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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:43:41 ; Search time 23 Seconds
(without alignments)
22.446 Million cell updates/sec

Title: US-09-761-636A-13
Perfect score: 56
Sequence: 1 CUSVPLSVPC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 103740

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/2/aaa/5B.COMB.pep.*
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5: /cgn2_6/ptodata/2/aaa/PTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/aaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query %		Match	Length	DB ID	Description
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1	36	64.3	9	1	US-08-331-383-33		Sequence 33, Appl
2	36	64.3	9	1	US-08-549-008-43		Sequence 43, Appl
3	36	64.3	9	3	US-08-802-981-143		Sequence 143, Appl
4	33	58.9	9	1	US-08-331-383-31		Sequence 31, Appl
5	33	58.9	9	1	US-08-549-008-42		Sequence 42, Appl
6	33	58.9	9	3	US-08-802-981-142		Sequence 142, Appl
7	25	44.6	10	1	US-08-212-190A-5		Sequence 5, Appl
8	25	44.6	10	2	US-08-900-321-5		Sequence 5, Appl
9	25	44.6	10	3	US-09-461-697-21		Sequence 21, Appl
10	25	44.6	10	5	PCT-US95-03610-5		Sequence 5, Appl
11	24	42.9	6	1	US-08-483-434A-21		Sequence 21, Appl
12	24	42.9	6	3	US-08-476-134A-30		Sequence 30, Appl
13	24	42.9	6	6	5190920-26		Patent No. 5190920
14	24	42.9	6	6	5506208-28		Patent No. 5506208
15	24	42.9	9	1	US-08-331-383-35		Sequence 35, Appl
16	24	42.9	9	1	US-08-549-008-40		Sequence 40, Appl
17	24	42.9	9	3	US-08-802-981-1		Sequence 1, Appl
18	24	42.9	10	1	US-08-033-857A-5		Sequence 5, Appl
19	24	42.9	10	1	US-08-374-983A-5		Sequence 5, Appl
20	24	42.9	10	3	US-08-377-781A-17		Sequence 17, Appl
21	23	41.1	6	1	US-07-994-133-3		Sequence 3, Appl
22	23	41.1	6	1	US-08-221-078A-8		Sequence 8, Appl
23	23	41.1	8	1	US-08-221-171A-8		Sequence 8, Appl
24	23	41.1	8	1	US-08-189-331-147		Sequence 147, Appl
25	23	41.1	8	1	US-08-189-331-148		Sequence 148, Appl
26	23	41.1	8	1	US-08-189-331-149		Sequence 149, Appl
27	23	41.1	8	1	US-08-189-331-150		Sequence 150, Appl

SUMMARIES

28 23 41.1 8 2 US-08-471-068-147 Sequence 147, Appl
29 23 41.1 8 2 US-08-471-068-148 Sequence 148, Appl
30 23 41.1 8 2 US-08-471-068-149 Sequence 149, Appl
31 23 41.1 8 2 US-08-471-068-150 Sequence 150, Appl
32 23 41.1 8 4 US-03-311-784A-371 Sequence 371, Appl
33 23 41.1 8 4 US-09-187-330-6 Sequence 6, Appl
34 23 41.1 9 4 US-09-997-579-19 Sequence 19, Appl
35 23 41.1 9 4 US-09-187-330-28 Sequence 28, Appl
36 23 41.1 10 4 US-09-187-330-33 Sequence 33, Appl
37 23 41.1 10 4 US-09-535-852-1686 Sequence 1686, Appl
38 22.5 40.2 9 3 US-08-831-271-4 Sequence 4, Appl
39 22.5 40.2 9 3 US-08-660-092-126 Sequence 126, Appl
40 22.5 40.2 9 4 US-09-160-513-126 Sequence 126, Appl
41 22 39.3 7 2 US-08-934-222-13 Sequence 13, Appl
42 22 39.3 7 2 US-08-933-402-13 Sequence 13, Appl
43 22 39.3 7 2 US-09-207-621-13 Sequence 13, Appl
44 22 39.3 7 2 US-08-532-818-13 Sequence 13, Appl
45 22 39.3 7 3 US-09-231-797-13 Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-331-383-33
; Sequence 33, Application US/08331383
; Patent No. 5605809
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of
; TITLE OF INVENTION: Proteases in Biological Samples and Methods and Use
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Hourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,383
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 16865-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-331-383-33

Query Match 64.3%; Score 36; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 4; Mismatches 0; Gaps 0;

QY 3 SVPLSVPC 10
Db 2 AIPWSIPC 9

RESULT 2
US-08-549-008-43
; Sequence 43, Application US/08549008
; Patent No. 5714342
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of
; TITLE OF INVENTION: Protease in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/549,008
; FILING DATE: 27-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,383
; FILING DATE: 28-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 016865-000110US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-549-008-43
; Query Match 64.3%; Score 36; DB 1; Length 9;
; Best Local Similarity 50.0%; Pred. No. 3e+05;
; Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 3 SVPLSVPC 10
Db 2 AIPMSIPC 9
RESULT 3
US-08-602-981-143
; Sequence 143, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,383
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 16865-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-000300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-802-981-143
; Query Match 64.3%; Score 36; DB 3; Length 9;
; Best Local Similarity 50.0%; Pred. No. 3e+05;
; Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 3 SVPLSVPC 10
Db 2 AIPMSIPC 9
RESULT 4
US-08-331-383-31
; Sequence 31, Application US/08331383
; Patent No. 5605809
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of
; TITLE OF INVENTION: Proteases in Biological Samples and Methods of Use
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,383
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 16865-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: one-of(5)
; OTHER INFORMATION: /note= "Xaa is norleucine."
US-08-331-383-31

Query Match 58.9%; Score 33; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 SVPLSVPC 10
Db 2 AIPXSIPC 9

RESULT 5
US-08-549-008-42
; Sequence 42, Application US/08549008
; Patent No. 5714342
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of
; TITLE OF INVENTION: Protease in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 27-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,383
; FILING DATE: 28-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 016865-000110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /product= "Nle"
US-08-549-008-42

Query Match 58.9%; Score 33; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 SVPLSVPC 10
Db 2 AIPXSIPC 9

RESULT 6
US-08-802-981-142
; Sequence 142, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-000300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 142:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /product= "Nle"
US-08-802-981-142

Query Match 58.9%; Score 33; DB 3; Length 9;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 SVPLSVPC 10
Db 2 AIPXSIPC 9

RESULT 7
US-08-212-190A-5
; Sequence 5, Application US/08212190A
; Patent No. 5652223
; GENERAL INFORMATION:
; APPLICANT: KOHN, Elise C.
; APPLICANT: LIOTTA, Lance A.
; APPLICANT: KIM, Young Sook
; TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
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1 COUNTRY: US
2 ZIP: 94105-1493
3 COMPUTER READABLE FORM:
4 MEDIUM TYPE: Floppy disk
5 COMPUTER: IBM PC compatible
6 OPERATING SYSTEM: PC-DOS/MS-DOS
7 SOFTWARE: Patent In Release #1.0, Version #1.25
8 CURRENT APPLICATION DATA:
9 APPLICATION NUMBER: US/08/212,190A
10 FILING DATE: 14-MAR-1994
11 CLASSIFICATION: 435
12 ATTORNEY/AGENT INFORMATION:
13 NAME: Hunter, Tom
14 REGISTRATION NUMBER: 38,498
15 REFERENCE/DOCKET NUMBER: 15280-204US
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: (415) 543-9600
18 TELEFAX: (415) 543-5043
19 INFORMATION FOR SEQ ID NO: 5:
20 SEQUENCE CHARACTERISTICS:
21 LENGTH: 10 amino acids
22 TYPE: amino acid
23 STRANDEDNESS: single
24 TOPOLOGY: linear
25 MOLECULE TYPE: peptide
26 US-08-212-190A-5

Query Match 44.6%; Score 25; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLSVPC 10
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Db 3 PAPVPC 8

RESULT 8
US-08-900-321-5
; Sequence 5, Application US/08900321
; Patent No. 5981712
; GENERAL INFORMATION:
; APPLICANT: Kohn, Elise C.
; APPLICANT: Liotta, Lance A.
; APPLICANT: Kim, Young S.
; TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,321
; FILING DATE: 25-JUL-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,190
; FILING DATE: 14-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-204100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200

1 TELEFAX: (415) 576-0300
2 INFORMATION FOR SEQ ID NO: 5:
3 SEQUENCE CHARACTERISTICS:
4 LENGTH: 10 amino acids
5 TYPE: amino acid
6 STRANDEDNESS:
7 TOPOLOGY: linear
8 MOLECULE TYPE: peptide
9 US-08-900-321-5

Query Match 44.6%; Score 25; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLSVPC 10
| | | | |
Db 3 PAPVPC 8

RESULT 9
US-09-461-697-21
; Sequence 21, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COSENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Purnam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-461-697-21

Query Match 44.6%; Score 25; DB 3; Length 10;
Best Local Similarity 44.4%; Pred. No. 2.7e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 C1SVPLSVP 9
| : | : | : |
Db 2 CVMTHSLP 10

RESULT 10
PCT-US95-03610-5
; Sequence 5, Application PC/TUS9503610
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03610
; FILING DATE: 14-MAR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,190

; FILING DATE: 14-MAR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Weber, Kenneth A.
 ; REGISTRATION NUMBER: 31,677
 ; REFERENCE/DOCKET NUMBER: 15280-204000PC
 ; REFERENCE/DOCKET NUMBER: DHHS Ref. No. E-112-94/0
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 543-9600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; PCT-US95-03610-5

Query Match 44.6%; Score 25; DB 5; Length 10;
 Best Local Similarity 66.7%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PLSVPC 10
 Db 3 PAPVPC 8

RESULT 11
 US-08-483-434A-21
 ; Sequence 21, Application US/08483434A
 ; Patent No. 5648461
 ; GENERAL INFORMATION:
 ; APPLICANT: EVAL, Jacob
 ; APPLICANT: HAMILTON, Bruce K.
 ; APPLICANT: TUSZYNSKI, George P.
 ; TITLE OF INVENTION: Synthetic Analogs of Thrombospondin and
 ; TITLE OF INVENTION: Therapeutic Use Thereof
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
 ; STREET: 1601 Market Street, 36th Floor
 ; CITY: Philadelphia
 ; STATE: Pennsylvania
 ; COUNTRY: USA
 ; ZIP: 19103-2398
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/483,434A
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/450,738
 ; FILING DATE: 25-MAY-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/185,614
 ; FILING DATE: 24-JAN-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/024,436
 ; FILING DATE: 01-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/587,197
 ; FILING DATE: 24-SEP-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/483,527
 ; FILING DATE: 22-FEB-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Leary Ph.D., Kathryn
 ; REGISTRATION NUMBER: 36,317
 ; REFERENCE/DOCKET NUMBER: 9598-306 (9049)

; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 567-2020
 ; TELEFAX: (215) 567-2991
 ; TELEX: 831-494
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-483-434A-21

Query Match 42.9%; Score 24; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SVPC 10
 Db 2 SVPC 5

RESULT 12
 US-08-476-134A-30
 ; Sequence 30, Application US/08476134A
 ; Patent No. 6239110
 ; GENERAL INFORMATION:
 ; APPLICANT: EVAL, JACOB
 ; APPLICANT: HAMILTON, BRUCE K.
 ; APPLICANT: TUSZYNSKI, GEORGE P.
 ; TITLE OF INVENTION: SYNTHETIC ANALOGS OF THROMBOSPONDIN AND THERAPEUTIC USE
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: 07206-0009
 ; CURRENT APPLICATION NUMBER: US/08/476,134A
 ; CURRENT FILING DATE: 1995-06-07
 ; PRIOR APPLICATION NUMBER: 07/587,197
 ; PRIOR FILING DATE: 1990-09-24
 ; PRIOR APPLICATION NUMBER: 07/483,527
 ; PRIOR FILING DATE: 1990-02-22
 ; PRIOR APPLICATION NUMBER: 08/450,738
 ; PRIOR FILING DATE: 1995-05-25
 ; PRIOR APPLICATION NUMBER: 08/185,614
 ; PRIOR FILING DATE: 1994-01-24
 ; PRIOR APPLICATION NUMBER: 08/024,436
 ; PRIOR FILING DATE: 1993-03-01
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 30
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: analog of thrombospondin
 ; US-08-476-134A-30

Query Match 42.9%; Score 24; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SVPC 10
 Db 2 SVPC 5

RESULT 13
 5190920-26
 ; Patent No. 5190920
 ; APPLICANT: EVAL, JACOB; HAMILTON, BRUCE K.; TUSZYNSKI,
 ; GEORGE P.
 ; TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS
 ; OF THROMBOSPONDIN FOR INHIBITING METASTASIS ACTIVITY
 ; NUMBER OF SEQUENCES: 32

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/587,197
; FILING DATE: 24-SEP-1990
; SEQ ID NO:26:
; LENGTH: 6
5190920-26

Query Match
Best Local Similarity 42.9%; Score 24; DB 6; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SVPC 10
Db 2 SVPC 5

RESULT 14
5506208-28
;PATENT NO. 5506208
;APPLICANT: EYAL, JACOB;HAMILTON, BRUCE K.;TUSZYNSKI,
;GEORGE P.
; TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS OF
; THROMBOSPONDIN FOR INHIBITING ANGIOGENESIS ACTIVITY
; NUMBER OF SEQUENCES: 45
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,181
; FILING DATE: 22-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 131,565
; FILING DATE: 04-OCT-1993
; APPLICATION NUMBER: 895,764
; FILING DATE: 09-JUN-1992
; APPLICATION NUMBER: 587,197
; FILING DATE: 24-SEP-1990
; SEQ ID NO:28:
; LENGTH: 6
5506208-28

Query Match
Best Local Similarity 42.9%; Score 24; DB 6; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SVPC 10
Db 2 SVPC 5

RESULT 15
US-08-331-383-35
; Sequence 35, Application US/08331383
; Patent No. 5605809
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of
; TITLE OF INVENTION: Proteases in Biological Samples and Methods and Use
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,383
; FILING DATE: 28-OCT-1994
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; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 16865-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: one-of(5)
; OTHER INFORMATION: /note= "Xaa is Met or norleucine."
; FEATURE:
; NAME/KEY: Region
; LOCATION: one-of(8)
; OTHER INFORMATION: /note= "Xaa is Pro or aminoisobutyric
; OTHER INFORMATION: acid."
; US-08-331-383-35

Query Match
Best Local Similarity 42.9%; Score 24; DB 1; Length 9;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SVPLSVPC 10
Db 2 AIPXSIXC 9

Search completed: March 8, 2004, 12:47:08
Job time : 24 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:36:04 ; Search time 23 Seconds
(without alignments)
13.468 Million cell updates/sec

Title: US-09-761-636A-12

Perfect score: 38

Sequence: 1 CVPLTC 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 40703

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 3: /cgn2_6/prodata/2/iaa/6A COMB.pdp.*
- 4: /cgn2_6/prodata/2/iaa/6B COMB.pdp.*
- 5: /cgn2_6/prodata/2/iaa/PCRU COMB.pdp.*
- 6: /cgn2_6/prodata/2/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	68.4	6	4	US-09-187-859-1374
2	26	68.4	6	4	US-09-839-542B-1374
3	25	65.8	6	4	US-09-187-859-1798
4	25	65.8	6	4	US-09-187-859-3970
5	25	65.8	6	4	US-09-187-859-4046
6	25	65.8	6	4	US-09-839-542B-1798
7	25	65.8	6	4	US-09-839-542B-3970
8	25	65.8	6	4	US-09-839-542B-4046
9	24	63.2	6	4	US-09-187-859-3573
10	24	63.2	6	4	US-09-839-542B-3573
11	23	60.5	6	4	US-09-187-859-2154
12	23	60.5	6	4	US-09-187-859-4040
13	23	60.5	6	4	US-09-839-542B-2154
14	23	60.5	6	4	US-09-839-542B-4040
15	22	57.9	4	2	US-08-429-964-41
16	22	57.9	4	4	US-09-665-362A-35
17	22	57.9	4	5	PCT-US93-08062-41
18	22	57.9	6	4	US-09-187-859-1737
19	22	57.9	6	4	US-09-187-859-2719
20	22	57.9	6	4	US-09-839-542B-1737
21	22	57.9	6	4	US-09-839-542B-2719
22	21	55.3	5	4	US-09-082-350B-90
23	21	55.3	5	4	US-09-050-861B-24
24	21	55.3	6	4	US-09-187-859-1885
25	21	55.3	6	4	US-09-187-859-2747
26	21	55.3	6	4	US-09-839-542B-1885
27	21	55.3	6	4	US-09-839-542B-2747

28 20 52.6 4 1 US-08-548-540-120 Sequence 120, App
29 20 52.6 4 5 PCT-US96-09809-120 Sequence 120, App
30 20 52.6 5 4 US-09-322-791-4 Sequence 4, Appli
31 20 52.6 5 4 US-09-322-791-6 Sequence 6, Appli
32 20 52.6 5 4 US-09-394-630-13 Sequence 13, Appli
33 20 52.6 6 3 US-08-750-142B-21 Sequence 21, Appl
34 20 52.6 6 4 US-09-187-859-1591 Sequence 1591, Ap
35 20 52.6 6 4 US-09-839-542B-1344 Sequence 1344, Ap
36 20 52.6 6 4 US-09-535-852-1344 Sequence 1344, Ap
37 20 52.6 6 4 US-09-535-852-1670 Sequence 1670, Ap
38 19 50.0 5 3 US-09-248-588-109 Sequence 109, App
39 19 50.0 6 1 US-08-201-046A-4 Sequence 4, Appli
40 19 50.0 6 1 US-08-433-318A-181 Sequence 181, App
41 19 50.0 6 2 US-08-922-048-181 Sequence 181, App
42 19 50.0 6 3 US-08-750-142B-23 Sequence 23, Appl
43 19 50.0 6 4 US-09-460-384-20 Sequence 20, Appl
44 19 50.0 6 4 US-09-187-859-738 Sequence 738, App
45 19 50.0 6 4 US-09-187-859-824 Sequence 824, App

ALIGNMENTS

RESULT 1

US-09-187-859-1374
; Sequence 1374, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1374
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-09-187-859-1374

Query Match 68.4%; Score 26; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
| | | |
Db 1 CBPKTC 6

RESULT 2

US-09-839-542B-1374
; Sequence 1374, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1374
; LENGTH: 6
; TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-09-839-542B-1374

Query Match      68.4%; Score 26; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 1 CEPKTC 6

RESULT 3
US-09-187-859-1798
; Sequence 1798, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1798
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
US-09-187-859-1798

Query Match      65.8%; Score 25; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 1 CEPKTC 6

RESULT 4
US-09-187-859-3970
; Sequence 3970, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3970
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence
US-09-187-859-3970

Query Match      65.8%; Score 25; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 CVPLTC 6
Db 1 CDPKTC 6

RESULT 5
US-09-187-859-4046
; Sequence 4046, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4046
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-09-187-859-4046

Query Match      65.8%; Score 25; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 1 CDPKTC 6

RESULT 6
US-09-839-542B-1798
; Sequence 1798, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1798
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
US-09-839-542B-1798

Query Match      65.8%; Score 25; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 1 CDPKTC 6

RESULT 7
US-09-839-542B-3970
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; Sequence 3970, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3970
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence
US-09-839-542B-3970
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Query Match 65.8%; Score 25; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 CVPLTC 6
Db 1 CDPKTC 6
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RESULT 8

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US-09-839-542B-4046
; Sequence 4046, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4046
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-09-839-542B-4046
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Query Match 65.8%; Score 25; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 CVPLTC 6
Db 1 CDPKTC 6
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RESULT 9

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US-09-187-859-3573
; Sequence 3573, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
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; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3573
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-09-187-859-3573
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Query Match 63.2%; Score 24; DB 4; Length 6;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 1 CVPLTC 6
Db 1 CDPVSC 6
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RESULT 10

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US-09-839-542B-3573
; Sequence 3573, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3573
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-09-839-542B-3573
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Query Match 63.2%; Score 24; DB 4; Length 6;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 1 CVPLTC 6
Db 1 CDPVSC 6
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RESULT 11

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US-09-187-859-2154
; Sequence 2154, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2154
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; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-15 cell adhesion recognition sequence
US-09-187-859-2154

Query Match      60.5%; Score 23; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CVPLTC 6
Db      1 CDELTC 6

RESULT 12
US-09-187-859-4040
; Sequence 4040, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4040
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-09-187-859-4040

Query Match      60.5%; Score 23; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CVPLTC 6
Db      1 CDELTC 6

RESULT 13
US-09-839-542B-2154
; Sequence 2154, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2154
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-15 cell adhesion recognition sequence
US-09-839-542B-2154

Query Match      60.5%; Score 23; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CVPLTC 6
Db      1 CDELTC 6

RESULT 14
US-09-839-542B-4040
; Sequence 4040, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4040
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-09-839-542B-4040

Query Match      60.5%; Score 23; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CVPLTC 6
Db      1 CDELTC 6

RESULT 15
US-08-429-964-41
; Sequence 41, Application US/08429964
; Patent No. 5962243
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: GOLDSTEIN, JOSEPH L.
; APPLICANT: REISS, YUVAL
; APPLICANT: JAMES, GUY L.
; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
; TITLE OF INVENTION: TRANSFERASE INHIBITORS
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P. O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/429,964
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 435
; OTHER INFORMATION:
; APPLICATION NUMBER: US 08/021,625
; FILING DATE: 16-FEB-1993
```

```
;
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/822,011
; FILING DATE: ABANDONED
; CLASSIFICATION: 435
; APPLICATION NUMBER: PCT/US/91/02650
; FILING DATE: 18-APR-1991
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/615,715
; FILING DATE: 20-NOV-1990
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/510,706
; FILING DATE: 18-APR-1990 (ABANDONED)
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PARKER, DAVID L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSD:432/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-429-964-41

Query Match          57.9%; Score 22; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CVPL 4
Db      1 CVPM 4
      |||
      |||

Search completed: March 8, 2004, 12:39:28
Job time : 23 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:42:56 ; Search time 21 Seconds

(without alignments)
45.805 Million cell updates/sec

Title: US-09-761-636A-13

Perfect score: 56

Sequence: 1 CISVPLSVPC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1101

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	35.7	6	2 I65546	MHC H2-L antigen -
2	19	33.9	5	2 A60521	glycogen phosphory
3	19	33.9	10	2 C39111	Ig heavy chain C r
4	18	32.1	9	2 PT0247	Ig heavy chain CRD
5	17	30.4	10	2 A61622	vitellogenin, 190k
6	17	30.4	10	2 PH0944	T-cell receptor be
7	16	28.6	4	2 I51049	metallothionein-A
8	16	28.6	8	2 G33098	205K exoantigen -
9	16	28.6	10	2 S62880	polygalacturonase
10	16	28.6	10	2 PH0926	T-cell receptor be
11	15	26.8	8	2 A42689	major postsynaptic
12	15	26.8	9	2 B49712	ATP-binding protei
13	15	26.8	10	2 S43630	cytochrome-c oxida
14	15	26.8	10	2 E86128	hypothetical prote
15	14	25.0	5	2 B22565	R-phycocerythrin al
16	14	25.0	7	2 A28340	myomodulin - Calif
17	14	25.0	8	2 I57018	gene cfr protein
18	14	25.0	9	2 A60356	118K stomach cance
19	14	25.0	9	2 S26508	collagen alpha 2(V
20	14	25.0	10	2 A24407	amicyanin - Paraco
21	14	25.0	10	2 C39745	sphingomyelinase -
22	14	25.0	10	2 D28027	protein P7 - curle
23	14	25.0	10	2 S65715	aryl hydrocarbon (
24	14	25.0	10	2 A61218	alpha-gliadin 4Ha
25	14	25.0	10	2 B61218	alpha-gliadin 6Ha
26	14	25.0	10	2 A32195	Na+/K+-exchanging
27	13	23.2	5	2 E42364	flagellar protein
28	13	23.2	9	2 B28495	conopressin S - co
29	13	23.2	9	2 S77984	cytochrome-c oxida

30	13	23.2	9	2 PT0268	Ig heavy chain CRD
31	13	23.2	10	2 S51912	hemagglutinin - in
32	13	23.2	10	2 B45482	platelet activatin
33	13	23.2	10	2 C39398	Fc mu (IgM) recept
34	12	21.4	5	2 S11127	phosphoprotein, bo
35	12	21.4	6	2 B34835	dnAA protein - Pse
36	12	21.4	6	2 B36206	alpha-1,4-glucan-p
37	12	21.4	6	2 A35039	hypothetical colla
38	12	21.4	7	2 A61081	tryptophyllin, bas
39	12	21.4	7	2 E61491	seed protein ws-5
40	12	21.4	7	2 S42620	aggrecaan - bovine
41	12	21.4	7	2 PH1602	Ig H chain V-D-J r
42	12	21.4	7	2 A39690	neural cell adhesi
43	12	21.4	7	2 PH0932	T-cell receptor be
44	12	21.4	8	2 S68802	nitrate reductase
45	12	21.4	8	2 S10783	enamelin f - bovin

ALIGNMENTS

RESULT 1

I65546

MHC H2-L antigen - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999

C:Accession: I65546

R:Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.

Cell 44, 261-272, 1986

A>Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and th

A:Reference number: 152778; MUID:86106202; PMID:3510743

A:Accession: I65546

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-6 <RES>

A:Cross-references: GB:M12483; NID:g199565; PIDN:AAA39663.1; PID:g554234

Query Match 35.7%; Score 20; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPC 10

DB 2 VPC 4

RESULT 2

A60521

glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)

N:Alternate names: glycogen phosphorylase b

C:Species: Liza ramada

C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003

C:Accession: A60521

R:Bonomusa, L.; Baanante, I.V.

Comp. Biochem. Physiol. B 95, 295-301, 1990

A>Title: Purification and characterization of glycogen phosphorylase B from skeletal m

A:Reference number: A60521; MUID:90227907; PMID:2109665

A:Accession: A60521

A:Molecule type: protein

A:Residues: 1-5 <BON>

C:Superfamily: glucan phosphorylase

C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein

F:3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status exper

Query Match

Best Local Similarity 33.9%; Score 19; DB 2; Length 5;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVP 5

DB 2 ISVP 5


```

RESULT 3
C39111
Ig heavy chain C region - Pacific hagfish (fragment)
C:Species: Eptatretus stoutii (Pacific hagfish)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C:Accession: C39111
R:Varner, J.; Neame, P.; Litman, G.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991
A>Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural similarity to the heavy chain of the immunoglobulin heavy chain diversity and
A:Reference number: A39111; MUID:91156684; PMID:2000382
A:Accession: C39111
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <VAR>
C:Keywords: heterotetramer; immunoglobulin

Query Match 33.9%; Score 19; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISVPLSV 8
DB 4 ISSPLW 10

RESULT 4
PT0247
Ig heavy chain CRD3 region (clone 2-106A) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0247
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0247
A:Molecule type: DNA
A:Residues: 1-9 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 32.1%; Score 18; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 SVPLSVP 9
DB 2 SAPIDSP 8

RESULT 5
A61622
vitellogenin, 190k chain - gypsy moth (fragment)
N/Contains: vitellin
C:Species: Lymantria dispar (gypsy moth)
C>Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 15-Oct-1999
C:Accession: A61622
R:Hiremath, S.; Behita, S.
Insect Biochem. Mol. Biol. 22, 605-611, 1992
A>Title: Purification and characterization of vitellogenin from the gypsy moth, Lymantria
A:Reference number: A61622
A:Accession: A61622
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <HIR>
C:Keywords: egg yolk; hemolymph

Query Match 30.4%; Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLVSVP 9
DB 1 1 1 1 1 1 1 1 1 1

RESULT 6
PH0944
T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0944
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenberg, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A>Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0944
A:Molecule type: mRNA
A:Residues: 1-10 <GOL>
A:Experimental source: complete Freund's adjuvant-immunized lymph node
A>Note: the authors translated the codon GAC for residue 9 as Glu
C:Keywords: T-cell receptor

Query Match 30.4%; Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CUSVP 5
DB 1 CASSP 5

RESULT 7
IS1049
metallothionein-A - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: IS1049
R:Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.
Eur. J. Biochem. 230, 344-349, 1995
A>Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss)
A:Reference number: IS1049; MUID:95324545; PMID:7601121
A:Accession: IS1049
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <OLS>
A:Cross-references: EMBL:X80181; NID:gl019799; PID:CAA56466.1; PID:94379328

Query Match 28.6%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PC 10
DB 3 PC 4

RESULT 8
G33098
205K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C>Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C:Accession: G33098
R:Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A:Reference number: A33098
A:Accession: G33098
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <NIC>

Query Match 28.6%; Score 16; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPLSV 8
DB 1 1 1 1 1 1 1 1

```

Query Match	26.8%	Score 15; DB 2; Length 8;
Best Local Similarity	75.0%	Pred. No. 2.8e+05;
Matches 3; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	A.Accession: E86128 A.Status: preliminary A.Molecule type: DNA A.Residues: 1-10 <STO>

A;Cross-references: GB:AE005174; NID:gl2519314; PIDN:AGS9489.1; GSPDB:GN00145; UWGP:Z59
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z5903

Query Match 26.8%; Score 15; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LSVPC 10
| | |
Db 5 LQVVC 9

RESULT 15

B22565
R-phycoerythrin alpha-2 chain - red alga (Gastrocloonium coulteri) (fragment)
C;Species: Gastrocloonium coulteri
C;Date: 07-Mar-1998 #sequence_revision 07-Mar-1998 #text_change 23-Mar-1993
C;Accession: B22565
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Reference number: A22565; MUID:85182601; PMID:3886644
A;Accession: B22565
A;Molecule type: protein
A;Residues: 1-5 <KIO>

Query Match 25.0%; Score 14; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 LSVPC 9
| | |
Db 1 LCVP 4

Search completed: March 8, 2004, 12:46:32
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:39:35 ; Search time 11 seconds
(without alignments)
47.337 Million cell updates/sec

Title: US-09-761-636A-13
Perfect score: 56
Sequence: 1 C1SVPLSVPC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 371

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	26	46.4	9	1 MGMT_BOVIN	P29177 bos taurus
2	19	33.9	10	1 LPK2_LOCOMI	P41488 locusta mig
3	18	32.1	8	1 COM2_CONPU	P58785 conus purpu
4	15	26.8	10	1 COXH_ONCMY	P80331 oncorhynch
5	15	26.8	10	1 NS1_MYCTU	P81135 mycobacteri
6	15	26.8	10	1 TXG2_LOCOMI	P62224 locusta mig
7	15	26.8	10	1 UPA2_HUMAN	P30088 homo sapien
8	14	25.0	7	1 TPFF_FACDA	P83455 pachymedusa
9	14	25.0	10	1 TRP7_LEUMA	P81739 leucophaea
10	13	23.2	6	1 E101_LITRU	P82096 litoria rub
11	13	23.2	9	1 CONO_CONST	P05487 conus stria
12	13	23.2	9	1 COXE_THUOB	P80975 thunnus obe
13	13	23.2	10	1 COXQ_SHEEP	P80337 ovis aries
14	12	21.4	7	1 MNPI_LEPDE	P42984 lepidotars
15	12	21.4	8	1 ALL6_CVDPO	P82157 cydia pomon
16	12	21.4	8	1 FUSS_FUSSO	P81010 fusarium so
17	12	21.4	8	1 UPA1_HUMAN	P30087 homo sapien
18	12	21.4	9	1 FAR5_PENMO	P83320 penaeus mon
19	12	21.4	9	1 FLA2_TREHY	P80159 treponema h
20	12	21.4	9	1 OXYT_BUFRE	P42995 bufo regula
21	12	21.4	9	1 RT33_BOVIN	P82926 bos taurus
22	12	21.4	9	1 SAP_STOVA	P24047 stomopneute
23	12	21.4	10	1 ANCT_CHICK	P61018 gallus gall
24	12	21.4	10	1 COXQ_RABIT	P80336 oryctolagus
25	12	21.4	10	1 UPA8_HUMAN	P30094 homo sapien
26	11	19.6	6	1 C1P1_MYTED	P13736 mytilus edu
27	11	19.6	6	1 C1P2_MYTED	P13737 mytilus edu
28	11	19.6	6	1 VP19_HSVIK	P23210 herpes simp
29	11	19.6	7	1 CARP_MYTED	P10440 mytilus edu
30	11	19.6	8	1 ALL3_CVDPO	P82154 cydia pomon
31	11	19.6	8	1 PPK3_PERAM	P82618 periplaneta
32	11	19.6	8	1 VGLG_HSV2B	P81780 herpes simp
33	11	19.6	9	1 DNFI_LOCOMI	P16339 locusta mig

```

34 11 19.6 9 1 FAR9_ASCSU P43172 ascaris suu
35 11 19.6 9 1 LMT3_LOCOMI P41489 locusta mig
36 11 19.6 9 1 OXYA_SQUTAC P42999 squalus aca
37 11 19.6 9 1 OXYT_RABIT P32878 oryctolagus
38 11 19.6 9 1 UPA3_HUMAN P30089 homo sapien
39 11 19.6 9 1 UPA7_HUMAN P30093 homo sapien
40 11 19.6 10 1 AH3_FRUSE P29261 prunus sero
41 11 19.6 10 1 BPP8_BOTIN P30426 bothrops in
42 11 19.6 10 1 BPP_VIPAS P31351 vipera aspi
43 11 19.6 10 1 BRK_ONCMY Q9prz1 oncorhynch
44 11 19.6 10 1 COXK_ONCMY P80332 oncorhynch
45 11 19.6 10 1 GS09_BACSU P80243 bacillus su

```

ALIGNMENTS

```

RESULT 1
MGMT_BOVIN
ID MGMT_BOVIN STANDARD; PRT; 9 AA.
AC P29177;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-
DE methylguanine-DNA methyltransferase) (fragment).
GN MGMT.
OS Bos taurus (Bovine).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=90174912; PubMed=2308822;
RA Rydberg B., Hall J., Karan P.;
RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA
RT methyltransferase."
RL Nucleic Acids Res. 18:17-21(1990).
CC -!- FUNCTION: Repair of alkylated guanine in DNA by stoichiometrically
CC transferring the alkyl group at the O-6 position to a cysteine
CC residue in the enzyme. This is a suicide reaction: the enzyme is
CC irreversibly inactivated.
CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) +
CC [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein
CC S-methyl-L-cysteine.
CC -!- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OGT METHYLTRANSFERASE
CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
CC InterPro; IPR001437; Methyltransf_1.
DR PROSITE; PS00374; MGMT; PARTIAL.
KW DNA repair; Transferase; Methyltransferase.
FT ACT_SITE 1 1
FT NON_TER 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

```

```

Query Match 46.4%; Score 26; DB 1; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.4e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 4 VPLSVPC 10
Db 3 IPILTFC 9

```

```

RESULT 2
LPK2_LOCOMI
ID LPK2_LOCOMI STANDARD; PRT; 10 AA.
AC P41488;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

```

DE Locustapyrokinin 2 (LOW-PK-2) (FXPL-amide).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=94094539; PubMed=7903606;
 RA Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,
 RA de Loof A.;
 RA "Isolation, identification and synthesis of locustapyrokinin II from
 RT Locusta migratoria, another member of the FXPL-amide peptide
 RT family";
 RL Comp. Biochem. Physiol. 106C:103-109(1993).
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 CC activity).
 CC -!- SIMILARITY: Belongs to the Pyrokinin family.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; 1
 KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1145 MW; CFAF4271A9D1B772 CRC64;
 Query Match 33.9%; Score 19; DB 1; Length 10;
 Best Local Similarity 57.1%; Pred. No. 8.8e+02;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 SVPLSVP 9
 |||||
 Db 2 SVPTFP 8

RESULT 3
 COW2_CONFU
 ID COW2_CONFU STANDARD; PRT; 8 AA.
 AC P58785;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Leu-contryphan-P.
 OS Conus purpurascens (Purple cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=41690;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC STRAIN=Clipperton Island; TISSUE=Venom;
 RX MEDLINE=99388839; PubMed=10461743;
 RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
 RA Olivera B.M.;
 RT "A novel D-leucine-containing Conus peptide: diverse conformational
 RT dynamics in the contryphan family";
 RL J. Pept. Res. 54:93-99(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
 CC -!- SIMILARITY: Belongs to the contryphan family.
 KW Toxin; Hydroxylation; D-amino acid.
 FT DISULFID 2 8
 FT MOD RES 4 4 D-LEUCINE.
 SQ SEQUENCE 8 AA; 890 MW; 75A36762732CEB8 CRC64;
 Query Match 32.1%; Score 18; DB 1; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CISVP 5
 ||:|
 Db 2 CVLLP 6

RESULT 4
 COXH_ONCMY
 ID COXH_ONCMY STANDARD; PRT; 10 AA.
 AC P80331;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Cytochrome c oxidase polypeptide Vfc (EC 1.9.3.1) (Fragment).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=94237150; PubMed=8181469;
 RA Freund R., Kadenbach B.;
 RT "Identification of tissue-specific isoforms for subunits Vb and VIIa
 RT of cytochrome c oxidase isolated from rainbow trout";
 RL Eur. J. Biochem. 221:1111-1116(1994).
 CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
 CC chains of cytochrome c oxidase, the terminal oxidase in
 CC mitochondrial electron transport.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 DR PIR; S43630; S43630.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 977 MW; E11B40769DC772DA CRC64;
 Query Match 26.8%; Score 15; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 4.5e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 LSVP 9
 |||||
 Db 2 LXVP 5

RESULT 5
 NS1_MYCTU
 ID NS1_MYCTU STANDARD; PRT; 10 AA.
 AC P81135;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 30 kDa non-secretory protein 1 (Fragment).
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=H37Rv;
 RA Prasad H.K., Annapurna P.S.;
 RL Submitted (DEC-1997) to Swiss-Prot.
 CC -!- CAUTION: We are unable to find this protein in the translation of
 CC the genome of strain H37Rv.
 CC NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1042 MW; 8767FE6AB2C73771 CRC64;
 Query Match 26.8%; Score 15; DB 1; Length 10;
 Best Local Similarity 37.5%; Pred. No. 4.5e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 ISVPLSVP 9
 ::|||
 Db 1 MATPLVDP 8

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RESULT 6
TKL2 LOCM1
ID TKL2 LOCM1 STANDARD; PRT; 10 AA.
AC P16224;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin II (TK-II).
OS Locustatachykinin (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=90184489; PubMed=2311766;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Locustatachykinin I and II, two novel insect neuropeptides with
RT homology to peptides of the vertebrate tachykinin family.";
RL FEBS Lett. 261:397-401(1990).
CC -!- FUNCTION: Myoactive peptide. Stimulates the contraction of the
CC oviduct and foregut.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
DR PIR; S08266; ECLQ2M.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
FT SEQUENCE 10 AA; 1066 MW; 5D52CD6B59C865B7 CRC64;

Query Match 26.8%; Score 15; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLS 7
Db 2 PLS 4

RESULT 7
UPA2 HUMAN
ID UPA2 HUMAN STANDARD; PRT; 10 AA.
AC P30088;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 10) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 4.4, its MW is: 49 kDa.
DR SWISS-2DPAGE; P30088; HUMAN.
FT NON_TER 1 1
FT UNSURE 6 6
FT NON_TER 10 10
FT SEQUENCE 10 AA; 1079 MW; 51AC54AAB77775B7 CRC64;

Query Match 26.8%; Score 15; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.5e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 4 VPLSVP 9
Db 1 VKLSPP 6

RESULT 8
TFYF PACDA
ID TFYF PACDA STANDARD; PRT; 7 AA.
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE tryptophyllin-1 (Pdt-1).
OS Pachymedusa danielcolor (Giant mexican leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylloidea; Hylidae;
OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
RP PRO-7.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Shaw C.;
RT "Pachymedusa danielcolor tryptophyllin-1 (Pdt-1): structural
RT characterization, pharmacological activity and cloning of precursor
RT cDNA.";
RL Submitted (SEP-2002) to Swiss-Prot.
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
CC smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0045986; P:negative regulation of smooth muscle contra. .; NAS.
KW Amphibian defense peptide; Amidation; Hydroxylation.
FT MOD_RES 3 3
FT MOD_RES 7 7
FT SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;

Query Match 25.0%; Score 14; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLSVP 9
Db 3 PAWVP 7

RESULT 9
TRP7 LEUMA
ID TRP7 LEUMA STANDARD; PRT; 10 AA.
AC P81739;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tachykinin-related peptide 7 (LemTRP 7).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Brain;
RX MEDLINE=9726266; PubMed=9114447;
RA Muren J.E., Naessel D.R.;
RT "Seven tachykinin-related peptides isolated from the brain of the
RT madeira cockroach; evidence for tissue-specific expression of
RT isoforms.";
RL Peptides 18:7-15(1997).
CC -!- FUNCTION: Myoactive peptide. Increases the amplitude and frequency
CC of spontaneous contractions and tonus of hindgut muscle.

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CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Brain.
CC -1- MASS SPECTROMETRY: MW=1069.7; METHOD=WALDI.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1068 MW; C4541679C9C865BD CRC64;

Query Match 25.0%; Score 14; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPLS 7
DB 1 VPAS 4

RESULT 10
ID E101 LITRU STANDARD; PRT; 6 AA.
AC P82096;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Electrin 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hyliidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
[1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella."
RL Aust. J. Chem. 52:639-645(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 6 6 AMIDATION.
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 23.2%; Score 13; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPL 6
DB 2 VPI 4

RESULT 11
ID CONO CONST STANDARD; PRT; 9 AA.
AC P05487;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Arg-conopressin S.
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbecconcha; Hypogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6493;
[1]
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
RT peptides from Conus geographus and Conus striatus venoms.";
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RL J. Biol. Chem. 262:15821-15824(1987).
RN [2]
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -1- FUNCTION: Targets vasopressin-oxytocin related receptors.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR PIR; B28495; B28495.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1031 MW; 17EB176EB4540050 CRC64;

Query Match 23.2%; Score 13; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CI 2
DB 1 CI 2

RESULT 12
ID COXE THUOB STANDARD; PRT; 9 AA.
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).
OS Thunus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
[1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -1- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC chains of cytochrome c oxidase, the terminal oxidase in
CC mitochondrial electron transport.
CC -1- CATALYTIC ACTIVITY: 4 ferrocycochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase Via family.
DR PIR; S77984; S77984.
DR InterPro; IPR001349; COX6A.
DR PROSITE; PS01329; COX6A; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON TER 1 1
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

Query Match 23.2%; Score 13; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLSVP 9
|||
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Db 4 PEFVP 8

RESULT 13

COXQ SHEEP STANDARD; PRT; 10 AA.
 ID COXQ SHEEP STANDARD; PRT; 10 AA.
 AC P80337;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)
 DE (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart, and Liver;
 RA Freund R., Kadenbach B.;
 RL Submitted (MAR-1994) to Swiss-Prot.
 CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
 chains of cytochrome c oxidase, the terminal oxidase in
 CC mitochondrial electron transport.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIII family.
 CC Oxidoreductase; Mitochondrion.
 KW NON TER 10
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1027 MW; C4E95CA33DC7633D CRC64;

Query Match 23.2%; Score 13; DB 1; Length 10;

Best Local Similarity 40.0%; Pred. No. 1e+04; 3; Indels 0; Gaps 0;

QY 5 PLSVP 9

Db 5 PAKTP 9

RESULT 14

MNPI LEPDE STANDARD; PRT; 7 AA.
 ID MNPI LEPDE STANDARD; PRT; 7 AA.
 AC P42984;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Myotropic neuropeptide 1 (led-MNP-I).
 OS Leptinotarsa decemlineata (Colorado potato beetle).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
 OC Chrysomelini; Leptinotarsa.
 OX NCBI_TaxID=7539;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RX MEDLINE=95350343; PubMed=7651886;
 RA Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
 RA Grauwels L., van Leuven F., de Loof A.;
 RT "Identification, characterization, and immunological localization of
 RT a novel myotropic neuropeptide in the Colorado potato beetle,
 RT Leptinotarsa decemlineata";
 RL Peptides 16:365-374(1995).
 CC -!- FUNCTION: Myotropic peptide. Stimulates the contractions of the
 CC oviduct.
 KW Neuropeptide; Amidation.
 FT MOD RES 7
 SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;

Query Match 21.4%; Score 12; DB 1; Length 7;

Best Local Similarity 66.7%; Pred. No. 1.4e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLS 7

Db 5 PLA 7

RESULT 15

ALL6 CYDPO STANDARD; PRT; 8 AA.
 ID ALL6 CYDPO STANDARD; PRT; 8 AA.
 AC P82157;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydastatin 6.
 OS Cydia pomonella (Codling moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily."
 RL Peptides 18:1301-1309(1997).
 CC -!- SIMILARITY: Belongs to the allatostatin family.
 KW Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 21.4%; Score 12; DB 1; Length 8;

Best Local Similarity 66.7%; Pred. No. 1.4e+05; 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPL 6

Db 1 LPL 3

Search completed: March 8, 2004, 12:45:07

Job time : 11 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:42:36 ; Search time 38 Seconds
(without alignments)
83.031 Million cell updates/sec

Title: US-09-761-636A-13
Perfect score: 56
Sequence: 1 C1SVPLSVPC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1443

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	20	35.7	9	11	Q35953 mus musculus
2	20	35.7	10	15	Q85598 moloney mur
3	20	35.7	10	15	Q85563 moloney mur
4	20	35.7	10	15	Q85619 moloney mur
5	19	33.9	8	2	Q56140 streptococc
6	19	33.9	10	2	Q7WUG2 escherichia
7	17	30.4	8	4	Q9Y4X6 homo sapien
8	17	30.4	9	10	Q7XGA3 zea mays su
9	17	30.4	10	8	Q96041 oenothera b
10	17	30.4	10	10	Q7Y018 zea mays su
11	17	30.4	10	12	Q39957 hepatitis g
12	16	28.6	8	4	Q15898 homo sapien
13	16	28.6	8	6	Q02831 oryctolagus
14	16	28.6	8	6	Q9TRV3 sus sp. ins
15	16	28.6	9	12	Q8QVD3 ovine respi
16	16	28.6	9	13	Q8AYL5 carassius a

17	16	28.6	9	13	Q8AUM7
18	16	28.6	10	6	Q8SPN8
19	16	28.6	10	8	Q85AZ9
20	16	28.6	10	10	Q94IS6
21	15	26.8	7	13	Q42564
22	15	26.8	10	2	Q9L5W6
23	15	26.8	10	16	Q8X4E5
24	14	25.0	7	15	Q07624
25	14	25.0	8	2	Q9X3K1
26	14	25.0	9	2	P72345
27	14	25.0	9	2	Q9K4M6
28	14	25.0	9	4	Q9UCS8
29	14	25.0	9	5	Q9TWV0
30	14	25.0	9	10	Q9FXL0
31	14	25.0	10	4	Q9H3R9
32	14	25.0	10	4	Q9H121
33	14	25.0	10	8	Q8MAZ9
34	14	25.0	10	8	Q8MBB7
35	14	25.0	10	8	Q8SL54
36	14	25.0	10	10	P83091
37	14	25.0	10	12	O90347
38	14	25.0	10	12	Q8U7V8
39	14	25.0	10	13	Q9PRU1
40	13	23.2	7	12	O67113
41	13	23.2	8	2	Q8KPX4
42	13	23.2	8	2	Q49534
43	13	23.2	8	2	O32560
44	13	23.2	8	4	Q8IUB8
45	13	23.2	8	8	Q8WFR5

ALIGNMENTS

RESULT 1
O35953 PRELIMINARY; PRT; 9 AA.
AC O35953;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
GN SCN8A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIII;
RX MEDLINE=97442476; PubMed=9295353;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97672; AAB80914.1;
DR MGD; MGI-103169; Scn8a.
DR GO; GO:0007628; P:adult walking behavior; IMP.
KW Ionic channel.
FT NON TER 1
SQ SEQUENCE 9 AA; 898 MW; 22D92865B735B737 CRC64;

Query Match 35.7%; Score 20; DB 11; Length 9;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPLSL 8
Db 1 VPLSL 5

RESULT 2
Q85598

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ID Q85598 PRELIMINARY; PRT; 10 AA.
AC Q85598;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Moloney murine sarcoma virus (Strain Hri) env/mos 5' junction
DE (Fragment).
OS Moloney murine leukemia virus.
OC Viruses; Retrovirdae; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83164305; PubMed=6300424;
RA Donoghue D.J., Hunter T.;
RT "Recombination junctions of variants of Moloney murine sarcom virus:
RT Generation and divergence of a mammalian transforming gene.";
RL J. Virol. 45:607-617(1983).
DR EMBL; K03106; AAA46492.1; -.
FT NON TER 10
SQ SEQUENCE 10 AA; 1081 MW; 7BECFCBEA771B5A4 CRC64;

Query Match 35.7%; Score 20; DB 15; Length 10;
Best Local Similarity 75.0%; Pred. No. 3.8e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 SVPC 10
DB 4 STPC 7

RESULT 3
Q85563 PRELIMINARY; PRT; 10 AA.
ID Q85563;
AC Q85563;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Env-mos fusion protein (Fragment).
OS Moloney murine leukemia virus.
OC Viruses; Retrovirdae; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82196891; PubMed=6281735;
RA Donoghue D.J., Hunter T.;
RT "A generalized method of subcloning DNA fragments by restriction site
RT reconstruction: Application to sequencing the amino-terminal region of
RT the transforming gene of Gazdar murine sarcoma virus.";
RL Nucleic Acids Res. 10:2549-2564(1982).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83164305; PubMed=6300424;
RA Donoghue D.J., Hunter T.;
RT "Recombination junctions of variants of Moloney murine sarcom virus:
RT Generation and divergence of a mammalian transforming gene.";
RL J. Virol. 45:607-617(1983).
DR EMBL; K03105; AAA46491.1; -.
FT NON TER 10
SQ SEQUENCE 10 AA; 1062 MW; F9ECFCBEA771B5B1 CRC64;

Query Match 35.7%; Score 20; DB 15; Length 10;
Best Local Similarity 75.0%; Pred. No. 3.8e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 SVPC 10
DB 4 STPC 7

RESULT 4
Q85619 PRELIMINARY; PRT; 10 AA.
ID Q85619
AC Q85619;
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DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Moloney murine sarcoma virus (Strain mi) env/mos 5' junction
DE (Fragment).
OS Moloney murine leukemia virus.
OC Viruses; Retrovirdae; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83164305; PubMed=6300424;
RA Donoghue D.J., Hunter T.;
RT "Recombination junctions of variants of Moloney murine sarcom virus:
RT Generation and divergence of a mammalian transforming gene.";
RL J. Virol. 45:607-617(1983).
DR EMBL; K03108; AAA46494.1; -.
FT NON TER 10
SQ SEQUENCE 10 AA; 1081 MW; 7BECFCBEA771B5A4 CRC64;

Query Match 35.7%; Score 20; DB 15; Length 10;
Best Local Similarity 75.0%; Pred. No. 3.8e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 SVPC 10
DB 4 STPC 7

RESULT 5
Q56140 PRELIMINARY; PRT; 8 AA.
ID Q56140;
AC Q56140;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE STP6 protein (Fragment).
GN STP6.
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ST11;
RX MEDLINE=95047254; PubMed=7958782;
RA Constable A., Mollet B.;
RT "Isolation and characterisation of promoter regions from Streptococcus
RT thermophilus.";
RL FEMS Microbiol. Lett. 122:85-90(1994).
DR EMBL; X78210; CAA55045.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 846 MW; ED086772D5B045B6 CRC64;

Query Match 33.9%; Score 19; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVP 5
DB 3 ISVP 6

RESULT 6
Q7WUG2 PRELIMINARY; PRT; 10 AA.
ID Q7WUG2;
AC Q7WUG2;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DE 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE TnpIS1 (Fragment).
GN INSA.
OS Escherichia coli.
OG Plasmid p541.
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OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Miriagou V., Tzouvelekis L.S., Villa L., Lelessi E., Vatopoulos A.C.,
RA Carattoli A., Tzelepi E.;
RT "Antibiotic Resistance Region of an IncN Plasmid Carrying an Integron-
RT Located blaVIM-1-Metallo- $\beta$ -lactamase Gene and a Novel CMY-type
RT Cephalosporinase Gene.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY339625; AAQ16673.1; -.
DR EMBL; AY339625; AAQ16673.1; -.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 991 MW; 882D57A5B045A2D5 CRC64;

Query Match 33.9%; Score 19; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 5.8e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SVPLSVP 9
DB 3 SVSISCP 9

RESULT 7
QY4X6 PRELIMINARY; PRT; 8 AA.
AC QY4X6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Nuclear LIM interactor (Fragment).
GN NLI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20108806; PubMed=10640831;
RA Drechsler M., Schumacher V., Friedrich S., Wildhardt G., Giesler S.,
RA Schroth A., Bodem J., Royer-Pokora B.;
RT "Genomic structure, alternative transcripts and chromosome location of
RT the human LIM domain binding protein gene LDB1.";
RL Cytogenet. Cell Genet. 87:119-124 (1999).
DR EMBL; AJ243097; CAB45408.1; -.
FT NON TER 8 8
SQ SEQUENCE 8 AA; 767 MW; EE6BDDDEB862D5B6 CRC64;

Query Match 30.4%; Score 17; DB 4; Length 8;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 LSVPC 10
DB 1 MSVGC 5

RESULT 8
QY4X6 PRELIMINARY; PRT; 9 AA.
AC QY4X6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Isoamylase (Fragment).
GN SUL.
OS Zea mays subsp. mays (maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4578;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. 38-11, and cv. A632;
RA Wilson L.M., Whitt S.R., Ibanez A.M., Rocheford T.R., Goodman M.M.,
RA Buckler E.S. IV.;
RT "Dissection of maize starch production by candidate gene
RT association.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY290305; AAP45331.1; -.
DR EMBL; AY290311; AAP45337.1; -.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 976 MW; DF9BCEA76736C6DD CRC64;

Query Match 30.4%; Score 17; DB 10; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPC 10
DB 5 LPC 7

RESULT 9
QY6041 PRELIMINARY; PRT; 10 AA.
AC QY6041;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NADH-ubiquinone oxidoreductase subunit 3 (Fragment).
GN NAD3.
OS Oenothera bertiana (Bertero's evening primrose).
OC Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Onagraceae; Oenothera.
OX NCBI_TaxID=3950;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94019250; PubMed=8413195;
RA Schuster W.;
RT "Ribosomal protein gene rpl5 is cotranscribed with the nad3 gene in
RT Oenothera mitochondria.";
RL Mol. Gen. Genet. 240:445-449 (1993).
DR EMBL; X69553; CAA49285.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion; Ubiquinone.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1097 MW; 723067B0476D9C9B CRC64;

Query Match 30.4%; Score 17; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CIS 3
DB 8 CIS 10

RESULT 10
QYV018 PRELIMINARY; PRT; 10 AA.
AC QYV018;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Isoamylase (Fragment).
GN SUL.
OS Zea mays subsp. mays (maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4578;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. K144;
RA Wilson L.M., Whitt S.R., Ibanez A.M., Rocheford T.R., Goodman M.M.,
RA Buckler E.S. IV.;
RT "Dissection of maize starch production by candidate gene
RT association.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY290360; RAP45386.1; -.
FT NON TER 10
SQ SEQUENCE 10 AA; 1063 MW; D0FF9BCEA76736C6 CRC64;

Query Match 30.4%; Score 17; DB 10; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.4e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPC 10
DB 5 LPC 7

RESULT 11
ID O39957 PRELIMINARY; PRT; 10 AA.
AC O39957;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE El protein (Fragment).
OS Hepatitis GB virus C.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=39839;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Edinburgh haemophilic;
RX MEDLINE=97368412; PubMed=9225026;
RA Smith D.B., Cuccaneu N., Davidson P., Jarvis L.M., Mokili J.L.,
RA Hamid S., Ludlam C.A., Simmonds P.;
RT "Discrimination of hepatitis G virus/GBV-C geographical variants by
RT analysis of the 5' non-coding region.";
RL J. Gen. Virol. 78:1533-1542(1997).
DR EMBL; AF003175; AAC57986.1; -.
FT NON TER 10
SQ SEQUENCE 10 AA; 1067 MW; CC88FE27273772 CRC64;

Query Match 30.4%; Score 17; DB 12; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVPL 6
DB 1 MAVPL 5

RESULT 12
ID Q15898 PRELIMINARY; PRT; 8 AA.
AC Q15898;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP6A11B) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chihault C.A., Baldini A., Lindsey E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;

RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Genet. 0:0-0(1995).
DR EMBL; L32078; AAA73888.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 938 MW; 34AA15B0477B45BB CRC64;

Query Match 28.6%; Score 16; DB 4; Length 8;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SVPLS 7
DB 2 SYPIS 6

RESULT 13
ID O02831 PRELIMINARY; PRT; 8 AA.
AC O02831;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE pro alpha 1 type III collagen protein (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96377339; PubMed=8783186;
RA Metearanta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
RA Vuorio E.;
RT "Evidence for insufficient chondrocytic differentiation during repair
RT of full-thickness defects of articular cartilage.";
RL Matrix Biol. 15:39-47(1996).
DR EMBL; S83371; AADI4433.1; -.
KW Collagen.
FT NON TER 1
SQ SEQUENCE 8 AA; 1028 MW; B859C7272EA77371 CRC64;

Query Match 28.6%; Score 16; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PC 10
DB 3 PC 4

RESULT 14
ID Q9TRY3 PRELIMINARY; PRT; 8 AA.
AC Q9TRY3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Insulin-like growth factor-binding protein-6, IGFBP-6 (Fragment).
OS Sus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9826;
RN [1]
RP SEQUENCE.
RX MEDLINE=92049376; PubMed=1719383;
RA Shimazaki S., Gao L., Shimonaka M., Ling N.;
RT "Isolation and molecular cloning of insulin-like growth factor-binding
RT protein-6.";
RL Mol. Endocrinol. 5:938-948(1991).
FT NON TER 1
SQ SEQUENCE 8 AA; 850 MW; 9FB2CEA37EA7687D CRC64;
```

Query Match 28.6%; Score 16; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PC 10
||
Db 3 PC 4

RESULT 15

Q8QVD3 PRELIMINARY; PRT; 9 AA.
AC Q8QVD3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Matrix protein 2 (fragment).
GN M2.
OS Ovine respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=28869;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21580659; PubMed=11724134;
RA Eleraky N.Z., Kania S.A., Potgieter L.N.;
RT "The ovine respiratory syncytial virus F gene sequence and its
diagnostic application.";
RL J. Vet. Diagn. Invest. 13:455-461(2001).
DR EMBL; AF334398; AAL91343.1; -.
FT NON TER 9
SQ SEQUENCE 9 AA; 1154 MW; 8B6A3EA764541415 CRC64;

Query Match 28.6%; Score 16; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PC 10
||
Db 6 PC 7

Search completed: March 8, 2004, 12:45:59
Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:39:00 ; Search time 52 Seconds
(without alignments)
54.336 Million cell updates/sec

Title: US-09-761-636A-13

Perfect score: 56

Sequence: 1 CUSVPLSVPC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 325896

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq 29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	4	AAU04532
2	41.5	74.1	9	4	AAU04533
3	36	64.3	9	2	AAR96138
4	36	64.3	9	2	AAW82212
5	36	64.3	9	2	AAW46562
6	33	58.9	9	2	AAR96137
7	33	58.9	9	2	AAW82094
8	33	58.9	9	2	AAW46561
9	33	58.9	9	4	AACT73245
10	33	58.9	9	5	ABU60357
11	32	57.1	10	4	AAU00643
12	32	57.1	10	7	ADB88786
13	31.5	56.2	9	5	AAU94301
14	31.5	56.2	10	5	AAU94201
15	31.5	56.2	10	5	AAU94811
16	31.5	56.2	10	5	AAU94577
17	31	55.4	10	5	AAW50003
18	30	53.6	9	5	AAU95231
19	30	53.6	9	5	AAU94696
20	30	53.6	9	5	AAU95023
21	29	51.8	10	4	AACT73418
22	29	51.8	10	4	AAW85638
23	29	51.8	10	5	ABG64264
24	28	50.0	9	6	ABR19062
25	28	50.0	10	6	ABR19524

26	28	50.0	10	6	ABR18877
27	27	48.2	8	2	AAR74541
28	27	48.2	9	7	ADC71003
29	27	48.2	9	7	ADC70887
30	27	48.2	10	7	ADC70636
31	27	48.2	10	7	ADC70959
32	27	48.2	10	7	ADC70732
33	27	48.2	10	7	ADC70653
34	27	48.2	10	7	ADC71049
35	26	46.4	9	1	AAAP82102
36	26	46.4	9	5	ABG34945
37	26	46.4	9	5	ABJ04424
38	26	46.4	9	5	AAW48672
39	26	46.4	10	2	AAW12561
40	25	44.6	7	6	ABU96540
41	25	44.6	9	4	AAU04529
42	25	44.6	10	2	AAR77368
43	25	44.6	10	4	AAW98618
44	24	42.9	6	4	AAE05003
45	24	42.9	6	4	AAW60620

ALIGNMENTS

RESULT 1
AAU04532
ID AAU04532 standard; peptide; 10 AA.
XX
AC AAU04532;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 10.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Disulfide-bond 1..10
FT /note= "This bond cyclises the peptide"
XX
PN WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stacker S, Cendron A;
XX WPI; 2001-442248/47.
XX
PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
PS Claim 49; Page 32; 102pp; English.
XX
CC The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the exposed loop of human
CC VEGF (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 56; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0098;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CISVPLSVPC 10
 |||||
 Db 1 CISVPLSVPC 10

RESULT 2
 AAU04533
 ID AAU04533 standard; peptide; 9 AA.
 XX
 AC AAU04533;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 11.
 XX
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 FH Disulfide-bond 1..9
 FT /note= "This bond cyclises the peptide"

XX WO200152875-A1.
 XX 26-JUL-2001.
 XX
 XX 18-JAN-2001; 2001WO-US001533.
 XX
 XX 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204530P.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX
 XX Achen MG, Hughes RA, Stacker S, Cendron A;
 XX WPI; 2001-442248/47.
 XX

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 FT or lymphangiogenesis, is produced by cyclising a peptide loop fragment
 FT from an exposed loop of a growth factor protein by oxidizing the cysteine
 FT

PT residues.
 XX Claim 49; Page 32; 102pp; English.
 XX
 CC The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 9 AA;

Query Match 74.1%; Score 41.5; DB 4; Length 9;
 Best Local Similarity 90.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CISVPLSVPC 10
 |||||
 Db 1 CISVPL-VPC 9

RESULT 3
 AAR96138
 ID AAR96138 standard; peptide; 9 AA.
 XX
 AC AAR96138;

XX 25-MAR-2003 (revised)
 DT 18-DEC-1996 (first entry)
 XX
 DE Protease substrate peptide with fluorophore at each terminus.

XX Fluorogenic substrate; fluorophore; protease activity; assay;
 KW visible fluorescence; in situ detection; frozen tissue section;
 KW histology; arthritis; emphysema; thrombosis; cancer metastasis.
 XX
 OS Synthetic.

XX Key Location/Qualifiers

XX 1..3
 FT /label= C1
 FT /note= "the two conformation determining regions C1 and
 FT C2 which flank the protease recognition site peptide P
 FT are provided to position the two fluorophores within 100
 FT angstroms of each other"
 FT Modified-site 1
 FT /note= "labelled by donor fluorophore (Fl) 5'-
 FT carboxytetramethylrhodamine"
 FT 4..7
 FT /label= P
 FT /note= "peptide comprising a protease recognition site"
 FT

```

FT Region      8. .9
FT /label= C2
FT /note= "The two conformation determining regions C1 and
FT C2 which flank the protease recognition site peptide P
FT are provided to position the two fluorophores within 100
FT angstroms of each other"
FT Modified-site 9
FT /note= "labelled by acceptor fluorophore F2 rhodamine X
FT acetamide"
FT
FN W09613607-Al.
XX
XX
PD 09-MAY-1996.
XX
XX PF 27-OCT-1995; 95WO-US013936.
XX
XX PR 28-OCT-1994; 94US-00331383.
XX
XX PA (ONCO-) ONCOIMMUNIN INC.
XX
XX PI Komoriya A, Packard BS;
XX
XX DR WPI; 1996-239512/24.
XX
XX PT New fluorogenic peptide(s) with fluorophore at each terminus - for
PT detecting protease(s) in biological samples, emit intense visible
PT fluorescence when cleaved.
XX
XX PS Claim 16; Page 31; 89pp; English.
XX
CC The present sequence is a specific example of a fluorogenic substrate for
CC detecting activity of a protease. The substrate agrees with the generic
CC formula (S1)n-C1(F1)-P-C2(F2)-(S2)k in which a peptide P of 2-8 amino
CC acids comprising a recognition site for the protease is flanked by
CC conformation determining regions (C1 and C2) of 1-3 amino acids. C1 and
CC C2 are labelled by fluorophore groups (F1 and F2, respectively)
CC positioned within 100 angstroms of each other. Additional peptide spacers
CC of 1-50 amino acids (S1 and S2) may also be present (i.e. n and k = 0 or
CC 1). Fluorogenic substrates corresponding to the generic formula are used
CC to detect or localise proteases in biological specimens, esp. in frozen
CC tissue sections or to monitor protease activity in stored reagents.
CC Changes in protease activity are associated with e.g. arthritis,
CC emphysema, thrombosis and cancer metastasis. (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
XX SQ Sequence 9 AA;

Query Match 64.3%; Score 36; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLSVPC 10
Db ::||:|
2 AIPMSIPC 9

RESULT 5
AAW46562
ID AAW46562 standard; peptide; 9 AA.
XX
XX AC AAW46562;
XX
XX DT 20-MAY-1998 (first entry)
XX
XX DE Peptide backbone of a protease indicator.
XX
XX KW Protease binding site; protease; protease indicator; fluorescent signal;
XX detection; protease activity.
XX
XX OS Synthetic.
XX
XX PN US5714342-A.
XX
XX PD 03-FEB-1998.
XX
XX PF 27-OCT-1995; 95US-00549008.
XX
XX PR 28-OCT-1994; 94US-00331383.
XX
XX PA (ONCO-) ONCOIMMUNIN INC.
XX
XX PI Packard BS, Komoriya A;
XX
XX DR WPI; 1998-158345/14.
XX
XX PT Fluorogenic substrates for protease determination - having two closely

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PD 27-AUG-1998.
XX
XX PF 20-FEB-1998; 98WO-US003000.
XX
XX PR 20-FEB-1997; 97US-00802981.
XX
XX PA (ONCO-) ONCOIMMUNIN INC.
XX
XX PI Komoriya A, Packard BS;
XX
XX DR WPI; 1998-467579/40.
XX
XX PT New fluorogenic compositions - containing 2 fluorophores separated by a
PT peptide comprising a protease binding site, used for detecting protease
PT activity in samples.
XX
XX PS Example 1; Page 52; 90pp; English.
XX
XX CC AAW82023-W82240 are peptides used in the construction of a fluorogenic
CC composition which is used for the detection of protease activity in
CC biological samples. The products can be used for the detection of
CC conformation changes in nucleic acids, oligosaccharides, polysaccharides,
CC proteins, peptides, lipids, phospholipids, glycolipids, glycoproteins,
CC steroids or polymers. In addition, attachment of a hydrophobic group to a
CC molecule can be used to enhance uptake by cells. The composition is
CC composed of P = peptide comprising a protease binding site for the
CC protease, F1, F2 peptides = fluorophores where F1 is attached to the
CC amino terminal amino acid and F2 is attached to the carboxyl terminal
CC amino acid and S1, S2 peptides = when present, are peptide spacers where
CC S1, when present, is attached to the amino terminal acid, and S2, when
CC present, is attached to the carboxyl terminal amino acid
XX
XX SQ Sequence 9 AA;

Query Match 64.3%; Score 36; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLSVPC 10
Db ::||:|
2 AIPMSIPC 9

RESULT 5
AAW46562
ID AAW46562 standard; peptide; 9 AA.
XX
XX AC AAW46562;
XX
XX DT 20-MAY-1998 (first entry)
XX
XX DE Peptide backbone of a protease indicator.
XX
XX KW Protease binding site; protease; protease indicator; fluorescent signal;
XX detection; protease activity.
XX
XX OS Synthetic.
XX
XX PN US5714342-A.
XX
XX PD 03-FEB-1998.
XX
XX PF 27-OCT-1995; 95US-00549008.
XX
XX PR 28-OCT-1994; 94US-00331383.
XX
XX PA (ONCO-) ONCOIMMUNIN INC.
XX
XX PI Packard BS, Komoriya A;
XX
XX DR WPI; 1998-158345/14.
XX
XX PT Fluorogenic substrates for protease determination - having two closely

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PT spaced fluorophores flanking protease binding site.
 XX Example 1; Col 23; 39pp; English.
 PS
 CC The present peptide contains a protease binding site. It is used to
 CC produce novel reagents whose fluorescence increases in the presence of
 CC particular proteases. These fluorogenic protease indicators (substrates)
 CC provide a high intensity fluorescent signal at a visible wavelength when
 CC they are digested by a protease. The fluorogenic indicators have the
 CC general formula: F1-C1-P-C2-F2 | (S1)n (S2)k where: P is a peptide
 CC containing a protease binding site e.g. AAW46520-53, AAW46560, F1 and F2
 CC are fluorophores. S1 and S2 are peptide spacers e.g. AAW46554-58, n, k =
 CC 0 or 1. C1 and C2 are conformation-determining regions that introduce a
 CC bend into the composition which positions the fluorophores adjacent to
 CC each other with a separation of less than 100 Angstrom. When n is 1, S1
 CC is joined to the terminal alpha-amino group of C1 by a peptide bond, and
 CC when k is 1, S2 is joined to the terminal carboxy group of C2 by a
 CC peptide bond. The protease indicators are used for detecting protease
 CC activity in a biological sample. The sample is contacted with the
 CC indicator and any change in fluorescence is detected, an increase in
 CC fluorescence indicating protease activity
 XX
 SQ Sequence 9 AA;
 Query Match 64.3%; Score 36; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SVPLSVPC 10
 Db ::|||:
 2 AIPMSIPC 9
 RESULT 6
 AAR96137
 ID AAR96137 standard; peptide; 9 AA.
 AC AAR96137;
 XX
 XX 25-MAR-2003 (revised)
 DT 18-DEC-1996 (first entry)
 DT Protease substrate peptide with fluorophore at each terminus.
 DE
 XX Fluorogenic substrate; fluorophore; protease activity; assay;
 KW visible fluorescence; in situ detection; frozen tissue section;
 KW histology; arthritis; emphysema; thrombosis; cancer metastasis.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Region 1. .3
 FT /label= C1
 FT /note= "the two conformation determining regions C1 and
 FT C2 which flank the protease recognition site peptide P
 FT are provided to position the two fluorophores within 100
 FT angstroms of each other"
 FT Modified-site 1
 FT /note= "labelled by donor fluorophore (F1) 5'-
 FT carboxytetramethylrhodamine"
 FT Peptide 4. .7
 FT /label= P
 FT /note= "peptide comprising a protease recognition site"
 FT Modified-site 5
 FT /label= Nle
 FT Region 8. .9
 FT /label= C2
 FT /note= "the two conformation determining regions C1 and
 FT C2 which flank the protease recognition site peptide P
 FT are provided to position the two fluorophores within 100
 FT angstroms of each other"
 FT Modified-site 9
 FT /note= "labelled by acceptor fluorophore F2 rhodamine X

FT acetamide"
 XX
 PN WO9613607-A1.
 XX
 PD 09-MAY-1996.
 XX
 PF 27-OCT-1995; 95WO-US019936.
 XX
 PR 28-OCT-1994; 94US-00331383.
 XX
 PA (ONCO-) ONCOIMMUNIN INC.
 XX
 PI Komoriya A, Packard BS;
 XX
 DR WPI; 1996-239512/24.
 XX
 XX New fluorogenic peptide(s) with fluorophore at each terminus - for
 PT detecting protease(s) in biological samples, emit intense visible
 PT fluorescence when cleaved.
 XX
 PS Claim 15; Page 31; 88pp; English.
 XX
 CC The present sequence is a specific example of a fluorogenic substrate for
 CC detecting activity of a protease. The substrate agrees with the generic
 CC formula (S1)n-C1(F1)-P-C2(F2)-(S2)k in which a peptide P of 2-8 amino
 CC acids comprising a recognition site for the protease is flanked by
 CC conformation determining regions (C1 and C2) of 1-3 amino acids. C1 and
 CC C2 are labelled by fluorophore groups (F1 and F2, respectively)
 CC positioned within 100 angstroms of each other. Additional peptide spacers
 CC of 1-50 amino acids (S1 and S2) may also be present (i.e. n and k = 0 or
 CC 1). Fluorogenic substrates corresponding to the generic formula are used
 CC to detect or localise proteases in biological specimens, esp. in frozen
 CC tissue sections or to monitor protease activity in stored reagents.
 CC Changes in protease activity are associated with e.g. arthritis,
 CC emphysema, thrombosis and cancer metastasis. (Updated on 25-MAR-2003 to
 CC correct PA field.)
 XX
 SQ Sequence 9 AA;
 Query Match 58.9%; Score 33; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 3 SVPLSVPC 10
 Db ::|||:
 2 AIPXSIPC 9
 RESULT 7
 AAW82094
 ID AAW82094 standard; peptide; 9 AA.
 AC AAW82094;
 XX
 XX 18-FEB-1999 (first entry)
 DT
 XX D-NorFES-A protease inhibitor peptide.
 DE
 XX Protease activity; fluorophore; detection; fluorogenic; cellular uptake;
 KW conformation change.
 KW Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "Asp residue is modified by the presence of F1
 FT where F1 is the donor fluorophore 5'-
 FT carboxytetramethylrhodamine (C2211)"
 FT Modified-site 5
 FT /label= Nle
 FT /note= "Norleucine"
 FT Modified-site 9
 FT /note= "Cys residue is modified by the presence of F2

FT where F2 is the acceptor fluorophore rhodamine X
 FT acetamide (R492)"
 PN W09837226-A1.
 XX 27-AUG-1998.
 XX 20-FEB-1998; 98WO-US003000.
 PF 20-FEB-1997; 97US-00802981.
 XX (ONCO-) ONCOIMMUNIN INC.
 XX Komoriya A, Packard BS;
 XX WPI; 1998-467579/40.
 DR New fluorogenic compositions - containing 2 fluorophores separated by a
 PT peptide comprising a protease binding site, used for detecting protease
 PT activity in samples.
 XX Disclosure; Page 10; 90pp; English.
 XX AAW82023-W82240 are peptides used in the construction of a fluorogenic
 CC composition which is used for the detection of protease activity in
 CC biological samples. The products can be used for the detection of
 CC conformation changes in nucleic acids, oligosaccharides, polysaccharides,
 CC proteins, peptides, lipids, phospholipids, glycolipids, glycoproteins,
 CC steroids or polymers. In addition, attachment of a hydrophobic group to a
 CC molecule can be used to enhance uptake by cells. The composition is
 CC composed of P = peptide comprising a protease binding site for the
 CC protease, F1, F2 peptides = fluorophores where F1 is attached to the
 CC amino terminal amino acid and F2 is attached to the carboxyl terminal
 CC amino acid and S1, S2 peptides = when present, are peptide spacers where
 CC S1, when present, is attached to the amino terminal acid, and S2, when
 CC present, is attached to the carboxyl terminal amino acid
 XX Sequence 9 AA;
 SQ Query Match 58.9%; Score 33; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 3 SVPLSVC 10
 Db ::|||::|||
 2 AIPXSIPC 9
 RESULT 8
 AAW46561
 ID AAW46561 standard; peptide; 9 AA.
 XX AAW46561;
 AC AAW46561;
 XX 20-MAY-1998 (first entry)
 DT Peptide backbone of a protease indicator.
 DE Protease binding site; protease; protease indicator; fluorescent signal;
 KW Protease detection; protease activity.
 XX Synthetic.
 OS Key Location/Qualifiers
 PH Modified-site 5
 FT /label= Nle
 FT /note= "Norleucine"
 XX US5714342-A.
 PN 03-FEB-1998.
 PD 27-OCT-1995; 95US-00549008.
 PF

XX 28-OCT-1994; 94US-00331383.
 PR (ONCO-) ONCOIMMUNIN INC.
 XX Packard BS, Komoriya A;
 PI WPI; 1998-158345/14.
 XX Fluorogenic substrates for protease determination - having two closely
 DR spaced fluorophores flanking protease binding site.
 PT Example 1; Col 23; 39pp; English.
 XX The present peptide contains a protease binding site. It is used to
 CC produce novel reagents whose fluorescence increases in the presence of
 CC particular proteases. These fluorogenic protease indicators (substrates)
 CC provide a high intensity fluorescent signal at a visible wavelength when
 CC they are digested by a protease. The fluorogenic indicators have the
 CC general formula: F1-C1--P-C2--F2 || (S1)n (S2)k where: P is a peptide
 CC containing a protease binding site e.g. AAW46520-53, AAW46560, F1 and F2
 CC are fluorophores. S1 and S2 are peptide spacers e.g. AAW46554-58, n, k =
 CC 0 or 1. C1 and C2 are conformation-determining regions that introduce a
 CC bend into the composition which positions the fluorophores adjacent to
 CC each other with a separation of less than 100 Angstrom. When n is 1, S1
 CC is joined to the terminal alpha -amino group of C1 by a peptide bond, and
 CC when k is 1, S2 is joined to the terminal carboxy group of C2 by a
 CC peptide bond. The protease indicators are used for detecting protease
 CC activity in a biological sample. The sample is contacted with the
 CC indicator and any change in fluorescence is detected, an increase in
 CC fluorescence indicating protease activity
 XX Sequence 9 AA;
 SQ Query Match 58.9%; Score 33; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 3 SVPLSVC 10
 Db ::|||::|||
 2 AIPXSIPC 9
 RESULT 9
 AAW73245
 ID AAW73245 standard; peptide; 9 AA.
 XX AAW73245;
 AC AAW73245;
 XX 14-AUG-2001 (first entry)
 DT Protease indicator peptide #1.
 DE Protease detection; peptide cleavage; enzyme activity; fluorogenic;
 KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;
 XX haemophilia.
 XX Synthetic.
 OS Key Location/Qualifiers
 PH Modified-site 1
 FT /label= OTHER
 FT /note= "modified by fluorophore"
 FT Modified-site 9
 FT /label= OTHER
 FT /note= "modified by fluorophore"
 XX WO200118238-A1.
 PN 15-MAR-2001.
 PD 11-SEP-2000; 2000WO-US024882.
 PF

PR 10-SEP-1999; 99US-00394019.
 XX (ONCO-) ONCOIMMUNIN INC.
 XX Komoriya A, Packard BS;
 PI WPI; 2001-389573/41.
 XX
 XX New fluorogenic compositions whose fluorescence level increases in the
 PT presence of active proteases, useful for detecting and localizing
 PT protease activity in biological samples, particularly in frozen tissue
 PT samples.
 XX
 XX Example 2; Page 53; 86pp; English.
 XX
 XX The present invention describes fluorogenic compositions which can be
 CC used for the detection of protease activity. This can be useful as an
 CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,
 CC thrombosis and arthritis. The fluorogenic compositions comprise a
 CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The
 CC peptide is cleaved by a protease and the fluorophores can then be
 CC detected. The present sequence is one of the peptides described in the
 CC exemplification of the invention
 XX
 XX Sequence 9 AA;
 CC
 CC Query Match 58.9%; Score 33; DB 4; Length 9;
 CC Best Local Similarity 50.0%; Pred. No. 1.4e+06;
 CC Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC QY 3 SVPLSVPC 10
 CC ::|||::||
 CC Db 2 AIPXSIPC 9
 CC
 CC RESULT 10
 CC ASU60357
 CC ID ASU60357 standard; peptide; 9 AA.
 CC AC ASU60357;
 CC
 CC DT 29-APR-2003 (first entry)
 CC
 CC DE D-NorFES-A protease inhibitor peptide.
 CC
 CC KW Protease; indicator; chromophore; H-dimer; fluorescence; absorbance;
 CC nuclease; screening; fluorophore; substrate cleavage.
 CC
 CC OS Synthetic.
 CC
 CC FH Key Location/Qualifiers
 CC FT Modified-site 1
 CC FT /note= "F1, where F1 is a donor fluorophore 5'-
 CC FT carbocytetramethylrhodamine (C2211)"
 CC FT Modified-site 5
 CC FT /label= Wle
 CC FT /note= "norleucine"
 CC FT Modified-site 9
 CC FT /note= "F2, where F2 is an acceptor fluorophore rhodamine
 CC FT X acetamide (R492)"
 CC FT
 CC PN WO200261038-A2.
 CC
 CC PD 08-AUG-2002.
 CC
 CC XX 21-DEC-2001; 2001WO-US049781.
 CC
 CC PR 22-DEC-2000; 2000US-00747287.
 CC
 CC XX (ONCO-) ONCOIMMUNIN INC.
 CC
 CC PA Packard BS, Komoriya A;
 CC PI
 CC XX

DR WPI; 2002-698548/75.
 XX
 XX Indicator composition comprising polypeptide or nucleic acid backbone
 PT joining two same chromophores resulting in quenching of fluorescence
 PT of/change in absorbance of chromophores, useful for detecting protease
 PT activity.
 XX
 XX Example 2; Page 15; 97pp; English.
 XX
 XX This invention describes a novel indicator composition (referred as homo-
 CC doubly labeled compositions) comprising a polypeptide backbone or a
 CC nucleic acid backbone joining two chromophores of the same species
 CC whereby the chromophores form an H-dimer resulting in quenching of the
 CC fluorescence of or a change in the absorbance of the chromophore, a
 CC decrease in fluorescence or a change in absorbance indicates that the
 CC first molecule and the second molecule are interacting. The indicator is
 CC useful for detecting the activity of a protease, where an increase in
 CC fluorescence or a change in absorbance indicates that the protease
 CC cleaves the polypeptide backbone. The indicator is attached to a solid
 CC support inside a mammalian, yeast or insect cell. The composition bears a
 CC hydrophobic group such as Fmoc, 9-fluoreneacetyl group, 1-
 CC fluoreneacetyl group, 9-fluoreneacetyl group, and 9-fluorenone-1-
 CC carboxylic group, benzoyloxycarbonyl, Xanthyl (Xan), Trityl (Trt), 4-
 CC methyltrityl (Mtr), 4-methoxytrityl (Mmt), 4-methoxy-2,3, 6-trimethyl-
 CC benzene-sulphonyl (Mts), Mesitylene-2-sulphonyl (Mts), 4,4'-
 CC dimethoxybenzhydryl (Mbh), etc. The method described in the invention is
 CC useful for detecting protease or nuclease activity (or the presence of
 CC nucleic acid) in histological section, cells in culture, (e.g., seeded or
 CC cultured adherent cells), a biological sample such as tissue, biopsy,
 CC lymph, embryo, or whole animal, or cell suspension derived from a
 CC biological sample such as tissue, blood, urine, saliva, lymph, or biopsy.
 CC The indicator composition is also useful for screening a test agent for
 CC the ability to modulate a protease (or a nuclease, lipase, etc.). The
 CC indicator reagents allow rapid determination of protease activity in a
 CC matter of minutes in a single-step procedure. The fluorescent indicators
 CC both absorb and emit in the visible range (400-800 nm). These signals are
 CC therefore not readily quenched by, nor is activation of the fluorophores,
 CC that is, absorption of light, interfered with by background molecules;
 CC therefore they are easily detected in biological samples. The fluorogenic
 CC protease indicators utilise high efficiency fluorophores and are able to
 CC achieve a high degree of quenching while providing a strong signal when
 CC the quench is released by cleavage of the peptide substrate. The high
 CC signal allows detection of very low levels of protease activity. Thus the
 CC fluorogenic protease indicators are particularly well suited for in situ
 CC detection of protease activity. ASU60357-ASU60477 represent peptides use
 CC to illustrate the method described in the disclosure of the invention
 XX
 XX Sequence 9 AA;
 CC
 CC Query Match 58.9%; Score 33; DB 5; Length 9;
 CC Best Local Similarity 50.0%; Pred. No. 1.4e+06;
 CC Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC QY 3 SVPLSVPC 10
 CC ::|||::||
 CC Db 2 AIPXSIPC 9
 CC
 CC RESULT 11
 CC AAU00643
 CC ID AAU00643 standard; peptide; 10 AA.
 CC
 CC AC AAU00643;
 CC
 CC DT 07-SEP-2001 (first entry)
 CC
 CC DE Human membrane translocating peptide (MTLP) #12.
 CC
 CC KW Membrane translocating peptide; MTLP; human; intracellular gene delivery;
 CC epithelial cell layer; gastrointestinal tract; circulatory system.
 CC
 CC OS Homo sapiens.
 CC XX

XX WPI; 2002-269179/31.
 XX Monitoring 83P2H3 gene products for monitoring the presence of cancer in
 PT a subject, comprises determining the status of 83P2H3 gene products in a
 PT tissue sample from the subject and comparing it to a normal sample.
 XX
 XX Example 11; Page 173; 270pp; English.
 XX
 XX The invention relates to monitoring 83P2H3 (a calcium transport protein
 CC whose gene is located on chromosome 7q34) gene products in a biological
 CC sample from a patient who has or is suspected of having cancer
 CC (especially prostate cancer), comprises: (a) determining the status of
 CC 83P2H3 gene products expressed by cells in a tissue sample from an
 CC individual and (b) comparing the status to the status of 83P2H3 gene
 CC products in a normal sample. Also included are modulators of 83P2H3
 CC function or status, generating antibodies/immune response against 83P2H3
 CC (or related protein CatrF2E11 whose gene is located on chromosome
 CC 12q24.1) using identified HLA (human leukocyte antigen) binding peptides
 CC derived from the protein, delivering a cytotoxic agent to a cell
 CC expressing 83P2H3 by conjugating the agent to an anti-83P2H3 antibody, a
 CC recombinant protein comprising an antigen-binding region of the antibody,
 CC a non-human transgenic animal that produces the recombinant protein, a
 CC hybridoma that produces the recombinant protein, a single-chain
 CC monoclonal antibody that comprises the variable domains of the heavy and
 CC light chains of the anti-83P2H3 antibody, a vector comprising a
 CC polynucleotide that encodes the monoclonal antibody and inducing an
 CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
 CC epitope with an immune system T cell or B cell respectively. The method
 CC is useful for monitoring 83P2H3 gene products in a biological sample for
 CC cancer that expresses 83P2H3. The immunological methods are useful for
 CC generating an immune response against 83P2H3, and for detecting the
 CC presence of 83P2H3-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-
 CC idiotype antibodies that mimic the 83P2H3 protein. The present sequence
 CC is an HLA binding peptide motif from 83P2H3 or its related protein
 CC CatrF2E11
 XX
 XX Sequence 9 AA;
 XX
 XX Query Match 56.2%; Score 31.5; DB 5; Length 9;
 XX Best Local Similarity 60.0%; Pred. No. 1.4e+06;
 XX Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
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 XX QY 1 CTSVPLSVPC 10
 XX |::|||
 XX 1 CLT-PLSFPC 9
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 XX Db
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 XX RESULT 14
 XX AAU94201
 XX ID AAU94201 standard; peptide; 10 AA.
 XX AC AAU94201;
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 XX 02-JUL-2002 (first entry)
 XX
 XX Human novel protein CatrF2E11 HLA binding peptide #84.
 XX
 XX Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CatrF2E11;
 XX calcium transport protein; cancer; prostate cancer; cytostatic;
 XX chromosome 7q34; chromosome 12q24.1; T cell; B cell.
 XX
 XX Homo sapiens.
 XX
 XX WO200214361-A2.
 XX

XX
 PD 21-FEB-2002.
 XX
 XX 17-AUG-2001; 2001WO-US025782.
 XX
 XX 17-AUG-2000; 2000US-0226329P.
 XX
 XX (AGEN-) AGENSYS INC.
 XX
 XX Raitano AB, Challita-Eid PM, Faris M, Safran DC, Afar DEH;
 XX Levin E, Hubert RS, Ge W, Jakobovits A;
 XX
 XX WPI; 2002-269179/31.
 XX
 XX Monitoring 83P2H3 gene products for monitoring the presence of cancer in
 PT a subject, comprises determining the status of 83P2H3 gene products in a
 PT tissue sample from the subject and comparing it to a normal sample.
 XX
 XX Example 11; Page 169; 270pp; English.
 XX
 XX The invention relates to monitoring 83P2H3 (a calcium transport protein
 CC whose gene is located on chromosome 7q34) gene products in a biological
 CC sample from a patient who has or is suspected of having cancer
 CC (especially prostate cancer), comprises: (a) determining the status of
 CC 83P2H3 gene products expressed by cells in a tissue sample from an
 CC individual and (b) comparing the status to the status of 83P2H3 gene
 CC products in a normal sample. Also included are modulators of 83P2H3
 CC function or status, generating antibodies/immune response against 83P2H3
 CC (or related protein CatrF2E11 whose gene is located on chromosome
 CC 12q24.1) using identified HLA (human leukocyte antigen) binding peptides
 CC derived from the protein, delivering a cytotoxic agent to a cell
 CC expressing 83P2H3 by conjugating the agent to an anti-83P2H3 antibody, a
 CC recombinant protein comprising an antigen-binding region of the antibody,
 CC a non-human transgenic animal that produces the recombinant protein, a
 CC hybridoma that produces the recombinant protein, a single-chain
 CC monoclonal antibody that comprises the variable domains of the heavy and
 CC light chains of the anti-83P2H3 antibody, a vector comprising a
 CC polynucleotide that encodes the monoclonal antibody and inducing an
 CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
 CC epitope with an immune system T cell or B cell, respectively. The method
 CC is useful for monitoring 83P2H3 gene products in a biological sample for
 CC cancer that expresses 83P2H3. The immunological methods are useful for
 CC generating an immune response against 83P2H3, and for detecting the
 CC presence of 83P2H3-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-
 CC idiotype antibodies that mimic the 83P2H3 protein. The present sequence
 CC is an HLA binding peptide motif from 83P2H3 or its related protein
 CC CatrF2E11
 XX
 XX Sequence 10 AA;
 XX
 XX Query Match 56.2%; Score 31.5; DB 5; Length 10;
 XX Best Local Similarity 60.0%; Pred. No. 99;
 XX Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
 XX
 XX QY 1 CTSVPLSVPC 10
 XX |::|||
 XX 1 CLT-PLSFPC 9
 XX
 XX Db
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 XX RESULT 15
 XX AAU94811
 XX ID AAU94811 standard; peptide; 10 AA.
 XX
 XX AAU94811;
 XX
 XX AC

XX 02-JUL-2002 (first entry)
 DT Human novel protein CaTrF2E11 HLA binding peptide #394.
 DE Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
 XX calcium transport protein; cancer; prostate cancer; cytostatic;
 KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.
 XX Homo sapiens.
 OS WO200214361-A2.
 PN 21-FEB-2002.
 PD 17-AUG-2001; 2001WO-US025782.
 PF 17-AUG-2000; 2000US-0226329P.
 PR (AGEN-) AGENSYS INC.
 XX Raitano AB, Challita-Eid PM, Paris M, Saffran DC, Afar DEH;
 PI Levin E, Hubert RS, Ge W, Jakobovits A;
 PI WPI; 2002-269179/31.
 DR Monitoring 83P2H3 gene products for monitoring the presence of cancer in
 XX a subject, comprises determining the status of 83P2H3 gene products in a
 PT tissue sample from the subject and comparing it to a normal sample.
 PT Example 11; Page 191; 270pp; English.
 PS The invention relates to monitoring 83P2H3 (a calcium transport protein
 CC whose gene is located on chromosome 7q34) gene products in a biological
 CC sample from a patient who has or is suspected of having cancer
 CC (especially prostate cancer), comprises: (a) determining the status of
 CC 83P2H3 gene products expressed by cells in a tissue sample from an
 CC individual and (b) comparing the status to the status of 83P2H3 gene
 CC products in a normal sample. Also included are modulators of 83P2H3
 CC function or status, generating antibodies/immune response against 83P2H3
 CC (or related protein CaTrF2E11 whose gene is located on chromosome
 CC 12q24.1) using identified HLA (human leukocyte antigen) binding peptides
 CC derived from the protein, delivering a cytotoxic agent to a cell
 CC expressing 83P2H3 by conjugating the agent to an anti-83P2H3 antibody, a
 CC recombinant protein comprising an antigen-binding region of the antibody,
 CC a non-human transgenic animal that produces the recombinant protein, a
 CC hybridoma that produces the recombinant protein, a single-chain
 CC monoclonal antibody that comprises the variable domains of the heavy and
 CC light chains of the anti-83P2H3 antibody, a vector comprising a
 CC polynucleotide that encodes the monoclonal antibody and inducing an
 CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
 CC protein that comprises a T cell or B cell epitope, and contacting the
 CC epitope with an immune system T cell or B cell, respectively. The method
 CC is useful for monitoring 83P2H3 gene products in a biological sample for
 CC monitoring the presence of cancer in an individual. The modulator is
 CC useful for inhibiting the growth of cancer cells that express 83P2H3, for
 CC treating cancer and the vector is useful for treating a patient with a
 CC cancer that expresses 83P2H3. The immunological methods are useful for
 CC generating an immune response against 83P2H3, and for detecting the
 CC presence of 83P2H3-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-
 CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence
 CC is an HLA binding peptide motif from 83P2H3 or its related protein
 CC CaTrF2E11

XX Sequence 10 AA;

Query Match 56.2%; Score 31.5; DB 5; Length 10;
 Best Local Similarity 60.0%; Pred. No. 99;

Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
 Qy 1 CTSVPLSVEC 10
 Db 1 CLT-PLSVEC 9
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Search completed: March 8, 2004, 12:44:44
 Job time : 53 secs

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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:46:06 ; Search time 33 Seconds
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63.986 Million cell updates/sec

Title: US-09-761-636A-13
Perfect score: 56
Sequence: 1 CISVPLSVPC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues
Total number of hits satisfying chosen parameters: 122139

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Published Applications AA:

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11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep.*
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17: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	41.5	74.1	9	9	US-09-761-636A-13
3	32	57.1	10	14	US-10-126-845-13
4	32	57.1	10	14	US-10-126-845-13
5	32	57.1	10	15	US-10-126-845-71
6	31.5	56.2	9	10	US-09-932-165-284
7	31.5	56.2	10	10	US-09-932-165-184
8	31.5	56.2	10	10	US-09-932-165-560
9	31.5	56.2	10	10	US-09-932-165-794
10	31	55.4	9	15	US-10-154-884B-11221
11	30	53.6	9	10	US-09-932-165-679
12	30	53.6	9	10	US-09-932-165-1006
13	30	53.6	9	10	US-09-932-165-1214
14	29	51.8	10	11	US-09-833-245-1011
15	27	48.2	8	9	US-09-756-283A-66

Sequence 11228, A
Sequence 11250, A
Sequence 11254, A
Sequence 11258, A
Sequence 11259, A
Sequence 11265, A
Sequence 11275, A
Sequence 11280, A
Sequence 32, Appl
Sequence 43, Appl
Sequence 11276, A
Sequence 11287, A
Sequence 10, Appl
Sequence 21, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 9790, Ap
Sequence 9847, Ap
Sequence 10152, A
Sequence 10196, A
Sequence 12, Appl
Sequence 37, Appl
Sequence 456, App
Sequence 577, App
Sequence 12, Appl
Sequence 37, Appl
Sequence 456, App
Sequence 577, App
Sequence 9790, Ap
Sequence 9847, Ap

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9 15 US-10-154-884B-11276
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9 9 US-09-761-636A-10
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5 9 US-09-866-135-5
5 10 US-09-886-135-5
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9 14 US-10-277-292-577
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9 15 US-10-280-340-37
9 15 US-10-280-340-456
9 15 US-10-280-340-577
9 15 US-10-057-475B-9790
9 15 US-10-057-475B-9847

ALIGNMENTS

RESULT 1
US-09-761-636A-13
; Sequence 13, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761.636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-13

Query Match 100.0%; Score 56; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CISVPLSVPC 10
DB 1 CISVPLSVPC 10

RESULT 2
US-09-761-636A-14
; Sequence 14, Application US/09761636A
; Patent No. US20020065218A1

APPLICANT: GE, WANGMAO
APPLICANT: JAKOBOVITS, AYA
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
TITLE OF INVENTION: 83P2H3 AND CAT-F2E11 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20014.00
CURRENT APPLICATION NUMBER: US/09/932,165
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/226,329
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 1508
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 284
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-284

Query Match 56.2%; Score 31.5; DB 10; Length 9;
Best Local Similarity 60.0%; Pred. No. 7.2e+05;
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 CTSVPLSVPC 10
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Db 1 CLT-PLSPPC 9

RESULT 7
US-09-932-165-184
Sequence 184, Application US/09932165
Publication No. US20030134784A1
GENERAL INFORMATION:
APPLICANT: RAITANO, ARTHUR
APPLICANT: CHALLITA-EID, PIA M.
APPLICANT: FARIS, MARY
APPLICANT: SAFFRAN, DOUGLAS
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: HUBERT, RENE
APPLICANT: GE, WANGMAO
APPLICANT: JAKOBOVITS, AYA
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
TITLE OF INVENTION: 83P2H3 AND CAT-F2E11 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20014.00
CURRENT APPLICATION NUMBER: US/09/932,165
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/226,329
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 1508
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 184
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-184

Query Match 56.2%; Score 31.5; DB 10; Length 10;
Best Local Similarity 60.0%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 CTSVPLSVPC 10
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Db 1 CLT-PLSPPC 9

RESULT 8
US-09-932-165-560
Sequence 560, Application US/09932165

Publication No. US20030134784A1
GENERAL INFORMATION:
APPLICANT: RAITANO, ARTHUR
APPLICANT: CHALLITA-EID, PIA M.
APPLICANT: FARIS, MARY
APPLICANT: SAFFRAN, DOUGLAS
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: HUBERT, RENE
APPLICANT: GE, WANGMAO
APPLICANT: JAKOBOVITS, AYA
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
TITLE OF INVENTION: 83P2H3 AND CAT-F2E11 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20014.00
CURRENT APPLICATION NUMBER: US/09/932,165
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/226,329
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 1508
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 560
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-560

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Best Local Similarity 60.0%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 CTSVPLSVPC 10
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Db 1 CLT-PLSPPC 9

RESULT 9
US-09-932-165-794
Sequence 794, Application US/09932165
Publication No. US20030134784A1
GENERAL INFORMATION:
APPLICANT: RAITANO, ARTHUR
APPLICANT: CHALLITA-EID, PIA M.
APPLICANT: FARIS, MARY
APPLICANT: SAFFRAN, DOUGLAS
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: HUBERT, RENE
APPLICANT: GE, WANGMAO
APPLICANT: JAKOBOVITS, AYA
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
TITLE OF INVENTION: 83P2H3 AND CAT-F2E11 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20014.00
CURRENT APPLICATION NUMBER: US/09/932,165
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/226,329
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 1508
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 794
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-794

Query Match 56.2%; Score 31.5; DB 10; Length 10;
Best Local Similarity 60.0%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

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1  TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
2
3  TITLE OF INVENTION: 83P2H3 AND CatrT2E11 USEFUL IN TREATMENT AND
4
5  TITLE OF INVENTION: DETECTION OF CANCER
6
7  FILE REFERENCE: 51158-20014.00
8
9  CURRENT APPLICATION NUMBER: US/09/932,165
10
11 CURRENT FILING DATE: 2001-08-17
12
13 PRIOR APPLICATION NUMBER: 60/226,329
14
15 PRIOR FILING DATE: 2000-08-17
16
17 NUMBER OF SEQ ID NOS: 1508
18
19 SOFTWARE: PatentIn Ver. 2.1
20
21 SEQ ID NO 679
22
23 LENGTH: 9
24
25 TYPE: PRT
26
27 ORGANISM: Artificial Sequence
28
29 FEATURE:
30
31 OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
32
33 US-09-932-165-679

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Best Local Similarity	83.3%	Pred. No. 7.2e+05;		
Matches 5;	Conservative	0;	Mismatches 1;	Indels 0;
Qy	5	PzSVPC	10	
Dh	3	PzSVPC	8	

RESULT 12
US-09-932-165-1006
Sequence 1006, Application US/09932165
Publication No. US20030134784A1
GENERAL INFORMATION:
APPLICANT: RAITANO, ARTHUR
APPLICANT: CHALLITA-EID, PIA M.
APPLICANT: PARIS, MARY
APPLICANT: SAFFRAN, DOUGLAS
APPLICANT: APAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: HUBERT, RENE
APPLICANT: GE, WANGMAO
APPLICANT: JAKOBOVITS, AYA
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
TITLE OF INVENTION: 832H3 AND Cairfze11 USEFUL IN TREATMENT AND
TITLE OF INVENTION: DETECTION OF CANCER
FILE REFERENCE: 51158-20014.00
CURRENT APPLICATION NUMBER: US/09/932,165
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/226,329
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 1508
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1006
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1006

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Query Match          53.6%; Score 30; DB 10; Length 9;
Best Local Similarity 83.3%; Pred. No. 7.2e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 PLSVPC 10
      ||| |||
      2 PLSPPC 7

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RESULT 13
US-09-932-165-1214
; Sequence 1214, Application US/09932165
; Publication No. US2003013478A1
; GENERAL INFORMATION:

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QY      1  CISVPLSVPC 10
      |::|||
      |::|||
DB      1  CLT-ELSPFC 9

RESULT 10
US-10-154-884B-11221
; Sequence 11221, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154-884B

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CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 11290
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 11221
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-154--884B-11221

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Query Match          55.4%; Score 31; DB 15; Length 9;
Best Local Similarity 71.4%; Pred. No. 7.2e+05;
Matches 5: Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	CISVPLS	7
		: : :	
Db	2	CLSVPLS	8

RESULT 11
US-09-932-165-679
; Sequence 679, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITS, AVA

; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-BID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND Cat-F2E11 USEFUL IN TREATMENT AND
; FILE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1214
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1214

Query Match 53.6%; Score 30; DB 10; Length 9;
Best Local Similarity 83.3%; Pred. No. 7.2e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLSVPC 10
DB 2 PLSFPC 7

RESULT 14

US-09-833-245-1011
; Sequence 1011, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1011
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-1011

Query Match 51.8%; Score 29; DB 11; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 C1SVPLS 7
DB 4 C1SLPIS 10

RESULT 15

US-09-756-283A-66
; Sequence 66, Application US/09756283A
; Patent No. US20020151478A1

; GENERAL INFORMATION:
; APPLICANT: Chernajovsky, Yuti
; APPLICANT: Dreja, Hanna Stina
; APPLICANT: Adams, Gillian
; TITLE OF INVENTION: Latent Fusion Protein
; FILE REFERENCE: 0623.1000000
; CURRENT APPLICATION NUMBER: US/09/756,283A
; CURRENT FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 66
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Sequence source uncertain
US-09-756-283A-66

Query Match 48.2%; Score 27; DB 9; Length 8;
Best Local Similarity 42.9%; Pred. No. 7.2e+05;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLSVP 9
DB 2 AIPWSIP 8

Search completed: March 8, 2004, 12:51:19
Job time : 34 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:28:28 ; Search time 22 Seconds
(without alignments)
16.426 Million cell updates/sec

Title: US-09-761-636A-11
Perfect score: 42
Sequence: 1 CVPLTSC 7

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 57228

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/2/iaa/5A COMB.pcp.*
2: /cgn2_6/prodata/2/iaa/5B COMB.pcp.*
3: /cgn2_6/prodata/2/iaa/6A COMB.pcp.*
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6: /cgn2_6/prodata/2/iaa/backfile1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	73.8	7	1	US-08-526-710-21
2	31	73.8	7	3	US-08-862-855-21
3	31	73.8	7	3	US-09-226-985-21
4	31	73.8	7	4	US-09-227-906-21
5	26	61.9	7	4	US-09-187-859-1375
6	26	61.9	7	4	US-09-839-542B-1375
7	25	59.5	7	4	US-03-187-859-1799
8	25	59.5	7	4	US-09-187-859-3971
9	25	59.5	7	4	US-09-839-542B-1799
10	25	59.5	7	4	US-09-187-859-4047
11	25	59.5	7	4	US-09-839-542B-3971
12	25	59.5	7	4	US-09-839-542B-1799
13	24	57.1	7	4	US-09-839-542B-4047
14	24	57.1	7	4	US-03-187-859-3574
15	23	54.8	6	1	US-07-947-035-13
16	23	54.8	6	1	US-08-321-585A-11
17	23	54.8	7	4	US-09-187-859-1392
18	23	54.8	7	4	US-09-187-859-1740
19	23	54.8	7	4	US-03-187-859-2155
20	23	54.8	7	4	US-09-187-859-2720
21	23	54.8	7	4	US-09-187-859-3637
22	23	54.8	7	4	US-09-187-859-4041
23	23	54.8	7	4	US-09-839-542B-1392
24	23	54.8	7	4	US-09-839-542B-1740
25	23	54.8	7	4	US-09-839-542B-2155
26	23	54.8	7	4	US-09-839-542B-2720
27	23	54.8	7	4	US-09-839-542B-3637

28 23 54.8 7 4 US-09-839-542B-4041 Sequence 4041, Ap
29 23 54.8 7 4 US-09-535-852-1826 Sequence 1826, Ap
30 22 52.4 4 2 US-08-429-964-41 Sequence 41, Appl
31 22 52.4 4 4 US-09-665-362A-35 Sequence 35, Appl
32 22 52.4 4 5 PCT-US93-08062-41 Sequence 41, Appl
33 22 52.4 7 1 US-07-958-903A-26 Sequence 26, Appl
34 22 52.4 7 1 US-08-463-018-26 Sequence 26, Appl
35 22 52.4 7 1 US-08-823-245-26 Sequence 26, Appl
36 22 52.4 7 4 US-07-963-329A-26 Sequence 26, Appl
37 22 52.4 7 4 US-09-187-859-1888 Sequence 1888, Ap
38 22 52.4 7 4 US-09-187-859-2750 Sequence 2750, Ap
39 22 52.4 7 4 US-09-187-859-3606 Sequence 3606, Ap
40 22 52.4 7 4 US-09-187-859-3621 Sequence 3621, Ap
41 22 52.4 7 4 US-09-839-542B-1888 Sequence 1888, Ap
42 22 52.4 7 4 US-09-839-542B-2750 Sequence 2750, Ap
43 22 52.4 7 4 US-09-839-542B-3606 Sequence 3606, Ap
44 22 52.4 7 4 US-09-839-542B-3621 Sequence 3621, Ap
45 22 52.4 7 4 US-09-535-852-918 Sequence 918, Ap

ALIGNMENTS

RESULT 1
US-08-526-710-21
; Sequence 21, Application US/08526710
; Patent No. 5622699
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/526,710
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-526-710-21

Query Match 73.8%; Score 31; DB 1; Length 7;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
Db 1 CLPVASC 7

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RESULT 2
US-08-862-855-21
; Sequence 21, Application US/08862855
; Patent No. 6068829
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,855
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,855
; FILING DATE: 23-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-862-855-21

Query Match 73.8%; Score 31; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPULTSC 7
DB 1 CLPVASC 7

RESULT 3
US-09-226-985-21
; Sequence 21, Application US/09226985
; Patent No. 6296832
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules That Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2621
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-862-855-21

Query Match 73.8%; Score 31; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPULTSC 7
DB 1 CLPVASC 7

RESULT 4
US-09-227-906-21
; Sequence 21, Application US/09227906
; Patent No. 6306365
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-226-985-21

Query Match 73.8%; Score 31; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPULTSC 7
DB 1 CLPVASC 7
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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/862,855
;; FILING DATE: 23-MAY-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-LJ 3424
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-227-906-21

Query Match 73.8%; Score 31; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
Db 1 CLPVASC 7

RESULT 5
US-09-187-859-1375
; Sequence 1375, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1375
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-09-187-859-1375

Query Match 61.9%; Score 26; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
Db 1 CEPKTGC 7

RESULT 6
US-09-839-542B-1375
; Sequence 1375, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052

;; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1375
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-09-839-542B-1375

Query Match 61.9%; Score 26; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
Db 1 CEPKTGC 7

RESULT 7
US-09-187-859-1799
; Sequence 1799, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1799
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
US-09-187-859-1799

Query Match 59.5%; Score 25; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
Db 1 CDPKTGC 7

RESULT 8
US-09-187-859-3971
; Sequence 3971, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3971
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence
US-09-187-859-3971

Query Match 59.5%; Score 25; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 3e+05; 3; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 CVPLTSC 7
| | | | |
Db 1 CDPKTCG 7

RESULT 9
US-09-187-859-4047
; Sequence 4047, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4047
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-09-187-859-4047

Query Match 59.5%; Score 25; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 3e+05; 3; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 CVPLTSC 7
| | | | |
Db 1 CDPKTCG 7

RESULT 10
US-09-839-542B-1799
; Sequence 1799, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1799
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
US-09-839-542B-1799

Query Match 59.5%; Score 25; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 3e+05; 3; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 CVPLTSC 7
| | | | |
Db 1 CDPKTCG 7

RESULT 11
US-09-839-542B-3971
; Sequence 3971, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3971
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence
US-09-839-542B-3971

Query Match 59.5%; Score 25; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 3e+05; 3; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 CVPLTSC 7
| | | | |
Db 1 CDPKTCG 7

RESULT 12
US-09-839-542B-4047
; Sequence 4047, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4047
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-09-839-542B-4047

Query Match 59.5%; Score 25; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 3e+05; 3; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 CVPLTSC 7
| | | | |
Db 1 CDPKTCG 7

RESULT 13
US-09-187-859-3574
; Sequence 3574, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:

```
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3574
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-09-187-859-3574

Query Match          57.1%; Score 24; DB 4; Length 7;
Best Local Similarity 42.9%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
Db 1 CDPVSGC 7

RESULT 14
US-09-839-542B-3574
; Sequence 3574, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3574
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-09-839-542B-3574

Query Match          57.1%; Score 24; DB 4; Length 7;
Best Local Similarity 42.9%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
Db 1 CDPVSGC 7

RESULT 15
US-07-947-035-13
; Sequence 13, Application US/07947035
; Patent No. 5444045
; GENERAL INFORMATION:
; APPLICANT: Francis, Geoffrey L.
; APPLICANT: Walton, Paul E.
; APPLICANT: Ballard, Francis J.
; APPLICANT: McMurty, John P.
; APPLICANT: Phelps, Patricia V.
; TITLE OF INVENTION: Method of Administering IGF-1, IGF-2,
```

```
; TITLE OF INVENTION: and Analogs Thereof to Birds
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 5444045th Carolina
; COUNTRY: US
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/947,035
; FILING DATE: 17-SEP-1992
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5175-59
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
US-07-947-035-13

Query Match          54.8%; Score 23; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PLTSC 7
Db 2 PLTLC 6

Search completed: March 8, 2004, 12:31:51
Job time : 23 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:35:19 ; Search time 21 Seconds
(without alignments)
27.493 Million cell updates/sec

Title: US-09-761-636A-12

Perfect score: 38

Sequence: 1 CVPLTC 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 316

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PTR_78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	52.6	5	2 B22565	R-phycoerythrin al
2	15	39.5	6	2 I65546	MHC H2-L antigen -
3	14	36.8	5	2 E60274	major protein anti
4	14	36.8	5	2 F22565	R-phycoerythrin ga
5	14	36.8	6	2 I49421	laminin B1 - waste
6	11	28.9	4	2 A32039	tyrosine-melanocyt
7	11	28.9	4	2 I54357	schwannomin - mous
8	11	28.9	5	2 A60521	glycogen phosphory
9	11	28.9	6	2 I37263	Y protein - human
10	11	28.9	6	2 H48394	glycoprotein compo
11	10	26.3	6	2 C22565	R-phycoerythrin be
12	9	23.7	3	3 A22565	R-phycoerythrin al
13	9	23.7	4	2 I51049	metallothionein-A
14	9	23.7	4	2 S43959	Ig mu chain v regi
15	9	23.7	4	2 S5238	pallidipin - assas
16	9	23.7	5	2 A37882	cadmium-binding pe
17	9	23.7	5	2 B37988	acid proteinase li
18	9	23.7	5	2 B45525	actin I - malaria
19	9	23.7	5	2 S65726	hemoglobin, extrac
20	9	23.7	5	2 S11127	phosphoprotein, bo
21	9	23.7	6	2 A61049	halo-toxin - Pseud
22	9	23.7	6	2 J00355	lipopeptide WS1279
23	9	23.7	6	2 P00008	angiotensin-conver
24	9	23.7	6	2 A27696	contraction-inhibi
25	9	23.7	6	2 B27696	contraction-inhibi
26	9	23.7	6	2 I37027	protamine P1 - gor
27	9	23.7	6	2 I67345	MHC H2-K-k cell su
28	9	23.7	6	2 F0652	T-cell receptor be
29	9	23.7	6	2 F41946	T-cell receptor ga

30 9 23.7 6 2 S29881 Na+/K+-exchanging
31 9 23.7 6 4 I79564 hypothetical TCL3
32 8 21.1 3 3 I78890 tyrosine protein k
33 8 21.1 5 1 HOROHA proctolin - Americ
34 8 21.1 5 2 JN0862 peptidyl-dipeptida
35 8 21.1 5 2 JN0860 peptidyl-dipeptida
36 8 21.1 5 2 E42364 flagellar protein
37 8 21.1 5 2 PQ0009 angiotensin-conver
38 8 21.1 5 2 A60411 proctolin - Atlant
39 8 21.1 5 2 S53595 hypothetical proce
40 8 21.1 6 4 A35039 hypothetical colla
41 7 18.4 3 3 RHDTTO thyroliberin - Bom
42 7 18.4 3 3 RHPGT thyroliberin - pig
43 7 18.4 3 3 RSHST thyroliberin - she
44 7 18.4 3 3 A92971 thyroliberin - eas
45 7 18.4 3 3 A33802 thyrotropin-releas

ALIGNMENTS

RESULT 1
B22565
R-phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: B22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601; PMID:3886644
A:Accession: B22565
A:Molecule type: protein
A:Residues: 1-5 <KLO>

Query Match 52.6%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVP 3
|||
DB 2 CVP 4

RESULT 2
I65546
MHC H2-L antigen - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I65546
R:Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
Cell 44, 261-272, 1986
A:Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and the
A:Reference number: I52778; MUID:86106202; PMID:3510743
A:Accession: I65546
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: GB:M12483; NID:g199565; PIDN:AAA39663.1; PID:g554234

Query Match 39.5%; Score 15; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VPLT 5
|||
DB 2 VECT 5

RESULT 3
E60274
major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)
C:Species: Mycobacterium tuberculosis

C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
 C;Accession: E60274
 R;Negat, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
 Infect. Immun. 59, 372-382, 1991
 A;Title: Isolation and partial characterization of major protein antigens in the culture
 A;Reference number: A60274; MUID:9109989; PMID:1898899
 A;Accession: E60274
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-5 <NAG>

Query Match 36.8%; Score 14; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PLT 5
 ||
 3 PIT 5

Db

RESULT 4
 F22565
 R-phycoerythrin gamma-A chain - red alga (Gastrocloonium coulteri) (fragment)
 C;Species: Gastrocloonium coulteri
 C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
 C;Accession: F22565
 R;Klotz, A.V.; Glazer, A.N.
 J. Biol. Chem. 260, 4856-4863, 1985
 A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
 A;Reference number: A22565; MUID:85182601; PMID:3886644
 A;Accession: F22565
 A;Molecule type: protein
 A;Residues: 1-5 <KLO>

Query Match 36.8%; Score 14; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TC 6
 ||
 2 TC 3

Db

RESULT 5
 I49421
 laminin B1 - western wild mouse (fragment)
 C;Species: Mus spretus (western wild mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C;Accession: I49421
 R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Mazaraki, Y.; Nadeau, J.H.
 Mamm. Genome 5, 349-355, 1994
 A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
 A;Reference number: I49421; MUID:94319082; PMID:8043949
 A;Accession: I49421
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-6 <RES>

Query Match 36.8%; Score 14; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TC 6
 ||
 4 TC 5

Db

RESULT 6
 A32039
 tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000

C;Accession: A32039
 R;Horvath, A.; Kastin, A.J.
 J. Biol. Chem. 264, 2175-2179, 1989
 A;Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor
 A;Reference number: A32039; MUID:89123285; PMID:2563371
 A;Accession: A32039
 A;Molecule type: protein
 A;Residues: 1-4 <HOR>
 A;Experimental source: brain
 A;Superfamily: unassigned animal peptides
 C;Keywords: amidated carboxyl end
 F;4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.9%; Score 11; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PL 4
 ||
 2 PL 3

Db

RESULT 7
 I54357
 Schwannomin - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C;Accession: I54357
 R;Ruyh, D.P.; Nechiporuk, T.; Pulst, S.
 Hum. Mol. Genet. 3, 1075-1079, 1994
 A;Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are c
 A;Reference number: I54357; MUID:95072570; PMID:7981675
 A;Accession: I54357
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-4 <RES>
 A;Cross-references: GB:I28838; NID:9454836; PIDN:AAA57150.1; PID:IG601923
 C;Genetics:
 A;Gene: NF2

Query Match 28.9%; Score 11; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VP 3
 ||
 1 VP 2

Db

RESULT 8
 A60521
 glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
 A;Alternate names: glycogen phosphorylase b
 C;Species: Liza ramada
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003
 C;Accession: A60521
 R;Bonamus, L.; Baanante, I.V.
 Comp. Biochem. Physiol. B 95, 295-301, 1990
 A;Title: Purification and characterization of glycogen phosphorylase B from skeletal mu
 A;Reference number: A60521; MUID:90227907; PMID:2109669
 A;Accession: A60521
 A;Molecule type: protein
 A;Residues: 1-5 <BON>
 C;Superfamily: glucan phosphorylase
 C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
 F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experi

Query Match 28.9%; Score 11; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VP 3
 ||

Db 4 VP 5

RESULT 9

I37263
Y protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999
C:Accession: I37263
R:Waechter, G.; Habener, J.F.
Endocrinology 131, 2010-2015, 1992
A>Title: Novel testis germ cell-specific transcript of the CREB gene contains an alternative exon
A:Reference number: I37263; MUID:93010691; PMID:1396344
A:Accession: I37263
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579916
C:Genetics:
A:Gene: CREB

Query Match 28.9%; Score 11; DB 2; Length 6;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTC 6

Db 2 LFC 4

RESULT 10

H48394
glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr
C:Species: Bos primigenius taurus (cattle)
C>Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C:Accession: H48394
R:Mathier, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A>Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
II-like sequences
A:Reference number: H48394; MUID:93250576; PMID:8485470
A:Accession: H48394
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-6 <MAT>
A:Experimental source: milk
A>Note: sequence extracted from NCBI backbone (NCBIP:131518)
C:Keywords: glycoprotein

Query Match 28.9%; Score 11; DB 2; Length 6;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTC 6

Db 4 LGC 6

RESULT 11

R22565
R-phycoerythrin beta-1 chain - red alga (Gastrocloonium coulteri) (fragment)
C:Species: Gastrocloonium coulteri
C>Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: C22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A>Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601; PMID:3886644
A:Accession: C22565
A:Molecule type: protein
A:Residues: 1-6 <KLO>

Query Match

26.3%; Score 10; DB 2; Length 6;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CV 2

Db 4 CL 5

RESULT 12

A22565
R-phycoerythrin alpha-1 chain - red alga (Gastrocloonium coulteri) (fragment)
C:Species: Gastrocloonium coulteri
C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: A22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A>Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601; PMID:3886644
A:Accession: A22565
A:Molecule type: protein
A:Residues: 1-3 <KLO>

Query Match 23.7%; Score 9; DB 3; Length 3;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1

Db 1 C 1

RESULT 13

I51049
metallothionein-A - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51049
R:Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.
Eur. J. Biochem. 230, 344-349, 1995
A>Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) m
A:Reference number: I51049; MUID:95324545; PMID:7601121
A:Accession: I51049
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <OLS>
A:Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match

23.7%; Score 9; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1

Db 4 C 4

RESULT 14

S43959
Ig mu chain V region (clone 13) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C:Accession: S43959
R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.
Nucleic Acids Res. 22, 1389-1393, 1994
A>Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A:Reference number: S43956; MUID:94248036; PMID:8190629
A:Accession: S43959
A:Molecule type: DNA
A:Residues: 1-4 <WAG>
C:Keywords: immunoglobulin

Query Match

23.7%; Score 9; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 2 C 2

RESULT 15
S55238
pallidipin - assassin bug (fragment)
C:Species: Triatoma pallidipennis (assassin bug)
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 19-May-2000
C:Accession: S55238
R:Haendler, B.; Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Schleunin
Biochem. J. 307, 465-470, 1995
A:Title: Expression of active recombinant pallidipin, a novel platelet aggregation inhib
A:Reference number: S55238; PMID:95251610; PMID:7733884
A:Accession: S55238
A:Molecule type: protein
A:Residues: 1-4 <HAB>

Query Match 23.7%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 3 C 3

Search completed: March 8, 2004, 12:38:53
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:31:54 ; Search time 10 Seconds
(without alignments)
31.242 Million cell updates/sec

Title: US-09-761-636A-12
Perfect score: 38
Sequence: 1 CVPLTC 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	13	34.2	6	1	E101_LITRU	P82096 Litoria rub
2	11	28.9	6	1	VP19_HSVIK	P23210 herpes simp
3	9	23.7	5	1	E103_LITRU	P82099 Litoria rub
4	9	23.7	6	1	CIP1_MYTED	P13736 mytilus edu
5	9	23.7	6	1	CIP2_MYTED	P13737 mytilus edu
6	8	21.1	5	1	PCT2_PERAM	P01373 peripianeta
7	8	21.1	6	1	TRP1_PSEPU	P36414 pseudomonas
8	7	18.4	3	1	THYL_PIG	P01151 sus scrofa
9	7	18.4	4	1	DCML_PSECH	P19916 pseudomonas
10	7	18.4	4	1	RM01_YEAST	P36515 saccharomyc
11	7	18.4	4	1	TUFT_HUMAN	P01858 homo sapien
12	7	18.4	5	1	BIOA_CITFR	P13071 citrobacter
13	7	18.4	5	1	BPF7_BOTIN	P30425 bochrops in
14	7	18.4	5	1	E104_LITRU	P82100 Litoria rub
15	7	18.4	5	1	PAP2_PARMA	P81864 pardachirus
16	7	18.4	5	1	SUGA_ACHDO	P19991 acheta dome
17	7	18.4	6	1	OVN_LEPDE	P42985 leptonotars
18	7	18.4	6	1	TMOF_SARBU	P41495 sarcophaga
19	5	13.2	5	1	PSK_DAUCA	P58261 daucus caro
20	5	13.2	5	1	RE31_LITRU	P82072 Litoria rub
21	5	13.2	5	1	RE32_LITRU	P82073 Litoria rub
22	5	13.2	6	1	UN06_CLOPA	P81351 clostridium
23	4	10.5	4	1	ES01_HUMAN	P02731 homo sapien
24	4	10.5	4	1	FAR3_HIRME	P42562 hirudo medi
25	4	10.5	4	1	FLRF_HIRME	P42561 hirudo medi
26	4	10.5	4	1	FLRN_ATEL	P58707 anthopleura
27	4	10.5	5	1	AL14_CARMA	P81817 carcinus ma
28	4	10.5	5	1	RE11_LITRU	P82070 Litoria rub
29	4	10.5	5	1	TPIS_CANFA	P54714 canis famil
30	4	10.5	5	1	UC22_MAZE	P80628 zea mays (m
31	4	10.5	6	1	ACPH_RABIT	P25154 oryctolagus
32	3	7.9	3	1	LUXE_VIBFI	P24272 vibrio fisc
33	3	7.9	4	1	FYRI_ATEL	P58706 anthopleura

34	3	7.9	5	1	FARP_ARTTR	P41853 artiopesthi
35	3	7.9	5	1	RE21_LITRU	P82071 Litoria rub
36	3	7.9	5	1	UF01_MOUSE	P38639 mus musculus
37	2	5.3	4	1	DCMS_PSECH	P19918 pseudomonas
38	2	5.3	4	1	FAR4_HIRME	P42563 hirudo medi
39	2	5.3	4	1	FMRF_MACNI	P01162 macrocallis
40	2	5.3	5	1	BIOB_CITFR	P12997 citrobacter
41	1	2.6	4	1	OCF3_OCTMI	P58649 octopus min
42	1	2.6	5	1	UXA4_CHLTR	P38005 chlamydia t
43	1	2.6	6	1	LOK1_LOCOMI	P41491 locusta mig
44	0	0.0	3	1	GRWM_HUMAN	P01157 homo sapien
45	0	0.0	4	1	ACH1_ACHFU	P35904 achatina fu

ALIGNMENTS

RESULT 1
E101_LITRU
ID E101_LITRU STANDARD; PRT; 6 AA.
AC P82096;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Electrin 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
PP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella".
RL Aust. J. Chem. 52:639-645 (1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 6
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 34.2%; Score 13; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VPL 4
DB 2 VPI 4

RESULT 2
VP19_HSVIK
ID VP19_HSVIK STANDARD; PRT; 6 AA.
AC P23210;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Capsid assembly and DNA maturation protein (Virion protein UL38)
DE (Capsid protein VP19C) (Fragment).
GN UL38.
OS Herpes simplex virus (type 1 / strain KOS).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10306;
RN [1]
PP SEQUENCE FROM N.A.
RX MEDLINE=91101287; PubMed=1846198;
RA Flanagan W.M., Papavasiliou A.G., Rice M., Hecht L.B.,
RA Silverstein S., Wagner E.K.;
RT "Analysis of the herpes simplex virus type 1 promoter controlling the

RT expression of UL38, a true late gene involved in capsid assembly.";
RL J. Virol. 65:769-786(1991).
CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
CC EMBEDDED. BINDS DNA.
CC -!- SIMILARITY: Belongs to the herpesviruses VP19C family.
CC -----
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CC -----
DR EMBL: M57646; AAA45830.1; -;
KW Capsid assembly; Coat protein; DNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;

Query Match 28.9%; Score 11; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PL 4
|
|
|
Db 5 PL 6

RESULT 3
E103 LITRU
ID E103 LITRU STANDARD; PRT; 5 AA.
AC P82099;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Electrin 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella".
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 5
SQ SEQUENCE 5 AA; 630 MW; 568761F2C9A00000 CRC64;

Query Match 23.7%; Score 9; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PL 4
|
|
|
Db 4 PL 5

RESULT 4
C1P1 MYTED
ID C1P1 MYTED STANDARD; PRT; 6 AA.
AC P13736;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Contraction-inhibiting peptide I (MIP I).
OS Mytilus edulis (Blue mussel).

OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
OC Mytiloidae; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RC TISSUE=Pedal ganglion;
RX MEDLINE=88240357; PubMed=3377776;
RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
RT "Structures and actions of Mytilus inhibitory peptides.";
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -!- FUNCTION: Inhibitory action on contractions in several molluscan
CC muscles.
CC -!- SIMILARITY: TO MIP II.
DR PIR; A27696; A27696.
KW Hormone; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA; 637 MW; 72C9C68775B81000 CRC64;

Query Match 23.7%; Score 9; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PL 4
|
|
|
Db 3 PL 4

RESULT 5
C1P2 MYTED
ID C1P2 MYTED STANDARD; PRT; 6 AA.
AC P13737;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Contraction-inhibiting peptide II (MIP II).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
OC Mytiloidae; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RC TISSUE=Pedal ganglion;
RX MEDLINE=88240357; PubMed=3377776;
RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
RT "Structures and actions of Mytilus inhibitory peptides.";
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -!- FUNCTION: Inhibitory action on contractions in several molluscan
CC muscles.
CC -!- SIMILARITY: TO MIP I.
DR PIR; B27696; B27696.
KW Hormone; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;

Query Match 23.7%; Score 9; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PL 4
|
|
|
Db 3 PL 4

RESULT 6
PCT PERAM
ID PCT PERAM STANDARD; PRT; 5 AA.
AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach),
OS Limulus polyphemus (Atlantic horseshoe crab), and

OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978, 6850, 6759;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=76074708; PubMed=576;
 RA Starratt A.N., Brown B.E.;
 RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
 RT in insects";
 RL Life Sci. 17:1253-1256 (1975).
 RN [2]
 RP BIOLOGICAL SOURCE.
 RC SPECIES=P.americana;
 RX MEDLINE=81225865; PubMed=6113690;
 RA O'Shea M., Adams M.E.;
 RT "Pentapeptide (proctolin) associated with an identified neuron";
 RL Science 213:567-569 (1981).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=L.polyphemus;
 RX MEDLINE=90287800; PubMed=2356151;
 RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
 RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
 RA Shabanowitz J.;
 RT "Identification of proctolin in the central nervous system of the
 RT horseshoe crab, Limulus polyphemus";
 RL Peptides 11:205-211 (1990).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=C.maenas;
 RX MEDLINE=86232789; PubMed=2872661;
 RA Stangier J., Dirksen H., Keller R.;
 RT "Identification and immunocytochemical localization of proctolin in
 RT pericardial organs of the shore crab, Carcinus maenas";
 RL Peptides 7:67-72 (1986).
 CC -/- FUNCTION: Stimulates cardiac output and hindgut motility,
 CC modulates visceral and skeletal muscle in many arthropods.
 CC -/- TISSUE SPECIFICITY: Found in the lateral white neurons and in
 CC the crab pericardial organs.
 DR PIR; A01644; HOROHA.
 DR PIR; A60411; A60411.
 KW Neuropeptide.
 SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;
 Query Match 21.1%; Score 8; DB 1; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VP 3
 DB 3 LP 4
 RESULT 7
 ID TRPI_PSEPU STANDARD; PRT; 6 AA.
 AC P36414.
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE HTH-type transcriptional regulator trpi (TrpBA operon transcriptional
 DE activator) (fragment).
 GN TRPI.
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PPGI C15;

RX MEDLINE=99335826; PubMed=2503057;
 RA Eberly L., Crawford I.P.;
 RT "DNA sequence of the tryptophan synthase genes of Pseudomonas
 RT putida";
 RL Biochimie 71:521-531 (1989).
 CC -/- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING
 CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
 CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE
 CC TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
 CC -/- SIMILARITY: Contains 1 HTH lyase-type DNA-binding domain.
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 CC -----
 DR EMBL; X13299; CAA31660.1; --
 DR InterPro; IPR000847; HTH_LYSE.
 DR PROSITE; PS50931; HTH_LYSE; PARTIAL.
 KW Tryptophan biosynthesis; Transcription regulation; Activator;
 FT DNA-binding.
 FT NON_TER 6 6
 SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;
 Query Match 21.1%; Score 8; DB 1; Length 6;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VP 3
 DB 5 LP 6
 RESULT 8
 ID THYL_PIG STANDARD; PRT; 3 AA.
 AC F01151;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Thyroliberin (thyrotropin releasing hormone) (TRH) (Protirelin).
 OS Sus scrofa (Pig).
 OS Ovis aries (Sheep).
 OS Bombina orientalis (Oriental fire-bellied toad), and
 OS Neophthalmus viridescens (Eastern newt) (Triturus viridescens).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823, 9940, 8346, 8316;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Pig; TISSUE=Hypothalamus;
 RX MEDLINE=70136150; PubMed=4984938;
 RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
 RT "Structure of porcine thyrotropin releasing hormone";
 RL Biochemistry 9:1103-1106 (1970).
 RN [2]
 RP SYNTHESIS.
 RC SPECIES=Pig;
 RX MEDLINE=70039904; PubMed=4992117;
 RA Bolter J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
 RT "The identity of chemical and hormonal properties of the thyrotropin
 RT releasing hormone and pyroglutamyl-histidyl-proline amide";
 RL Biochem. Biophys. Res. Commun. 37:705-710 (1969).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=Sheep; TISSUE=Hypothalamus;
 RA Desiderio D.M. Jr., Burgus R., Dunn T.F., Vale W., Guillemin R.,
 RA Ward D.N.;
 RT "The elucidation of the primary structure of the hypothalamic thyroid
 RT stimulating hormone releasing factor of ovine origin by means of mass

RL spectrometry.";
 RL Org. Mass Spectrom. 5:221-228 (1971).
 RN [4]
 RP SYNTHESIS.
 RC SPECIES=Sheep;
 RX MEDLINE=70163396; PubMed=4985794;
 RA Burgess R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
 RA Guillemain R.;
 RT "Characterization of ovine hypothalamic hypophysiotropic
 RT TSH-releasing factor.";
 RL Nature 226:321-325 (1970).
 RN [5]
 RP SEQUENCE.
 RC SPECIES=B.orientalis; TISSUE=Skin;
 RX MEDLINE=76138399; PubMed=815011;
 RA Yasuhara T., Nakajima T.;
 RT "Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
 RL Chem. Pharm. Bull. 23:3301-3303 (1975).
 RN [6]
 RP SEQUENCE.
 RC SPECIES=N.viridescens;
 RX MEDLINE=75035605; PubMed=4214528;
 RA Grimm-Joergensen Y., McKelvy J.F.;
 RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus
 RT viridescens) brain in vitro. Isolation and characterization of
 RT thyrotropin releasing factor.";
 RL J. Neurochem. 23:471-478 (1974).
 CC -!- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH
 CC in the anterior pituitary gland and as a neurotransmitter/
 CC neuromodulator in the central and peripheral nervous systems.
 DR PIR; A90919; RHTOTO.
 DR PIR; A92971; A92971.
 DR PIR; A93750; RHSHF.
 KW Amidation; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 3 3 AMIDATION.
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;
 Query Match 18.4%; Score 7; DB 1; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 P 3
 Db 3 P 3

RESULT 9
 DCML PSECH
 ID DCML PSECH STANDARD; PRT; 4 AA.
 AC F19316;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
 DE dehydrogenase subunit L) (CO-DH L) (Fragment).
 GN CUTL.
 OS Pseudomonas carboxydohydrogena.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae.
 CX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydorophilic bacteria.";
 RL Arch. Microbiol. 152:335-341 (1989).
 CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 CC dioxide.
 CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 CC acceptor.
 CC -!- COFACTOR: Molybdenum (molybdopterin).

CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 DR PIR; F10140; F10140.
 KW Oxidoreductase; Molybdenum.
 FT NON TER 4 4
 SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;
 Query Match 18.4%; Score 7; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 P 3
 Db 4 P 4

RESULT 10
 RM01 YEAST
 ID RM01 YEAST STANDARD; PRT; 4 AA.
 AC P36515;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Mitochondrial 60S ribosomal protein L1 (Yml1) (Fragment).
 GN MRPL1.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91285106; PubMed=2060626;
 RA Grohmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.,
 RA Kitakawa M.;
 RT "Extended N-terminal sequencing of proteins of the large ribosomal
 RT subunit from yeast mitochondria.";
 RL FEBS Lett. 284:51-56 (1991).
 DR PIR; S17255; S17255.
 DR SGD; L0002681; MRPL1.
 KW Ribosomal protein; Mitochondrion.
 FT NON TER 4 4
 SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;
 Query Match 18.4%; Score 7; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 P 3
 Db 4 P 4

RESULT 11
 TUFT HUMAN
 ID TUFT HUMAN STANDARD; PRT; 4 AA.
 AC P01858;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Phagocytosis-stimulating peptide (Tuftsin).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72187087; PubMed=4112769;
 RA Nishioka K., Constantinopoulos A., Satoh P.S., Najjar V.A.;
 RT "The characteristics, isolation and synthesis of the phagocytosis
 RT stimulating peptide tuftsin.";
 RL Biochem. Biophys. Res. Commun. 47:172-179 (1972).
 RN [2]
 RP IMMUNOGLOBULIN CLASS.

RX MEDLINE=68091045; PubMed=4169272;
RA Fidalgo B.V., Najjar V.A.;
RT "The physiological role of the lymphoid system. VI. The stimulatory
RT effect of leucophilic gamma globulin (leucokinin) on the phagocytic
RT activity of human polymorphonuclear leucocyte.";
RL Biochemistry 6:3386-3392(1967).
CC -!- MISCELLANEOUS: An IgG (called leucokinin) binds reversibly to the
CC cell membrane of neutrophils in the blood. Leucokininase on the
CC membrane releases the active peptide tuftsin from the gamma chain.
CC Tuftsin is essential for maximum stimulation of the phagocytic
CC activity of neutrophils.
DR PIR; A02147; A02147.
DR MIN; 191150; -.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006909; P:phagocytosis; NAS.
SQ SEQUENCE 4 AA; 501 MW; 74176321C00000000 CRC64;

Query Match 18.4%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 P 3
DB 3 P 3

RESULT 12
BIOA_CITFR STANDARD; PRT; 5 AA.
ID P13071;
AC P13071;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
DE (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
DE aminotransferase) (Fragment).
GN BIOA.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
SQ SEQUENCE FROM N.A.
RX MEDLINE=89006280; PubMed=2971595;
RA Shivan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-diaminononanoate.
CC -!- COFACTOR: Pyridoxal phosphate.
CC -!- PATHWAY: Biotin biosynthesis.
CC -!- SUBUNIT: Homodimer.
CC -!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent aminotransferases.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC
DR ENBL; M21922; -; NOT_ANNOTATED CDS.
DR PIR; I40697; I40697.
DR InterPro; IPR005814; Aminotrans 3.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
KW Biotin biosynthesis; Transferase; Aminotransferase;
KW Pyridoxal phosphate. 5
FT NON_TER 5
SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 18.4%; Score 7; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 LT 5
DB 1 MT 2

RESULT 13
BPP7_BOTIN STANDARD; PRT; 5 AA.
ID BPP7_BOTIN
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5,2 (SA) (Angiotensin-converting enzyme inhibitor).
DE OS Bothrops insularis (Island jararaca) (Queimada Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
SQ SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it. It acts as an indirect hypotensive agent.
CC PIR; G37196; G37196.
DR Hypotensive agent; Pyrrolidone carboxylic acid.
KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 18.4%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 P 3
DB 5 P 5

RESULT 14
E104_LITRU STANDARD; PRT; 5 AA.
ID E104_LITRU
AC P82100;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Electrin 4.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hyliidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
SQ SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog Litoria electrica. Comparison with the skin peptides from Litoria rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.

KW Amphibian defense peptide; Amidation.
 FT MOD RES 5 5 AMIDATION.
 SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 18.4%; Score 7; DB 1; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 LT 5
 |
 Db 2 IT 3

RESULT 15
 PAP2 PARMA
 ID PAP2 PARMA STANDARD; PRT; 5 AA.
 AC P81864;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Pardaxin II (PXII) (Fragment).
 OS Pardachirus marmoratus (Red sea mores sole).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
 OC Soleiidae; Soleidae; Pardachirus.
 OK NCBI_TaxID=31087;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=87057369; PubMed=3782138;
 RA Lazarovici P., Primor N., Loew L.M.;
 RT "Purification and pore-forming activity of two hydrophobic
 RT polypeptides from the secretion of the Red sea mores sole (Pardachirus
 RT marmoratus).";
 RL J. Biol. Chem. 261:16704-16713 (1986).
 CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
 CC properties. Forms voltage-dependent, ion-permeable channels
 CC in membranes. At high concentration causes cell membrane lysis.
 CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the pardaxin family.
 KW Toxin.
 FT NON TER 5 5
 SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 18.4%; Score 7; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 P 3
 |
 Db 5 P 5

Search completed: March 8, 2004, 12:37:29
 Job time : 11 secs

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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:34:59 ; Search time 39 Seconds
(without alignments)

48.541 Million cell updates/sec

Title: US-09-761-636A-12
Perfect score: 38
Sequence: 1 CVPLTC 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 11

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	31.6	5	13 P83308	P83308 gallus gall
2	9	23.7	6	5 P83569	P83569 sepiia offic
3	5	13.2	5	2 P83073	P83073 bacillus ce
4	5	13.2	6	2 P83533	P83533 lactobacill
5	5	13.2	6	10 P82181	P82181 spinacia ol
6	5	13.2	6	10 P82541	P82541 spinacia ol
7	5	13.2	6	10 P82182	P82182 spinacia ol
8	4	10.5	4	5 P83568	P83568 sepiia offic
9	4	10.5	4	11 Q08433	Q08433 rattus sp.
10	2	5.3	5	10 Q99007	Q99007 hordeum vul
11	0	0.0	2	5 P83570	P83570 sepiia offic

ALIGNMENTS

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RESULT 1
P83308
ID P83308 PRELIMINARY; PRT; 5 AA.
AC P83308;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE FMRFamide-like neuropeptide (LPLRF-amide).
OS Gallus gallus (Chicken).
OC Archosauria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RX PubMed=6137771;
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
RT "A novel active pentapeptide from chicken brain identified by
RT antibodies to FMRFamide.";
RL Nature 305:328-330(1983).
CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO: GO:0007218; P-neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD RES 5 5
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 31.6%; Score 12; DB 13; Length 5;
Best Local Similarity 66.7%; Pred. No. 1e+06; 0; Indels 0; Gaps 0;
Matches 2; Conservative 1; Mismatches 0;

QY 2 VPL 4
DB 1 LPL 3

RESULT 2
P83569
ID P83569 PRELIMINARY; PRT; 6 AA.
AC P83569;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Sperm attracting peptide SepSAP.
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidae; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP SEQUENCE, FUNCTION, DEVELOPMENTAL STAGE, MASS SPECTROMETRY, AND
RP AMIDATION.
RC TISSUE=Egg;
RX PubMed=12207899;
RA Zatylny C., Marvin L., Gagnon J., Henry J.;
RT "Fertilization in Sepia officinalis: the first mollusk sperm-
RT attracting peptide.";
RL Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
CC -!- FUNCTION: ATTRACTS SPERM INCREASING THE CHANCES OF GAMETE
CC COLLISION.
CC -!- DEVELOPMENTAL STAGE: FIRST APPEARS IN THE OVARIAN FOLLICLES FIRING
CC VITELLOGENESIS. ACCUMULATES IN THE OOCYTES BEFORE BEING SECRETED
CC DURING FERTILIZATION. EXPRESSION CONTINUES IN THE EMBEDDED OOCYTE.
CC ACCUMULATES IN THE EGG CAPSULE AFTER FERTILIZATION.
CC -!- MASS SPECTROMETRY: MW=596.6; METHOD=MALDI.
KW Amidation.
FT MOD RES 6 6
SQ SEQUENCE 6 AA; 597 MW; 72C8676AA0470000 CRC64;

Query Match 23.7%; Score 9; DB 5; Length 6;
Best Local Similarity 50.0%; Pred. No. 1e+06; 0; Indels 0; Gaps 0;
Matches 1; Conservative 1; Mismatches 0;

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QY 3 PL 4
DB 1 PI 2

RESULT 3
P83073 PRELIMINARY; PRT; 5 AA.
ID P83073
AC STRAIN=cv. ALVARO; TISSUE=Leaf;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DE 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DE 88 kDa protein (Fragment)
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE.
RC STRAIN=NCIMB 11796;
RA Browne N., Dowds B.C.A.;
EL Submitted (JUL-2001) to Swiss-Prot.
FT NON TER 5
SQ SEQUENCE 5 AA; 623 MW; 6B01AA336F00000 CRC64;

Query Match 13.2%; Score 5; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 T 5
DB 4 T 4

RESULT 4
P83533 PRELIMINARY; PRT; 6 AA.
ID P83533
AC P83533;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DE 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Unknown protein from 2D-page (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 20451;
RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Georg A.;
RT "High pressure effects step-wise altered protein expression in
Lactobacillus sanfranciscensis."
RL Proteomics 2:765-774(2002).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN
CC PROTEIN IS: 15 KDA.
FT NON TER 1
FT NON TER 6
SQ SEQUENCE 6 AA; 590 MW; 6DDDD452D1AAC000 CRC64;

Query Match 13.2%; Score 5; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 T 5
DB 2 T 2

RESULT 5
P82181 PRELIMINARY; PRT; 6 AA.
ID P82181
AC P82181;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chloroplast 30S ribosomal protein L10 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. ALVARO; TISSUE=Leaf;
DE MEDLINE=20435798; PubMed=10874039;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
the small subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28455-28465(2000).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
CC -1- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
CC -1- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA
FORM IS THE MINOR BASIC FORM.
CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0019843; F:rRNA binding; IEA.

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DR GO: 00003735; F: structural constituent of ribosome; IEA.
 DR InterPro: IPR002222; Ribosomal S19.
 DR PROSITE: PS00323; RIBOSOMAL S19. PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON TER 6
 SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 13.2%; Score 5; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 T 5
 Db 1 T 1

RESULT 7

ID P82182 PRELIMINARY; PRT; 6 AA.
 AC P82182;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Amaranthaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.

RC STRAIN=cv. ALVARO; TISSUE=Leaf;
 RX MEDLINE=20435798; PubMed=10874046;
 RA Yamaguchi K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 the 50 S subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 275:28466-28482(2000).
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
 CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 DR GO: 00003507; C: chloroplast; IEA.
 DR GO: 0019843; F: rRNA binding; IEA.
 DR GO: 00003735; F: structural constituent of ribosome; IEA.
 DR InterPro: IPR002363; Ribosomal L10eub.
 DR PROSITE: PS01109; RIBOSOMAL L10. PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON TER 6
 SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 13.2%; Score 5; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 T 5
 Db 5 T 5

RESULT 8

ID P83568 PRELIMINARY; PRT; 4 AA.
 AC P83568;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Pheromone peptide IIME.
 OS Sepia officinalis (Common cuttlefish).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Decapodiformes; Sepioidae; Sepiidae; Sepia.
 OX NCBI_TaxID=6610;
 RN [1]

RP SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
 RP SPECTROMETRY.
 RC TISSUE=Egg;
 RX PubMed=10944467;
 RA Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;
 RT "IIME: a waterborne pheromonal peptide released by the eggs of Sepia
 officinalis.";
 RL Biochem. Biophys. Res. Commun. 275:217-222(2000).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Egg;
 RX PubMed=12207899;
 RA Zatylny C., Marvin L., Gagnon J., Henry J.;
 RT "Fertilization in Sepia officinalis: the first mollusk sperm-
 attracting peptide.";
 RL Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
 CC -!- FUNCTION: HAS MYOTROPIC ACTIVITY TARGETING THE GENITAL TRACT.
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- TISSUE SPECIFICITY: FOLLICLE, FULLY GROWN OOCYTE AND EGG(EC2).
 CC -!- MASS SPECTROMETRY: MW=505.4; METHOD=MALDI.
 DR GO: 00005186; F: pheromone activity; IEA.
 KW Pheromone.
 SQ SEQUENCE 4 AA; 505 MW; 6B16972030000000 CRC64;

Query Match 10.5%; Score 4; DB 5; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
 Db 2 L 2

RESULT 9

ID Q08433 PRELIMINARY; PRT; 4 AA.
 AC Q08433;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Bilirubin UDP-glucuronosyltransferase (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Gunn;
 RX MEDLINE=91282758; PubMed=1840486;
 RA Sato H., Aono S., Kashiwamata S., Koizumi O.;
 RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
 hyperbilirubinemic Gunn rat.";
 RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
 DR EMBL: S38636; AAB19259.1;
 DR GO: 0016740; F: transferase activity; IEA.
 KW Transferase.
 FT NON TER 1
 SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 10.5%; Score 4; DB 11; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 V 2
 Db 2 V 2

RESULT 10

ID Q99007 PRELIMINARY; PRT; 5 AA.
 AC Q99007;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Alpha amylase (Fragment).
 GN AMY1 GENE.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91329704; PubMed=1831055;
 RA Jacobsen J.V., Close T.J.;
 RT "Control of transient expression of chimaeric genes by gibberellic
 RT acid and abscisic acid in protoplasts prepared from mature barley
 RT aleurone layers.";
 RL Plant Mol. Biol. 16:713-721(1991).
 DR EMBL: X54643; CAA38455.1; -.
 FT NON TER 5
 SQ SEQUENCE 5 AA; 600 MW; 51E3344DD6F00000 CRC64;

 Query Match 5.3%; Score 2; DB 10; Length 5;
 Best Local Similarity 0.0%; Pred. No. 1e+06;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 4 L 4
 Db 1 M 1

 RESULT 11
 P83570 PRELIMINARY; PRT; 2 AA.
 AC P83570;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Neuropeptide Gwa.
 OS Sepia officinalis (Common cuttlefish).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Decapodiformes; Sepioidae; Sepiidae; Sepia.
 OX NCBI_TaxID=6610;
 RN [1]
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
 RC TISSUE=Optic lobe;
 RX PubMed=9437704;
 RA Henry J., Favrel P., Boucaud-Camou E.;
 RT "Isolation and identification of a novel Ala-Pro-Gly-Tyr-amide-related
 RT peptide inhibiting the motility of the mature oviduct in the
 RT cuttlefish, Sepia officinalis.";
 RL Peptides 18:1469-1474(1997).
 CC -!- FUNCTION: REGULATORY NEUROPEPTIDE WITH MYOTROPIC ACTIVITY
 CC TARGETING THE DISTAL OVIDUCT. INHIBITS THE MOTILITY OF THE OVIDUCT
 CC BY DECREASING TONUS, FREQUENCY AND AMPLITUDE OF CONTRACTIONS.
 CC -!- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
 KW Neuropeptide; Amidation.
 FT MOD RES 2 2
 SQ SEQUENCE 2 AA; 261 MW; 73781000000000000000 CRC64;

 Query Match 0.0%; Score 0; DB 5; Length 2;
 Best Local Similarity 0.0%; Pred. No. 1e+06;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 3 P 3
 Db 1 G 1

Search completed: March 8, 2004, 12:38:20
 Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:31:19 ; Search time 52 Seconds
(without alignments)
32.602 Million cell updates/sec

Title: US-09-761-636A-12

Perfect score: 38

Sequence: 1 CVPLTC 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 59163

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	38	100.0	6	4	AAU04531
2	26	68.4	6	3	AY61488
3	25	65.8	6	3	AY62223
4	25	65.8	6	3	AY62763
5	25	65.8	6	3	AY62006
6	24	63.2	6	3	AY64259
7	23	60.5	6	3	AY85373
8	23	60.5	6	3	AY62757
9	23	60.5	6	3	AY62488
10	23	60.5	6	3	AY44431
11	22	57.9	4	2	AA15772
12	22	57.9	4	2	AA49769
13	22	57.9	4	2	AA77833
14	22	57.9	4	2	AA04459
15	22	57.9	5	2	AAW67428
16	22	57.9	6	2	AAW31456
17	22	57.9	6	3	AY63235
18	22	57.9	6	3	AY61927
19	21	55.3	6	3	AY62132
20	21	55.3	6	3	AY63263
21	20	52.6	4	2	AA51652
22	20	52.6	5	2	AA508270
23	20	52.6	5	2	AA78749
24	20	52.6	5	3	AY169213
25	20	52.6	5	3	AY56095

26	20	52.6	5	3	AY68185
27	20	52.6	5	4	AA78351
28	20	52.6	5	5	ABB83467
29	20	52.6	5	5	AA017897
30	20	52.6	5	5	ABB77196
31	20	52.6	5	5	ABB77197
32	20	52.6	6	2	AAW08703
33	20	52.6	6	2	AAW95842
34	20	52.6	6	2	AAW11026
35	20	52.6	6	2	AAW44954
36	20	52.6	6	2	AAW51950
37	20	52.6	6	2	AAW03380
38	20	52.6	6	2	AAW9219
39	20	52.6	6	3	AAW23802
40	20	52.6	6	3	AY61733
41	20	52.6	6	4	AAW31387
42	20	52.6	6	5	ABB46600
43	20	52.6	6	5	ABB46920
44	19	50.0	4	2	AAW43270
45	19	50.0	5	2	AY29743

ALIGNMENTS

RESULT 1
AAU04531
ID AAU04531 standard; peptide; 6 AA.

XX AC AAU04531;

DT 26-SEP-2001 (first entry)

XX DE VEGF based monocyclic peptide 9.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
XX neovascularisation; lymphangiogenesis; psoriasis; tumour;
XX diabetes induced neovascular sequelae; rheumatoid arthritis;
XX diabetic retinopathy; chronic inflammation; cyclic.
XX Synthetic.

XX Key Location/Qualifiers

XX Disulfide-bond 1..6 /note= "This bond cyclises the peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

XX 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stackler S, Cendron A;

XX WPI, 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
XX from an exposed loop of a growth factor protein by oxidizing the cysteine
XX residues.

XX Claim 49; Page 32; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,
XX whose 3-dimensional structure is modelled on the expose loop of human
XX VEGF (vascular endothelial growth factor). The invention relates to a
XX method of producing a monomeric monocyclic peptide by a measuring beta-
XX beta carbon separation distances on opposite antiparallel strands of a

PF 05-MAY-1999; 99WO-CA000363.
 XX
 PR 05-MAY-1998; 98US-00073040.
 FR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-00234395.
 XX 08-MAR-1999; 99US-00264516.
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 PI Blaschuk OW, Gour BJ, Byers S;
 XX WPI; 2000-038791/03.
 XX New cadherin modulating agents, used for modulating nonclassical cadherin mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX Claim 54; Page 184; 252pp; English.
 XX The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-expressing cell, preventing or treating obesity in a mammal, stimulating blood vessel regression in a mammal, enhancing drug delivery to the central nervous system, treating a demyelinating neurological disease, increasing vasopermeability in a mammal, enhancing adhesion of nonclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating wound healing or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bioreactors. AAY60592 to AAY64572 represent specifically claimed peptides, and AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in the exemplification of the present invention.
 XX Sequence 6 AA;
 SQ
 Query Match 65.8%; Score 25; DB 3; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CVPLTC 6
 Db 1 CDPKTC 6
 RESULT 4
 AAY62763
 ID AAY62763 standard; peptide; 6 AA.
 XX
 AC AAY62763;
 XX
 DT 02-MAR-2000 (first entry)
 XX
 DE PB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:4046.
 XX
 KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.
 XX

OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..6
 XX
 PN WO9957149-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 05-MAY-1999; 99WO-CA000363.
 XX
 PR 05-MAY-1998; 98US-00073040.
 PR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-00234395.
 PR 08-MAR-1999; 99US-00264516.
 XX
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 PI Blaschuk OW, Gour BJ, Byers S;
 XX WPI; 2000-038791/03.
 XX New cadherin modulating agents, used for modulating nonclassical cadherin mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX Claim 72; Page 193; 252pp; English.
 XX The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-expressing cell, preventing or treating obesity in a mammal, stimulating blood vessel regression in a mammal, enhancing drug delivery to the central nervous system, treating a demyelinating neurological disease, increasing vasopermeability in a mammal, enhancing adhesion of nonclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating wound healing or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bioreactors. AAY60592 to AAY64572 represent specifically claimed peptides, and AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in the exemplification of the present invention.
 XX Sequence 6 AA;
 SQ
 Query Match 65.8%; Score 25; DB 3; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CVPLTC 6
 Db 1 CDPKTC 6
 RESULT 5
 AAY62006
 ID AAY62006 standard; peptide; 6 AA.
 XX
 AC AAY62006;
 XX
 DT 02-MAR-2000 (first entry)
 XX
 DE Cadherin-12 cell adhesion recognition cyclic peptide SEQ ID NO:1798.

us-09-761-636a-12.closed.rag

Mon Mar 8 13:10:44 2004

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW OB-cadherin; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin; protocadherin;
 KW cadherin related neuronal receptor; LI-cadherin; cancer; tumour; obesity;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.
 XX Synthetic.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Disulfide-bond 1..6
 FT WO9957149-A2.
 PN 11-NOV-1999.
 PD 05-MAY-1999; 99WO-CA000363.
 XX 05-MAY-1999; 98US-00073040.
 PR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-00234395.
 PR 08-MAR-1999; 99US-00264516.
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 PA Blaschuk OW, Gour BJ, Byers S;
 PI WPI; 2000-038791/03.
 XX New cadherin modulating agents, used for modulating nonclassical cadherin
 DR mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX Claim 48; Page 180; 252pp; English.
 PS The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MAs can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC mammal, enhancing delivery of a drug to a tumour in a mammal, inhibiting
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, stimulating
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing synaptic stability in
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
 CC the exemplification of the present invention
 XX Sequence 6 AA;
 SQ Query Match 65.8%; Score 25; DB 3; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 2; Indels 0;
 QY 1 CVPLTC 6
 Db 1 CDPKTC 6

RESULT 6
 ID AAY64259 standard; peptide; 6 AA.
 XX AAY64259;
 AC AAY64259;
 XX 02-MAR-2000 (first entry)
 DT Cadherin-related neuronal receptor CAR cyclic peptide SEQ ID NO:3573.
 XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW OB-cadherin; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin; protocadherin;
 KW cadherin related neuronal receptor; LI-cadherin; cancer; tumour; obesity;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.
 XX Synthetic.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Disulfide-bond 1..6
 FT WO9957149-A2.
 PN 11-NOV-1999.
 PD 05-MAY-1999; 99WO-CA000363.
 XX 05-MAY-1999; 98US-00073040.
 PR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-00234395.
 PR 08-MAR-1999; 99US-00264516.
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 PA Blaschuk OW, Gour BJ, Byers S;
 PI WPI; 2000-038791/03.
 XX New cadherin modulating agents, used for modulating nonclassical cadherin
 DR mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX Claim 102; Page 217; 252pp; English.
 PS The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MAs can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC mammal, enhancing delivery of a drug to a tumour in a mammal, inhibiting
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, stimulating
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing synaptic stability in
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
 CC the exemplification of the present invention
 XX

SQ Sequence 6 AA;

Query Match 63.2%; Score 24; DB 3; Length 6;
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 1; Indels 0;

QY 1 CVPLTC 6
 | : | | |
 DB 1 CDPWSC 6

RESULT 7

AAV85373
 ID AAY85373 standard; peptide; 6 AA.

XX AC AAY85373;

XX DT 19-JUN-2000 (first entry)

XX DE IL-2 derived anti-inflammatory peptide pep11.

XX KW Interleukin-2; IL-2; antiinflammatory; antiarthritic; antirheumatic;
 KW antidiabetic; neuroprotective; dermatological; immunosuppressive;
 KW ophthalmological; autoimmune disease; multiple sclerosis; uveitis;
 KW systemic lupus erythematosus; Crohn's disease.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO200011028-A2.

XX PD 02-MAR-2000.

XX PF 19-AUG-1999; 99WO-IL000448.

XX PR 21-AUG-1998; 98GB-00018370.

XX PR 31-AUG-1998; 98IL-00126009.

XX PR 16-MAY-1999; 99IL-00129980.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PI Lider O, Ariel A, Hershkoviz R, Yavin EJ, Fridkin M;

XX WPI; 2000-256367/22.

XX Synthetic antiinflammatory peptide derived from IL-2 and its derivatives
 useful for treating inflammatory autoimmune diseases such as rheumatoid
 arthritis, multiple sclerosis and systemic lupus erythematosus.

PS Claim 6; Page 35; 49pp; English.

XX The invention provides synthetic antiinflammatory peptides derived from
 interleukin-2 (IL-2). They can be used for inhibition of adhesion of
 activated T-cells to ECM proteins such as fibronectin, laminin, collagen
 type-IV; inhibition of chemotactic migration of T-cell through ECM
 proteins preferably fibronectin; inhibition of cytokine or mitogen
 induced T-cell proliferation; inhibition of spontaneous or induced,
 preferably TNF-alpha induced cytokine secretion (e.g.IL-8, IL-1beta) by
 stimulated T-cells and intestinal epithelial cells. The anti-inflammatory
 peptides and their derivatives are useful for preparing compositions for
 treating and/or alleviating chronic or acute inflammatory disorders and
 autoimmune diseases such as rheumatoid arthritis, diabetes type-1,
 multiple sclerosis, systemic lupus erythematosus, bowel inflammation,
 uveitis, and Crohn's disease. Sequences AAY85366-374 represent modified
 anti-inflammatory derivative peptides derived from the IL-2 derived anti-
 inflammatory peptide pep1 (AAY85363)

XX Sequence 6 AA;

Query Match 60.5%; Score 23; DB 3; Length 6;
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;

Matches 3; Conservative 1; Mismatches 2; Indels 0;
 Gaps 0;

QY 1 CVPLTC 6
 | : | | |
 DB 1 CIVLAC 6

RESULT 8

AAV62757
 ID AAY62757 standard; peptide; 6 AA.

XX AC AAY62757;

XX DT 02-MAR-2000 (first entry)

XX DE PB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:4040.

XX KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PS-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.

XX OS Synthetic.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX FT Disulfide-bond 1..5

XX PN WO9957149-A2.

XX PD 11-NOV-1999.

XX PF 05-MAY-1999; 99WO-CA000363.

XX PR 05-MAY-1998; 98US-00073040.

XX PR 06-NOV-1998; 98US-00187859.

XX PR 20-JAN-1999; 99US-00234395.

XX PR 08-MAR-1999; 99US-00264516.

XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.

XX PI Blaschuk OW, Gour BJ, Byers S;

XX WPI; 2000-038791/03.

XX New cadherin modulating agents, used for modulating nonclassical cadherin
 mediated functions for treating e.g. cancers, obesity, rheumatoid
 arthritis, multiple sclerosis, diabetes or a neurological disease.

PS Claim 72; Page 193; 252pp; English.

XX The present invention describes cadherin modulating agents (MA)
 comprising peptides which comprise a nonclassical cadherin cell adhesion
 recognition (CAR) sequence. The MAs can be used for modulating
 nonclassical cadherin-mediated functions. They can be used for e.g.
 inhibiting adhesion of nonclassical-cadherin expressing cells in a
 mammal, enhancing delivery of a drug through the skin of a mammal,
 enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 expressing cell, preventing or treating obesity in a mammal, stimulating
 blood vessel regression in a mammal, enhancing drug delivery to the
 central nervous system, treating a demyelinating neurological disease,
 increasing vasopermeability in a mammal, enhancing synaptic stability in
 nonclassical cadherin-expressing cells, inhibiting synaptic adhesion of
 a mammal, or preventing pregnancy in a mammal. They can also be used for
 e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 related macular degeneration, multiple sclerosis and diabetes. The
 products can also be used for detection and diagnosis and in bioreactors.

CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in
 CC the exemplification of the present invention

SQ Sequence 6 AA;

Query Match 60.5%; Score 23; DB 3; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
 | | | |
 DB 1 CDELTC 6

RESULT 9

AAV62488
 ID AAY62488 standard; peptide; 6 AA.

XX AC AAY62488;

DT 02-MAR-2000 (first entry)

DE Cadherin-15 cell adhesion recognition cyclic peptide SEQ ID NO:2154.

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Disulfide-bond 1..6

PN WO957149-A2.

XX 11-NOV-1999.

XX 05-MAY-1999; 99WO-CA000363.

XX 05-MAY-1998; 98US-00073040.

PR 06-NOV-1998; 98US-00187859.

PR 20-JAN-1999; 99US-00234395.

PR 08-MAR-1999; 99US-00264516.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Gour BJ, Byers S;

XX WPI; 2000-038791/03.

XX New cadherin modulating agents, used for modulating nonclassical cadherin
 PT mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.

XX Claim 60; Page 188; 252pp; English.

XX The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MA can be used for modulating cell
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin
 CC expressing cell, preventing or treating obesity in a mammal, stimulating

CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing synaptic stability in
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in
 CC the exemplification of the present invention

SQ Sequence 6 AA;

Query Match 60.5%; Score 23; DB 3; Length 6;

Best Local Similarity 66.7%; Pred. No. 1.4e+06;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
 | | | |
 DB 1 CDELTC 6

RESULT 10

AAV44431
 ID AAY44431 standard; peptide; 6 AA.

XX AC AAY44431;

XX 22-MAR-2000 (first entry)

DE Peptide 1 derived from domain 1 of human beta-2 glycoprotein I.

XX Human beta-2 glycoprotein I; beta-2 GPI; toleragen; B cell anergy;
 KW beta-2 GPI-dependent antiphospholipid antibody; thrombosis;
 KW recurrent foetal loss; thrombocytopenia; autoimmune disease;
 KW systemic lupus erythematosus; coagulation assay.

XX Homo sapiens.

XX WO9964595-A1.

XX 16-DEC-1999.

XX 09-JUN-1999; 99WO-US013194.

XX 09-JUN-1998; 98US-0089656P.

PR 05-OCT-1998; 98US-0103088P.

PR 08-JUN-1999; 99US-00328199.

XX (LJOL-) LA JOLLA PHARM CO.

XX Marquis DM, Iverson GM, Victoria EJ, Jones DS, Linnik MD;

XX WPI; 2000-116542/10.

XX New isolated domain 1 beta-2 GPI polypeptides, used for inhibiting
 PT antiphospholipid antibodies for treating, e.g. thrombosis.

XX Claim 3; Page 19; 158pp; English.

XX The present sequence is a peptide fragment derived from domain 1 of human
 CC beta-2 glycoprotein, a phospholipid binding serum protein. Isolated
 CC domain 1 of beta-2 GPI protein binds to and inhibits beta-2 GPI-dependent
 CC antiphospholipid antibodies. The fragments are useful as toleragens when
 CC they bind to the antibodies at the surface of a B cell and triggers B
 CC cell anergy. The polypeptides and mimetics can be used for treating
 CC disorders associated with beta 2GPI-dependent aPL-associated pathologies,
 CC e.g. thrombosis, recurrent foetal loss, thrombocytopenia or autoimmune
 CC disease such as systemic lupus erythematosus. The polypeptides can also
 CC be used to detect and purify antibodies. They can also be used in

CC coagulation assays
XX
SQ Sequence 6 AA;

Query Match 60.5%; Score 23; DB 3; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVPLTC 6
| | | |
Db 1 CTPRCV 6

RESULT 11
AAR15772
ID AAR15772 standard; protein; 4 AA.

AC AAR15772;
XX 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 29-JAN-1992 (first entry)
XX Farnesyl-protein transferase inhibitor (25).
DE Farnesyl; transferase; FT; inhibitor; p21ras; rat.
XX
XX Synthetic.
OS
XX WO9116340-A.
PN
XX 31-OCT-1991.
PD

XX 18-APR-1990; 90US-00510706.
XX 18-APR-1990; 90US-00510706.
PR 20-NOV-1990; 90US-00615715.
XX (TEXA) UNIV TEXAS SYSTEM.
FA
XX Brown MS, Goldstein JL, Reiss Y;
PI WPI; 1991-339750/46.
DR

XX Compon. comprising purified farnesyl-protein transferase - used to
PT inhibit attachment of farnesyl moiety to RAS protein in malignant cells
PT and to treat cancer.
PT
XX Claim 25; Page 68; 87pp; English.

XX This peptide or the peptides represented in AAR15751-81, AAR14723 and
CC AAR14711 inhibit the rat FTs represented in AAR14712-22. They show FT
CC inhibition at an IC50 of 0.01-10 microm. The most potent inhibitors are
CC ones in which phenylalanine occurs at the third position of a
CC tetrapeptide whose N-terminus is cysteine. The inhibitors have a farnesyl
CC acceptor or inhibitor sequence within its structure and are capable of
CC inhibiting the farnesylation of p21ras by FT. See also AAR14711-23 and
CC AAR14541-47. (Updated on 09-JAN-2003 to add missing OS field.) (Updated
CC on 25-MAR-2003 to correct PA field.)

XX Sequence 4 AA;

Query Match 57.9%; Score 22; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPL 4
| | | |
Db 1 CVPM 4

RESULT 12
AAR49769

ID AAR49769 standard; peptide; 4 AA.

XX
AC AAR49769;
XX 25-MAR-2003 (revised)
DT 08-AUG-1994 (first entry)
XX Farnesyltransferase-inhibitor.

XX Farnesyltransferase-inhibitor; farnesyltransferase; FT; p21ras;
KW ras protein; farnesylation; cancer therapy.

XX Synthetic.

XX WO9404561-A1.

XX 03-MAR-1994.

XX 24-AUG-1993; 93WO-US008062.

XX 24-AUG-1992; 92US-00935087.

XX (TEXA) UNIV TEXAS SYSTEM.

XX (GETH) GENENTECH INC.

XX Brown MS, Goldstein JL, Reiss Y, Marsters JC;
PI WPI; 1994-083105/10.

XX New farnesyl-transferase inhibitors - used for inhibiting attachment of a
PT farnesyl moiety to a p21ras protein in malignant cells.

XX Disclosure; Page 33; 183pp; English.

XX Peptides given in AAR49741-75, AAR49777-78 and AAR49785-88, which include
CC a family of tetrapeptides based on the recognition site (AAR49776) of
CC farnesyltransferase (FT), are potential anticancer agents that inhibit
CC FT, thereby preventing expression of p21ras. (Updated on 25-MAR-2003 to
CC correct PN field.)

XX Sequence 4 AA;

Query Match 57.9%; Score 22; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPL 4
| | | |
Db 1 CVPM 4

RESULT 13
AAR77833
ID AAR77833 standard; protein; 4 AA.

XX AAR77833;

XX 25-MAR-2003 (revised)

DT 23-JAN-1996 (first entry)

XX Farnesyl transferase inhibitor tetrapeptide, CVPM.

XX Farnesyl transferase; inhibitor; cancer; ras; p21.

XX Synthetic.

XX US5420245-A.

XX 30-MAY-1995.

XX 03-APR-1992; 92US-00863169.

XX 18-APR-1990; 90US-00510706.

PR 20-NOV-1990; 90US-00615715.
 XX 16-JAN-1992; 92US-00822011.
 XX (TEXA) UNIV TEXAS.
 PA Reiss Y, Goldstein JL, Brown MS;
 PI WPI; 1995-206308/27.
 XX
 DR New farnesyl transferase inhibitor peptide(s) - based on farnesyl
 XX acceptor substrate carboxy terminal sequences, used for the treatment of
 PT cancer.
 PT
 XX
 PS Claim 2; Col 62; 55pp; English.
 XX
 XX AAR77800, AAR77805-R77838 are tetrapeptide inhibitors of farnesyl
 CC transferase. They all obey a generic formula for the C-terminal sequence
 CC of 4-10 amino acid inhibitory peptides; the formula is -CMA_x, where C=
 CC cysteine, A= any aliphatic, aromatic or hydroxy amino acid and X= any
 CC normal amino acid. Farnesyl transferase is involved in the farnesylation
 CC of various cellular proteins including the cancer related ras proteins.
 CC The transforming activity of ras is dependent on the localisation of the
 CC protein to membranes, a property which is thought to be dependent upon
 CC the addition of farnesyl groups. The peptide inhibitors are useful for
 CC treating cancers and ras-related cancers in particular. (Updated on 25-
 CC MAR-2003 to correct PF field.)
 XX
 XX Sequence 4 AA;
 SQ
 Query Match 57.9%; Score 22; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CVPL 4
 DB 1 CVPM 4
 |||
 RESULT 14
 AAW04459
 ID AAW04459 standard; peptide; 4 AA.
 XX
 AC AAW04459;
 XX
 DT 30-JUL-1997 (first entry)
 XX
 DE Farnesyl transferase peptide inhibitor used in cancer treatment.
 XX
 XX Farnesyl transferase; inhibitor; cancer; tumour; neoplasia; prenyl;
 KW ras protein; K-ras B; malignant; detection; identification.
 XX
 OS Synthetic.
 XX
 XX WO9634113-A2.
 PN
 XX 31-OCT-1996.
 PD
 XX 29-APR-1996; 96WO-US005969.
 PF
 XX 27-APR-1995; 95US-00429964.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Brown MS, Goldstein JL, James GL;
 PI WPI; 1996-497642/49.
 DR
 XX Assay for farnesyl transferase activity - by determining ability to
 PT transfer farnesyl moiety to K-Ras B protein, partic. useful for
 PT identifying inhibitors.
 XX
 PS Disclosure; Page 34; 257pp; English.
 XX

CC AAW04433-W04465 are peptide inhibitors of farnesyl transferase (FT)
 CC activity. The peptides block the attachment of prenyl groups to ras
 CC proteins in malignant cells of patients suffering from cancer or a
 CC precancerous state and as such are used to treat cancer. The peptides
 CC were identified by determining the ability of candidate substances to
 CC inhibit a FT enzyme, by inhibiting the transfer of a farnesyl moiety to a
 CC K-RasB protein
 XX
 XX Sequence 4 AA;
 SQ
 Query Match 57.9%; Score 22; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CVPL 4
 DB 1 CVPM 4
 |||
 RESULT 15
 AAW67428
 ID AAW67428 standard; peptide; 5 AA.
 XX
 AC AAW67428;
 XX
 DT 02-MAR-1999 (first entry)
 XX
 DE HCV peptide analogue #2.
 XX
 XX Hepatitis C virus; HCV; nucleocapsid; core protein; analogue; antibody;
 KW non-structural protein; thioamide bond; peptide bond.
 XX
 OS Synthetic.
 OS Hepatitis C virus.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "side chain protected by butyl group"
 FT Modified-site 2 /note= "side chain protected by tosyl group"
 FT Disulfide-bond 5 /note= "side chain protected by benzoyl group and C-
 FT terminus protected by benzyl group"
 XX
 XX JPI0226698-A.
 PN
 XX 25-AUG-1998.
 PD
 XX 19-FEB-1997; 97JP-00034702.
 PF
 XX 19-FEB-1997; 97JP-00034702.
 PR
 XX (KYOW) KYOWA MEDEX KK.
 PA
 XX WPI; 1998-515103/44.
 DR
 XX Determination of antibody in sample - uses peptide analog absorbed or
 PT chemically bound on carrier as antigen.
 PT
 XX Example 1; Page 9; 13pp; Japanese.
 PS
 XX This sequence represents an analogue peptide of the Hepatitis C virus
 CC (HCV) nucleocapsid core protein. The invention relates to peptide
 CC analogues derived from HCV proteins, e.g. AAW67417-W67426, which can be
 CC used for the determination of anti-HCV antibodies in a sample. Preferably
 CC the peptide analogues contain one or more thioamide peptide bonds where
 CC at least one oxygen atom of the peptide bond is replaced by sulphur atom.
 CC The peptide analogues can be adsorbed or chemically bound to a carrier
 XX
 XX Sequence 5 AA;
 SQ
 Query Match 57.9%; Score 22; DB 2; Length 5;
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPILT 5
| | | |
Db 1 CREILT 5

Search completed: March 8, 2004, 12:37:06
Job time : 53 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:38:25 ; Search time 33 Seconds
(without alignments)
38.392 Million cell updates/sec

Title: US-09-761-636A-12

Perfect score: 38

Sequence: 1 CVPLTC 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 21259

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubaa/US07_PUBCOMB.pep.*
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- 3: /cgn2_6/ptodata/2/pubaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubaa/US06_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/2/pubaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	100.0	6	9	US-09-761-636A-12
2	26	68.4	6	14	US-10-006-869-1374
3	26	68.4	6	15	US-10-395-032-1374
4	25	65.8	6	14	US-10-006-869-1798
5	25	65.8	6	14	US-10-006-869-3970
6	25	65.8	6	14	US-10-006-869-4046
7	25	65.8	6	15	US-10-395-032-1798
8	25	65.8	6	15	US-10-395-032-3970
9	25	65.8	6	15	US-10-395-032-4046
10	24	63.2	6	14	US-10-006-869-3573
11	24	63.2	6	15	US-10-395-032-3573
12	23	60.5	6	14	US-10-006-869-2154
13	23	60.5	6	14	US-10-006-869-4040
14	23	60.5	6	15	US-10-395-032-2154
15	23	60.5	6	15	US-10-395-032-4040

16	22	57.9	4	14	US-10-083-894-35	Sequence 35, Appl
17	22	57.9	6	11	US-09-943-944B-103	Sequence 103, App
18	22	57.9	6	14	US-10-006-869-1737	Sequence 1737, Ap
19	22	57.9	6	14	US-10-006-869-2719	Sequence 2719, Ap
20	22	57.9	6	15	US-10-395-032-1737	Sequence 1737, Ap
21	22	57.9	6	15	US-10-395-032-2719	Sequence 2719, Ap
22	21	55.3	6	9	US-09-911-838-184	Sequence 184, App
23	21	55.3	6	9	US-09-911-838-186	Sequence 186, App
24	21	55.3	6	10	US-09-792-286-222	Sequence 222, App
25	21	55.3	6	10	US-09-792-286-226	Sequence 226, App
26	21	55.3	6	10	US-09-792-286-278	Sequence 278, App
27	21	55.3	6	14	US-10-006-869-1885	Sequence 1885, Ap
28	21	55.3	6	14	US-10-006-869-2747	Sequence 2747, Ap
29	21	55.3	6	14	US-10-058-513-9	Sequence 9, Appli
30	21	55.3	6	15	US-10-395-032-1885	Sequence 1885, Ap
31	21	55.3	6	15	US-10-395-032-2747	Sequence 2747, Ap
32	20	52.6	5	10	US-09-753-139C-8	Sequence 8, Appli
33	20	52.6	6	9	US-09-911-838-90	Sequence 90, Appl
34	20	52.6	6	9	US-09-911-838-92	Sequence 92, Appl
35	20	52.6	6	9	US-09-911-838-94	Sequence 94, Appl
36	20	52.6	6	9	US-09-911-838-96	Sequence 96, Appl
37	20	52.6	6	14	US-10-006-869-1591	Sequence 1591, Ap
38	20	52.6	6	14	US-10-271-343-52	Sequence 52, Appl
39	20	52.6	6	14	US-10-436-826-50	Sequence 50, Appl
40	20	52.6	6	14	US-10-277-292-697	Sequence 697, App
41	20	52.6	6	15	US-10-280-340-697	Sequence 697, App
42	20	52.6	6	15	US-10-395-032-1591	Sequence 1591, Ap
43	19	50.0	6	9	US-09-234-395-124	Sequence 124, App
44	19	50.0	6	9	US-09-234-395-210	Sequence 210, App
45	19	50.0	6	9	US-09-305-928-124	Sequence 124, App

ALIGNMENTS

RESULT 1
US-09-761-636A-12
; Sequence 12, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09761.636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-12

Query Match 100.0%; Score 38; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 1 CVPLTC 6

RESULT 2
US-10-006-869-1374
; Sequence 1374, Application US/10006869
; Publication No. US20030082166A1


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; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1374
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-10-006-869-1374

Query Match 68.4%; Score 26; DB 14; Length 6;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
DB 1 CEPKTC 6

RESULT 3
US-10-395-032-1374
; Sequence 1374, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1374
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-10-395-032-1374

Query Match 68.4%; Score 26; DB 15; Length 6;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
DB 1 CEPKTC 6

RESULT 4
US-10-006-869-1798
; Sequence 1798, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1374
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-10-006-869-1798

Query Match 65.8%; Score 25; DB 14; Length 6;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
DB 1 CEPKTC 6

RESULT 5
US-10-006-869-3970
; Sequence 3970, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3970
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence
US-10-006-869-3970

Query Match 65.8%; Score 25; DB 14; Length 6;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
DB 1 CEPKTC 6

RESULT 6
US-10-006-869-4046
; Sequence 4046, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4046
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence
US-10-006-869-4046

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Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CVPLTC 6
Db 1 CDPKTC 6

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-10-006-869-4046

Query Match 65.8%; Score 25; DB 14; Length 6;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CVPLTC 6
Db 1 CDPKTC 6

Query Match 65.8%; Score 25; DB 14; Length 6;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CVPLTC 6
Db 1 CDPKTC 6

RESULT 9
US-10-395-032-4046
; Sequence 4046, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4046
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-10-395-032-4046

RESULT 7
US-10-395-032-1798
; Sequence 1798, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1798
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
US-10-395-032-1798

Query Match 65.8%; Score 25; DB 15; Length 6;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CVPLTC 6
Db 1 CDPKTC 6

Query Match 65.8%; Score 25; DB 15; Length 6;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CVPLTC 6
Db 1 CDPKTC 6

RESULT 10
US-10-006-869-3573
; Sequence 3573, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3573
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-10-006-869-3573

RESULT 8
US-10-395-032-3970
; Sequence 3970, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3970
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence
US-10-395-032-3970

Query Match 63.2%; Score 24; DB 14; Length 6;
Best Local Similarity 50.0%; Pred. No. 7.2e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CVPLTC 6
Db 1 CDPKTC 6

Query Match 65.8%; Score 25; DB 15; Length 6;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CVPLTC 6
Db 1 CDPKTC 6

US-10-006-869-3573
; Sequence 3573, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3573
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-10-006-869-3573

US-10-395-032-1798
; Sequence 1798, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1798
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
US-10-395-032-1798

Query Match 65.8%; Score 25; DB 15; Length 6;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CVPLTC 6
Db 1 CDPKTC 6

Query Match 65.8%; Score 25; DB 15; Length 6;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CVPLTC 6
Db 1 CDPKTC 6

RESULT 11

US-10-395-032-3573
; Sequence 3573, Application US/10395032
; Publication No. US20030229199A1

GENERAL INFORMATION:

; APPLICANT: Symonds, James Matthew
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3573
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-10-395-032-3573

Query Match 63.2%; Score 24; DB 15; Length 6;

Best Local Similarity 50.0%; Pred. No. 7.2e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTC 6

Db 1 CDPVSC 6

RESULT 12

US-10-006-869-2154
; Sequence 2154, Application US/10006869
; Publication No. US20030082166A1

GENERAL INFORMATION:

; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2154
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-15 cell adhesion recognition sequence
US-10-006-869-2154

Query Match 60.5%; Score 23; DB 14; Length 6;

Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6

Db 1 CDELTC 6

RESULT 13

US-10-006-869-4040
; Sequence 4040, Application US/10006869
; Publication No. US20030082166A1

GENERAL INFORMATION:

; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4040
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-10-006-869-4040

Query Match 60.5%; Score 23; DB 14; Length 6;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6

Db 1 CDELTC 6

RESULT 14

US-10-395-032-2154
; Sequence 2154, Application US/10395032
; Publication No. US20030229199A1

GENERAL INFORMATION:

; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2154
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-15 cell adhesion recognition sequence
US-10-395-032-2154

Query Match 60.5%; Score 23; DB 15; Length 6;

Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6

Db 1 CDELTC 6

RESULT 15

US-10-395-032-4040
; Sequence 4040, Application US/10395032
; Publication No. US20030229199A1

GENERAL INFORMATION:

; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C9

Mon Mar 8 13:10:44 2004

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; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4040
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-10-395-032-4040

Query Match      60.5%; Score 23; DB 15; Length 6;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CVELTC 6
      | | | |
Db      1 CDELTC 6

Search completed: March 8, 2004, 12:43:38
Job time : 33 secs
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Mon Mar 8 13:10:37 2004

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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:16:07 ; Search time 15.5 Seconds
(without alignments)
29.976 Million cell updates/sec

Title: US-09-761-636A-10

Perfect score: 50

Sequence: 1 CSVPPLTVC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 89883

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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6: /cgn2_6/ptodata/2/iaa/6D_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	52.0	9	4	US-09-760-599-34
2	25	50.0	9	3	US-09-258-754-199
3	25	50.0	9	3	US-09-042-107-199
4	25	50.0	9	4	US-09-187-859-3614
5	25	50.0	9	4	US-09-839-542B-3614
6	25	50.0	9	4	US-09-722-250D-199
7	25	50.0	9	4	US-09-760-599-25
8	25	50.0	9	4	US-09-483-550B-25
9	24	48.0	6	1	US-08-483-434A-21
10	24	48.0	6	3	US-08-476-134A-30
11	24	48.0	6	6	5190920-26
12	24	48.0	6	6	5506208-28
13	24	48.0	9	1	US-07-958-903A-43
14	24	48.0	9	1	US-08-462-018-43
15	24	48.0	9	1	US-08-823-245-43
16	24	48.0	9	2	US-08-598-873-49
17	24	48.0	9	3	US-08-605-430-49
18	24	48.0	9	4	US-07-963-329A-43
19	24	48.0	9	4	US-09-760-599-9
20	24	48.0	9	4	US-09-760-599-17
21	24	48.0	9	4	US-09-760-599-36
22	24	48.0	9	4	US-09-760-599-38
23	24	48.0	9	4	US-09-760-599-48
24	24	48.0	9	4	US-09-483-550B-9
25	24	48.0	9	4	US-09-483-550B-17
26	24	48.0	9	5	PCT-US92-09443A-43
27	23	46.0	8	4	US-08-475-955-67

28	23	45.0	9	1	US-08-195-075-4
29	23	46.0	9	1	US-08-467-083-3
30	23	46.0	9	1	US-08-414-417B-3
31	23	46.0	9	2	US-08-486-348A-3
32	23	46.0	9	2	US-08-468-545B-3
33	23	46.0	9	2	US-08-986-234-80
34	23	46.0	9	3	US-08-466-680B-3
35	23	46.0	9	3	US-09-258-754-146
36	23	46.0	9	3	US-09-258-754-308
37	23	46.0	9	3	US-09-139-802-92
38	23	46.0	9	3	US-08-660-082-122
39	23	46.0	9	3	US-09-042-107-146
40	23	46.0	9	3	US-09-042-107-308
41	23	46.0	9	4	US-09-160-513-122
42	23	46.0	9	4	US-09-659-786-92
43	23	46.0	9	4	US-08-403-459-25
44	23	46.0	9	4	US-08-926-914-92
45	23	46.0	9	4	US-09-722-250D-146

ALIGNMENTS

RESULT 1
US-09-760-599-34
; Sequence 34, Application US/09760599
; Patent No. 6630447
; GENERAL INFORMATION:
; APPLICANT: Larson Mr., Richard S.
; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CDM-1 Interaction
; FILE REFERENCE: SCI200/4-1CIP
; CURRENT APPLICATION NUMBER: US/09/760,599
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-760-599-34

Query Match 52.0%; Score 26; DB 4; Length 9;
Best Local Similarity 33.3%; Pred. No. 3e+05;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY	1	CSVPPLTVC 9
DB	1	CALMRMSIC 9

RESULT 2
US-09-258-754-199
; Sequence 199, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Ruoslahti, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence

Mon Mar 8 13:10:37 2004

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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-199

Query Match          50.0%; Score 25; DB 3; Length 9;
Best Local Similarity 55.6%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 4; Gaps 0;

QY 1 CSVPLTSVC 9
|||
Db 1 CSAVTTSPC 9

RESULT 3
US-09-042-107-199
; Sequence 199, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-199

Query Match          50.0%; Score 25; DB 3; Length 9;
Best Local Similarity 55.6%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 4; Gaps 0;

QY 1 CSVPLTSVC 9
|||
Db 1 CSAVTTSPC 9

RESULT 4
US-09-187-859-3614
; Sequence 3614, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3614
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
OTHER INFORMATION: recognition sequence
OTHER INFORMATION:
US-09-187-859-3614

Query Match          50.0%; Score 25; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

QY 1 CSVPLTSVC 9
|||
Db 1 CSAVTTSPC 9

RESULT 5
US-09-839-542B-3614
; Sequence 3614, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3614
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
OTHER INFORMATION: recognition sequence
OTHER INFORMATION:
US-09-839-542B-3614

Query Match          50.0%; Score 25; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

QY 1 CSVPLTSVC 9
|||
Db 1 CTFHDSVC 9

RESULT 6
US-09-722-250D-199
; Sequence 199, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-199

Query Match          50.0%; Score 25; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

QY 1 CSVPLTSVC 9
|||
Db 1 CSAVTTSPC 9

RESULT 7
US-09-760-599-25

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us-09-761-636a-10.closed.rai

Mon Mar 8 13:10:37 2004

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; Sequence 25, Application US/09760599
; Patent No. 6630447
; GENERAL INFORMATION:
; APPLICANT: Larson Mr., Richard S.
; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
; FILE REFERENCE: SCI200/4-1CIP
; CURRENT APPLICATION NUMBER: US/09/760,599
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-760-599-25

Query Match          50.0%; Score 25; DB 4; Length 9;
Best Local Similarity 33.3%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
Db 1 CMLRMNSIC 9

RESULT 8
US-09-483-550B-25
; Sequence 25, Application US/09483550B
; Patent No. 6649592
; GENERAL INFORMATION:
; APPLICANT: Larson Mr., Richard S.
; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
; FILE REFERENCE: SCI200/4-001
; CURRENT APPLICATION NUMBER: US/09/483,550B
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-483-550B-25

Query Match          50.0%; Score 25; DB 4; Length 9;
Best Local Similarity 33.3%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
Db 1 CMLRMNSIC 9

RESULT 9
US-08-483-434A-21
; Sequence 21, Application US/08483434A
; Patent No. 5648461
; GENERAL INFORMATION:
; APPLICANT: EVAL, Jacob
; APPLICANT: HAMILTON, Bruce K.
; APPLICANT: TUSZYNSKI, George P.
; TITLE OF INVENTION: Synthetic Analogs of Thrombospondin and
; TITLE OF INVENTION: Therapeutic Use Thereof
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA

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; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,434A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/450,738
; FILING DATE: 25-MAY-1995
; APPLICATION NUMBER: US 08/185,614
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: US 08/024,436
; FILING DATE: 01-MAR-1993
; APPLICATION NUMBER: US 07/587,197
; FILING DATE: 24-SEP-1990
; APPLICATION DATA: US 07/483,527
; APPLICATION NUMBER: 22-FEB-1990
; FILING DATE: 22-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9598-306 (9049)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 567-2020
; TELEFAX: (215) 567-2891
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-483-434A-21

Query Match          48.0%; Score 24; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSVP 4
Db 1 CSVP 4

RESULT 10
US-08-476-134A-30
; Sequence 30, Application US/08476134A
; Patent No. 6239110
; GENERAL INFORMATION:
; APPLICANT: EVAL, JACOB
; APPLICANT: HAMILTON, BRUCE K.
; APPLICANT: TUSZYNSKI, GEORGE P.
; TITLE OF INVENTION: SYNTHETIC ANALOGS OF THROMBOSPONDIN AND THERAPEUTIC USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 07206-0009
; CURRENT APPLICATION NUMBER: US/08/476,134A
; CURRENT FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/587,197
; PRIOR FILING DATE: 1990-09-24
; PRIOR APPLICATION NUMBER: 07/483,527
; PRIOR FILING DATE: 1990-02-22
; PRIOR APPLICATION NUMBER: 08/450,738
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/185,614
; PRIOR FILING DATE: 1994-01-24
; PRIOR APPLICATION NUMBER: 08/024,436

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us-09-761-636a-10.closed.ra1

Mon Mar 8 13:10:37 2004

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; PRIOR FILING DATE: 1993-03-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: analog of thrombospondin
US-08-476-134A-30

Query Match
Best Local Similarity 48.0%; Score 24; DB 3; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSVP 4
Db 1 CSVP 4

RESULT 11
5190920-26
; PATENT NO. 5190920
; APPLICANT: EYAL, JACOB; HAMILTON, BRUCE K.; TUSZYNSKI,
; GEORGE P.
; TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS
; OF THROMBOSPONDIN FOR INHIBITING METASTASIS ACTIVITY
; NUMBER OF SEQUENCES: 32
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/587,197
; FILING DATE: 24-SEP-1990
; SEQ ID NO: 26:
; LENGTH: 6
5190920-26

Query Match
Best Local Similarity 100.0%; Score 24; DB 6; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSVP 4
Db 1 CSVP 4

RESULT 12
5506208-28
; PATENT NO. 5506208
; APPLICANT: EYAL, JACOB; HAMILTON, BRUCE K.; TUSZYNSKI,
; GEORGE P.
; TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS OF
; THROMBOSPONDIN FOR INHIBITING ANGIOGENESIS ACTIVITY
; NUMBER OF SEQUENCES: 45
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,181
; FILING DATE: 22-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 131,565
; FILING DATE: 04-OCT-1993
; APPLICATION NUMBER: 895,764
; FILING DATE: 09-JUN-1992
; APPLICATION NUMBER: 587,197
; FILING DATE: 24-SEP-1990
; SEQ ID NO: 28:
; LENGTH: 6
5506208-28

Query Match
Best Local Similarity 100.0%; Score 24; DB 6; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSVP 4
Db 1 CSVP 4

RESULT 13
US-07-958-903A-43
; SEQUENCE 43, APPLICATION US/07958903A
; PATENT NO. 5652214
; GENERAL INFORMATION:
; APPLICANT: Lewis, Michael E.
; APPLICANT: Kauer, James C.
; APPLICANT: Smith, Kevin R.
; APPLICANT: Callison, Kathleen V.
; APPLICANT: Baldino, Frank
; APPLICANT: Neff, Nicola
; APPLICANT: Iqbal, Mohamed
; TITLE OF INVENTION: TREATING DISORDERS BY APPLICATION
; TITLE OF INVENTION: OF INSULIN-LIKE GROWTH FACTORS AND
; ANALOGS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/958,903A
; FILING DATE: October 7, 1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/361,595
; FILING DATE: June 5, 1989
; APPLICATION NUMBER: 07/534,139
; FILING DATE: June 5, 1990
; APPLICATION NUMBER: 07/869,913
; FILING DATE: April 15, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 02655/003004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-07-958-903A-43

Query Match
Best Local Similarity 48.0%; Score 24; DB 1; Length 9;
Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CSVP/TSVC 9
Db 1 CCTPAKSEC 9

RESULT 14
US-08-462-018-43
; SEQUENCE 43, APPLICATION US/08462018
; PATENT NO. 5703045
; GENERAL INFORMATION:
; APPLICANT: Lewis, Michael E.

```


us-09-761-636a-10.closed.ra1

Mon Mar 8 13:10:37 2004

APPLICANT: Kauer, James C.
 APPLICANT: Smith, Kevin R.
 APPLICANT: Callison, Kathleen V.
 APPLICANT: Baldino, Frank
 APPLICANT: Neff, Nicola
 APPLICANT: Iqbal, Mohamed
 TITLE OF INVENTION: TREATING DISORDERS BY APPLICATION
 TITLE OF INVENTION: OF INSULIN-LIKE GROWTH FACTORS AND
 TITLE OF INVENTION: ANALOGS
 NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM PS/2 Model 50Z or 55SX
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/462,018
 FILING DATE: 1992

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/958,903
 FILING DATE: October 7, 1992
 APPLICATION NUMBER: 07/361,595
 FILING DATE: June 5, 1989
 APPLICATION NUMBER: 07/534,139
 FILING DATE: June 5, 1990
 APPLICATION NUMBER: 07/869,913
 FILING DATE: April 15, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 02655/003005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLOGY: linear

US-08-462-018-43
 Query Match 48.0%; Score 24; DB 1; Length 9;
 Best Local Similarity 44.4%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
 Db 1 CCTPAKSEC 9

RESULT 15

US-08-823-245-43
 ; Sequence 43, Application US/08823245
 ; Patent No. 5776897
 ; GENERAL INFORMATION:
 ; APPLICANT: Lewis, Michael
 ; APPLICANT: Kauer, James C.
 ; APPLICANT: Smith, Kevin R.
 ; APPLICANT: Callison, Kathleen V.
 ; APPLICANT: Baldino, Frank
 ; APPLICANT: Neff, Nicola
 ; APPLICANT: Iqbal, Mohamed
 ; TITLE OF INVENTION: TREATING DISORDERS BY

TITLE OF INVENTION: APPLICATION
 TITLE OF INVENTION: OF INSULIN-LIKE GROWTH
 TITLE OF INVENTION: FACTORS AND
 TITLE OF INVENTION: ANALOGS
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM PS/2 Model 50Z or
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/823,245
 FILING DATE: March 24, 1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/361,595
 FILING DATE: June 6, 1989
 APPLICATION NUMBER: 07/534,139
 FILING DATE: June 5, 1990
 APPLICATION NUMBER: 07/869,913
 FILING DATE: April 15, 1992
 APPLICATION NUMBER: 07/958,903
 FILING DATE: October 7, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Creeson, Gary L.

REGISTRATION NUMBER: 34,310
 REFERENCE/DOCKET NUMBER: 02655/003008
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9
 TYPE: amino acid
 STRANDEDNESS: N/A
 TOPOLOGY: N/A
 US-08-823-245-43

Query Match 48.0%; Score 24; DB 1; Length 9;
 Best Local Similarity 44.4%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
 Db 1 CCTPAKSEC 9

Search completed: March 8, 2004, 12:21:08
 Job time : 15.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model
Run on: March 8, 2004, 12:27:23 ; Search time 20 Seconds
(without alignments)
33.667 Million cell updates/sec

Title: US-09-761-636A-11

Perfect score: 42

Sequence: 1 CVP LTRSC 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0*

Maximum Match 100*

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	20	47.6	5	2 B22565	R-phycoerythrin al
2	15	35.7	6	2 H48394	glycoprotein compo
3	15	35.7	6	2 I63546	MHC H2-L antigen -
4	15	35.7	7	2 B34818	vicilin 57K chain
5	15	35.7	7	2 A34026	acetylcholinestera
6	14	33.3	5	2 E60274	major protein anti
7	13	31.0	7	2 S42620	aggregran - bovine
8	12	28.6	6	2 C22565	R-phycoerythrin be
9	12	28.6	6	2 I67345	MHC H2-K-k cell su
10	12	28.6	7	2 S08606	hypothetical prote
11	11	26.2	4	2 A32039	tyrosine-melanocyt
12	11	26.2	4	2 I54357	schwannomin - mous
13	11	26.2	5	2 A60521	glycogen phosphory
14	11	26.2	6	2 I49421	laminin B1 - weste
15	11	26.2	7	2 E61491	seed protein ws-5
16	11	26.2	7	2 I48105	dihydrofolate redu
17	11	26.2	7	2 I48086	DNA topoisomerase
18	10	23.8	5	2 F22565	R-phycoerythrin ga
19	10	23.8	6	2 I37263	Y protein - human
20	10	23.8	7	2 E0MUCR	catch-relaxing pep
21	10	23.8	7	2 A61081	trypthophyllin, bas
22	10	23.8	7	2 S38516	mablin II chain
23	10	23.8	7	2 PT0087	ribulose-bisphosph
24	10	23.8	7	2 A28340	myomodulin - Calif
25	10	23.8	7	2 E30608	Ig kappa chain V-I
26	10	23.8	7	4 I56695	hypothetical L2 pr
27	10	23.8	7	4 A58725	virotaxin - destro
28	9	21.4	3	3 A22565	R-phycoerythrin al
29	9	21.4	4	2 I51049	metallothionein-A

Ig mu chain V regi
pallidipin - assas
cadmium-binding pe
acid proteinase li
actin I - malaria
hemoglobin, extrac
phosphoprotein, bo
34.5K structural p
34.5K structural p
35K structural pro
halo-toxin - Pseud
lipopeptide WS1279
angiotensin-conver
dihydrofolate redu
contraction-inhibi

ALIGNMENTS

RESULT 1

B22565
R-phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: B22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601; PMID:3886644
A:Accession: B22565
A:Molecule type: protein
A:Residues: 1-5 <KLO>

Query Match 47.6%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVP 3
Db 2 CVP 4

RESULT 2

H48394
glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C:Accession: H48394
R:Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-F
II-like sequences.
A:Reference number: A48394; MUID:93250576; PMID:8485470
A:Accession: H48394
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-6 <WAT>
A:Experimental source: milk
A>Note: sequence extracted from NCBI backbone (NCBIP:131518)
C:Keywords: glycoprotein

Query Match 35.7%; Score 15; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 VPLTSC 7
Db 1 VELLCC 6

RESULT 3

E60274 major protein antigen MP763 - Mycobacterium tuberculosis (fragment)
C:Species: Mycobacterium tuberculosis
C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C:Accession: E60274
R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A:Title: Isolation and partial characterization of major protein antigens in the culture
A:Reference number: A60274; PMID:9109989; PMID:1898899
A:Accession: E60274
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <NAG>

Query Match 33.3%; Score 14; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PLT 5
|:|
DB 3 PIT 5

RESULT 7
S42620
aggrecan - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
C:Accession: S42620
R:Vogel, K.G.; Sandy, J.D.; Pogany, G.; Robbins, J.R.
Matrix Biol. 14, 171-179, 1994
A:Title: Aggrecan in bovine tendon.
A:Reference number: S42620; PMID:94340214; PMID:7520336
A:Accession: S42620
A:Molecule type: protein
A:Residues: 1-7 <VOG>
A:Experimental source: flexor tendon
C:Keywords: cartilage

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Query Match          31.0%; Score 13; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 PLTS 6
      | |
Db      2 PIVS 5

RESULT 8
C22565
R-phycoerythrin beta-1 chain - red alga (Gastrocloonium coulteri) (fragment)
C-Species: Gastrocloonium coulteri
C-Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C-Accession: C22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A-Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A-Reference number: A22565; MUID:85182601; PMID:3886644
A-Accession: C22565
A-Molecule type: protein
A-Residues: 1-6 <KLO>

Query Match          28.6%; Score 12; DB 2; Length 6;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 2; Wismatches 1; Indels 0; Gaps 0;

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QY	4 LTSC 7
	: :
Db	1 MAAC 4
RESULT 9	
I67345	

MHC H2-K-k cell surface glycoprotein - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C:Accession: I67345
 R:Archibald, A.L.; Thompson, N.A.; Kvist, S.
 EMBL J. 5, 957-965, 1986
 A>Title: A single nucleotide difference at the 3' end of an intron causes differential splicing of the MHC H2-K-k gene
 A:Reference number: I53243; MUID:86247587; PMID:3013627
 A:Accession: I67345
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-6 <RES>
 A:Cross-references: GB:M26859; NID:G199439; PIDN:AAA39612.1; PID:G387458
 C:Genetics: 6/1
 C:Keywords: glycoprotein

Query Match 28.6%; Score 12; DB 2; Length 6;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 LTSC 7
 DB 1 LPDC 4

RESULT 10
 S08606
 hypothetical protein 2 estrogen receptor 5'-region - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 18-Aug-2000
 C:Accession: S08606
 R:Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, J.M.; Chambon, P.
 EMBL J. 5, 891-897, 1986
 A>Title: The chicken oestrogen receptor sequence: homology with v-erbA and the human oestrogen receptor
 A:Reference number: S07192; MUID:86247578; PMID:3755102
 A:Accession: S08606
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-7 <KKU>
 A:Cross-references: EMBL:X03805; NID:G63378; PIDN:CAA27432.1; PID:G584490
 C:Superfamily: unassigned leader peptides

Query Match 28.6%; Score 12; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 LTSC 7
 DB 3 LAHC 6

RESULT 11
 A32039
 tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
 C:Accession: A32039
 R:Horvath, A.; Kastin, A.J.
 J. Biol. Chem. 264, 2175-2179, 1989
 A>Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor
 A:Reference number: A32039; MUID:89123285; PMID:2563371
 A:Accession: A32039
 A:Molecule type: protein
 A:Residues: 1-4 <HOR>
 A:Experimental source: brain
 C:Superfamily: unassigned animal peptides
 C:Keywords: amidated carboxyl end
 F:4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 26.2%; Score 11; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PL 4
 DB 2 PL 3

RESULT 12
 I54357
 schwannomin - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C:Accession: I54357
 R:Hyunh, D.P.; Nechiporuk, T.; Pulat, S.
 Hum. Mol. Genet. 3, 1075-1079, 1994
 A>Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are
 A:Reference number: I54357; MUID:95072570; PMID:7981675
 A:Accession: I54357
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-4 <RES>
 A:Cross-references: GB:L28938; NID:G454836; PIDN:AAA57150.1; PID:G601923
 C:Genetics:
 A:Gene: NF2

Query Match 26.2%; Score 11; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VP 3
 DB 1 VP 2

RESULT 13
 A60521
 glycogen phosphorylase (BC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
 N:Alternate names: glycogen phosphorylase b
 C:Species: Liza ramada
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003
 C:Accession: A60521
 R:Bonamusa, L.; Baanante, I.V.
 Comp. Biochem. Physiol. B 95, 295-301, 1990
 A>Title: Purification and characterization of glycogen phosphorylase B from skeletal muscle
 A:Reference number: A60521; MUID:90227907; PMID:2109669
 A:Accession: A60521
 A:Molecule type: protein
 A:Residues: 1-5 <BON>
 C:Superfamily: glucan phosphorylase
 C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
 F:3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experimental

Query Match 26.2%; Score 11; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VP 3
 DB 4 VP 5

RESULT 14
 I49421
 laminin B1 - western wild mouse (fragment)
 C:Species: Mus spretus (western wild mouse)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: I49421
 R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maeraki, Y.; Nadeau, J.
 Mamm. Genome 5, 349-355, 1994
 A>Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
 A:Reference number: I48934; MUID:94319082; PMID:8043949
 A:Accession: I49421
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

us-09-761-636a-11.closed.rpr

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A;Residues: 1-6 <RES>
A;Cross-references: EMBL:U05736; NID:9497073; PIDN:AB60477.1; PID:g642829

Query Match 26.2%; Score 11; DB 2; Length 6;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TSC 7
Db 3 STC 5

RESULT 15

E61491
seed protein ws-5 - winged bean (fragment)
C;Species: Psophocarpus tetragonolobus (winged bean)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C;Accession: E61491
R;Hirano, H.
J. Protein Chem. 8, 115-130, 1989
A;Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dimensional gel electrophoresis
A;Reference number: A61491; MUID:89351606; PMID:2765119
A;Accession: E61491
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <HR>
C;Keywords: glycoprotein; seed

Query Match 26.2%; Score 11; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VP 3
Db 3 VP 4

Search completed: March 8, 2004, 12:31:15
Job time : 20 secs

Mon Mar 8 13:10:42 2004

us-09-761-636a-11.closed.rsp

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:21:13 ; Search time 11 Seconds
(without alignments)
33.136 Million cell updates/sec

Title: US-09-761-636A-11

Perfect score: 42

Sequence: 1 CVPLTSC 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 88

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	31.0	6	E101_LITRU	P82096 litoria rub
2	11	26.2	6	VLP19_HSVIK	P23210 herpes simp
3	11	26.2	7	MNEP1_LEPDE	P42984 leptinotars
4	11	26.2	7	TPFY_PACDA	P83455 pachymedusa
5	10	23.8	7	CARP_MYTED	P10420 mytilus edu
6	10	23.8	7	TVS1_LITRU	P82065 litoria rub
7	9	21.4	5	E103_LITRU	P82099 litoria rub
8	9	21.4	6	C1P1_MYTED	P13736 mytilus edu
9	9	21.4	6	C1P2_MYTED	P13737 mytilus edu
10	9	21.4	7	BRHP_CONIM	P58803 conus imper
11	8	19.0	5	B10A_CITFR	P13071 citrobacter
12	8	19.0	5	PRCT_PERAM	P01373 periplaneta
13	8	19.0	6	TRP1_PSEPU	P36414 pseudomonas
14	8	19.0	7	C1A_ENTFA	P11932 enterococcu
15	8	19.0	7	UNO6_PINFS	P81675 pinus pinas
16	7	16.7	3	THYL_PIG	P01151 sus scrofa
17	7	16.7	4	DCML_PSECH	P19916 pseudomonas
18	7	16.7	4	RM01_YEAST	P36515 saccharomyc
19	7	16.7	4	TUFT_HUMAN	P81858 homo sapien
20	7	16.7	5	BPP7_BOTIN	P30425 bothrops in
21	7	16.7	5	E104_LITRU	P82100 litoria rub
22	7	16.7	5	PAP2_PARMA	P81864 pardachirus
23	7	16.7	5	SUGA_ACHDO	P19991 acheta dome
24	7	16.7	6	OVN_LEPDE	P42985 leptinotars
25	7	16.7	6	TMOF_SARBU	P41495 sarcophaga
26	7	16.7	7	ALL3_CARMA	P81806 carcinus ma
27	7	16.7	7	ALL4_CARMA	P81807 carcinus ma
28	7	16.7	7	ALL5_CARMA	P81808 carcinus ma
29	7	16.7	7	CCF1_ENTFA	P20104 enterococcu
30	7	16.7	7	CHOX_ALCSP	P16101 alcaligenes
31	7	16.7	7	E105_LITRU	P82101 litoria rub
32	7	16.7	7	FAR1_HELTI	P41871 helisoma tr
33	7	16.7	7	FAR4_PANRE	P41875 panagrellus

34 7 16.7 7 1 FARB_CALVO
35 7 16.7 7 1 GFRP_MOUSE
36 7 16.7 7 1 LANC_CARUI
37 7 16.7 7 1 UF04_MOUSE
38 6 14.3 7 1 UN06_CLOPA
39 6 14.3 7 1 UC24_MAIZE
40 5 11.9 5 1 B10B_CITFR
41 5 11.9 5 1 PSK_DAUCA
42 5 11.9 5 1 RE31_LITRU
43 5 11.9 5 1 RE32_LITRU
44 5 11.9 6 1 LOK1_LOCOMI
45 5 11.9 7 1 IGAO_DACDE

ALIGNMENTS

RESULT 1
E101_LITRU STANDARD; PRT; 6 AA.
ID E101_LITRU
AC P82096;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Electrin 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wamnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
Litori electrica. Comparison with the skin peptides from Litoria
rubella".
RL Aust. J. Chem. 52:639-645 (1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 6
FT SEQUENCE 6 AA; 792 NW; 6683704772C9A000 CRC64;
Query Match 31.0%; Score 13; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VPL 4
DB 2 VPI 4

RESULT 2
VLP19_HSVIK STANDARD; PRT; 6 AA.
ID VLP19_HSVIK
AC P23210;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Capsid assembly and DNA maturation protein (Virion protein UL38)
DE (Capsid protein VP19C) (Fragment).
DE UL38
OS Herpes simplex virus (type 1 / strain KOS).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91101287; PubMed=1846198;
RA Flanagan W.M., Papavasiliou A.G., Rice M., Hecht L.B.,
RA Silverstein S., Wagner E.K.;
RT "Analysis of the herpes simplex virus type 1 promoter controlling the

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RT expression of UL39, a true late gene involved in capsid assembly. ";
RL J. Virol. 65:769-786(1991).
CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSID ARE
CC EMBEDDED. BINDS DNA.
CC -!- SIMILARITY: Belongs to the herpesviruses VP19C family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M57646; AAA5830.1; -.
DR Capsid assembly; Coat protein; DNA-binding.
KW NON_TER 6
FT SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;
SQ
Query Match 26.2%; Score 11; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PL 4
DB 5 PL 6
RESULT 3
MNP1_LEPDE STANDARD; PRT; 7 AA.
AC P42984;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE Myotropic neuropeptide 1 (Led-MNP-1).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cuculiformia;
OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
OC Chrysomelini; Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX TISSUE=Head;
RA Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
RA Grauwels L., van Leuven F., de Loof A.;
RT "Identification, characterization, and immunological localization of
RT a novel myotropic neuropeptide in the Colorado potato beetle,
RT Leptinotarsa decemlineata."
RL Peptides 16:363-374(1995).
CC -!- FUNCTION: Myotropic peptide. Stimulates the contractions of the
CC oviduct.
KW Neuropeptide; Amidation.
FT MOD_RES 7
FT SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;
SQ
Query Match 26.2%; Score 11; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PL 4
DB 5 PL 6
RESULT 4
TFYF_PACDA STANDARD; PRT; 7 AA.
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

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DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin-1 (Pdt-1).
OS Pachymedusa dactinolor (Giant mexican leaf frog).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylinae;
OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
RP PRO-7.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Shaw C.;
RA "Pachymedusa dactinolor tryptophyllin-1 (Pdt-1): structural
RT characterization, pharmacological activity and cloning of precursor
RT cDNA."
RL Submitted (SEP-2002) to Swiss-Prot.
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
CC smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0045986; P:negative regulation of smooth muscle contra. .; NAS.
KW Amphibian defense peptide; Amidation; Hydroxylation.
FT MOD_RES 3
FT SEQUENCE 7 AA; 794 MW; 7772D37DC776350 CRC64;
SQ
Query Match 26.2%; Score 11; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VP 3
DB 6 VP 7
RESULT 5
CARP_MYTED STANDARD; PRT; 7 AA.
ID CARP_MYTED
AC P10420;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Catch-relaxing peptide (CARP).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RX MEDLINE=88052022; PubMed=3676797;
RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
RA Muneoka Y.;
RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia."
RL Brain Res. 422:374-376(1987).
CC -!- FUNCTION: This peptide exhibits both potentiating (contraction)
CC and inhibitory (relaxation) effects on the anterior bysaeus
CC retractor muscle.
DR PIR; A29342; ECMUCK.
KW Hormone; Amidation.
FT MOD_RES 7
FT SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;
SQ
Query Match 23.8%; Score 10; DB 1; Length 7;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 VPL 4
DB 2 MPW 4

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RESULT 6
TY51_LITRU
ID TY51_LITRU STANDARD; PRT; 7 AA.
AC P82065;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Trypophyllin 5.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: May act as a neuromodulator or neurotransmitter.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -1- MASS SPECTROMETRY: MW=965; METHOD=MS.
KW Amphibian defense peptide; Amidation; Neuropeptide;
KW Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;

Query Match 23.8%; Score 10; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VP 3
DB 2 IP 3

RESULT 7
EI03_LITRU
ID EI03_LITRU STANDARD; PRT; 5 AA.
AC P82093;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Electrin 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria rubella. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 5 5 AMIDATION.
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 21.4%; Score 9; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PL 4

RESULT 8
CIP1_MYTED
ID CIP1_MYTED STANDARD; PRT; 6 AA.
AC P13736;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Contraction-inhibiting peptide I (MIP I).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RC TISSUE=Pedal ganglion;
RX MEDLINE=88240357; PubMed=3377776;
RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
RT "Structures and actions of Mytilus inhibitory peptides.";
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -1- FUNCTION: Inhibitory action on contractions in several molluscan
CC muscles.
CC -1- SIMILARITY: TO MIP II.
KW PIR; A27696; A27696.
DR Hormone; Amidation.
FT MOD RES 6 6 AMIDATION.
SQ SEQUENCE 6 AA; 637 MW; 72C9C68775B81000 CRC64;

Query Match 21.4%; Score 9; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PL 4
DB 3 PM 4

RESULT 9
CIP2_MYTED
ID CIP2_MYTED STANDARD; PRT; 6 AA.
AC P13737;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Contraction-inhibiting peptide II (MIP II).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RC TISSUE=Pedal ganglion;
RX MEDLINE=88240357; PubMed=3377776;
RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
RT "Structures and actions of Mytilus inhibitory peptides.";
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -1- FUNCTION: Inhibitory action on contractions in several molluscan
CC muscles.
CC -1- SIMILARITY: TO MIP I.
KW PIR; B27696; B27696.
DR Hormone; Amidation.
FT MOD RES 6 6 AMIDATION.
SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;

Query Match 21.4%; Score 9; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PL 4
DB 3 PM 4

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Db          3 PM 4

RESULT 10
BRHP CONTM          STANDARD;          PRT;          7 AA.
AC P58803;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bromheptapeptide Im.
OS Conus imperialis (Imperial cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=35631;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom.
RX MEDLINE=97184108; PubMed=9030520;
RA Craig A.G., Jimenez E.C., Dykert J., Nielsen D.B., Gulyas J.,
RA Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M.,
RA McIntosh J.M.;
RT "A novel post-translational modification involving bromination of
RT tryptophan. Identification of the residue, L-6-bromotryptophan, in
RT peptides from Conus imperialis and Conus radiatus venom.";
RL J. Biol. Chem. 272:4689-4698(1997).
CC -1- FUNCTION: Does not elicit gross behavioral symptoms when injected
CC centrally or peripherally in mice.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=853.19; METHOD=LSIMS.
DR PIR; A58512; A58512.
KW Bromination; Amidation; Pyrrolidone carboxylic acid.
FT DISULFID 2 7
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 6 6 BROMINATION.
FT MOD RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 795 MW; 6EA37DC6D87EA6B0 CRC64;

Query Match 21.4%; Score 9; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 2 C 2

RESULT 11
BIOA_CITFR          STANDARD;          PRT;          5 AA.
AC P13071;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
DE (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
DE aminotransferase) (Fragment).
GN BIOA.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89006280; PubMed=2971595;
RA Shivan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-

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CC diamononanoate.
CC -1- COFACTOR: Pyridoxal phosphate.
CC -1- PATHWAY: Biotin biosynthesis.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
CC aminotransferases.
CC -----
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CC -----
CC EMBL; W21922; -; NOT ANNOTATED_CDS.
DR PIR; I40697; I40697.
DR InterPro; IPR005814; Aminotrans_3.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
KW Biotin biosynthesis; Transferase; Aminotransferase;
KW Pyridoxal phosphate. 5
FT NON_TER 5
SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 19.0%; Score 8; DB 1; Length 5;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTS 6
Db 1 MTT 3

RESULT 12
PRCT PERAM          STANDARD;          PRT;          5 AA.
AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach), and
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 6850, 6759;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=76074708; PubMed=576;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RT in insects.";
RL Life Sci. 17:1253-1256(1975).
RN [2]
RP BIOLOGICAL SOURCE.
RC SPECIES=P.americana;
RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RN [3]
RP SEQUENCE.
RC SPECIES=L.polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
RT horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211(1990).

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RN [4]
RP SEQUENCE.
RC SPECIES=C.maenas; PubMed=2872661;
RA MEDLINE=86232789;
RX Stangier J., Dircksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
RL pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72(1986).
CC -!- FUNCTION: Stimulates cardiac output and hindgut motility.
CC modulates visceral and skeletal muscle in many arthropods.
CC -!- TISSUE SPECIFICITY: Found in the lateral white neurons and in
CC the crab pericardial organs.
DR PIR; A01644; HOROHA.
DR PIR; A60411; A60411.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 19.0%; Score 8; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VP 3
Db :
3 LP 4

RESULT 13
TRPI_PSEFU STANDARD; PRT; 6 AA.
AC P36414;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE HTH-type transcriptional regulator trpi (TrpBA operon transcriptional
DE activator) (Fragment).
GN TRPI.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=PPG1 C15;
RX MEDLINE=89335826; PubMed=2503057;
RA Eberly L., Crawford I.P.;
RT "DNA sequence of the tryptophan synthase genes of Pseudomonas
RL putida.";
RL Biochimie 71:521-531(1999).
CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING
CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE
CC TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
CC -!- SIMILARITY: Contains 1 HTH lyser-type DNA-binding domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; X13299; CAA31660.1;
DR InterPro; IPR000847; HTH Lyser.
DR PROSITE; PS0931; HTH LYSER; PARTIAL.
KW Tryptophan biosynthesis; transcription regulation; Activator;
KW DNA-binding.
FT NON TER 6
SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;

Query Match 19.0%; Score 8; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 2 VP 3
Db :
5 LP 6

RESULT 14
CIA_ENTFA STANDARD; PRT; 7 AA.
AC P11932;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CAM373 (Clumping-inducing agent) (CIA).
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
[1]
RN SEQUENCE.
RP MEDLINE=87005252; PubMed=3093276;
RA Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
RA White B.A., An F.Y., Clewell D.B., Suzuki A.;
RT "Isolation and structure of the Streptococcus faecalis sex pheromone,
RL CAM373.";
RL FEBS Lett. 206:69-72(1986).
CC -!- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
CC HARBORING PAM373.
CC -!- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR
CC SPECIFICITY OF PHEROMONES TO PLASMIDS.
CC -!- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
DR PIR; A25269; A25269.
KW Pheromone.
SQ SEQUENCE 7 AA; 734 MW; 75BDD72059C05DE80 CRC64;

Query Match 19.0%; Score 8; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTS 6
Db :
5 LAS 7

RESULT 15
UN06_PINFs STANDARD; PRT; 7 AA.
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 20-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
[1]
RN SEQUENCE.
RP TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RL proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.6, its MW is: 25 kDa.
FT NON TER 1
FT NON TER 7
SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 19.0%; Score 8; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 2 VP 3
Db : 1
5 LP 6

Search completed: March 8, 2004, 12:29:51
Job time : 12 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model
Run on: March 8, 2004, 12:26:58 ; Search time 39 Seconds
(without alignments)
56.631 Million cell updates/sec

Title: US-09-761-636A-11
Perfect score: 42
Sequence: 1 CVPLTSC 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 74

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL 25:*
- 1: sp_arChaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phase:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_arChaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	40.5	7	12	Q66113
2	15	35.7	7	13	O42564
3	12	28.6	5	13	P83308
4	12	28.6	7	12	Q67113
5	11	26.2	7	4	Q8NH7
6	11	26.2	7	8	Q8MFY6
7	11	26.2	7	10	P93233
8	10	23.8	7	2	P70804
9	10	23.8	7	2	P72081
10	10	23.8	7	2	Q8GL12
11	10	23.8	7	10	Q9C5B3
12	10	23.8	7	15	Q07624
13	9	21.4	6	5	P83569
14	9	21.4	7	2	O50556
15	9	21.4	7	2	Q54248
16	9	21.4	7	11	O55184

Q9YVE3 human adeno
Q9YI99 human adeno
Q9YI90 human adeno
Q8J120 gallus gall
O63668 rattus norv
Q47029 enterobacte
O34028 sphingomona
P83530 lactobacill
P83492 bionectria
Q721C0 caenorhabdi
P92214 amblyoppyrum
P92393 hordeum vul
P92403 loptopyrum
P92427 peridictyon
P92430 aegilops ta
P92221 bromus iner
O98866 spinacia ol
P92425 pseudoroegn
P92381 hordeum bra
P92387 henardia p
P92210 agropyron c
P92440 thynopyrum
P92218 australopyr
P92390 heteranthel
P92372 haynaldia v
P92442 taenitheru
P92226 crithopsis
P92385 hordeum mar
P92421 paathyrosta

ALIGNMENTS

RESULT 1

Q66113 ID Q66113 PRELIMINARY; PRT; 7 AA.
AC O66113;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE C-terminus of the viral replicase (Fragment).
OS Cherry leaf roll virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
OC Nepovirus.
OX NCBI_TaxID=12615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Walnut;
RA Borja M.;
RL Thesis (1992), Biologia Molecular y Virologia Vegetal, CIT-INTA.
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=Walnut;
RX MEDLINE=96124520; PubMed=8560786;
RA Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;
RT "Long, nearly identical untranslated sequences at the 3' terminal regions of the genomic RNAs of cherry leafroll virus (walnut strain).";
RT Virus Genes 10:245-252 (1995).
DR EMBL; Z34265; CAA84019.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 800 MW; 7417672EBDC6D740 CRC64;

Query Match 40.58; Score 17; DB 12; Length 7;
Best Local Similarity 66.77; Pred. No. 1e+06; Indels 0; Gaps 0;
Matches 2; Conservative 1; Mismatches 0

QY 1 CVP 3
DB 4 CLP 6

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RESULT 2
O42564 PRELIMINARY; PRT; 7 AA.
AC O42564;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
GN SCN8A.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97442476; PubMed=9295353;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
RT two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97673; AAB80916.1; -.
DR GO; GO:0005216; P:ion channel activity; IEA.
KW Ionic channel.
FT NON TER 1
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 35.7%; Score 15; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VPL 4
DB 1 VPL 3

RESULT 3
P83308 PRELIMINARY; PRT; 5 AA.
AC P83308;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE FMRFamide-like neuropeptide (LPLRF-amide).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE. AND SYNTHESIS.
RC TISSUE=Brain;
RX PubMed=613771;
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
RT "A novel active pentapeptide from chicken brain identified by
RT antibodies to FMRFamide.";
RL Nature 305:328-330(1983).
CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD RES 5
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 28.6%; Score 12; DB 13; Length 5;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VPL 4
DB 1 LPL 3

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RESULT 4
Q67113 PRELIMINARY; PRT; 7 AA.
AC Q67113;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Influenza virus type A (Udorn/72) hemagglutinin (Seg 4) cDNA, 3' end
DE (Fragment).
OS Influenzavirus A.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses.
OX NCBI_TaxID=197911;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81001892; PubMed=7407922;
RA Dhar R., Chanock R.M., Lai C.-J.;
RT "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza
RT viral mRNA deduced from cloned complete genomic sequences.";
RL Cell 21:495-500(1980).
DR EMBL; M25045; AAA43202.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;

Query Match 28.6%; Score 12; DB 12; Length 7;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CV 2
DB 6 CI 7

RESULT 5
Q8NH7 PRELIMINARY; PRT; 7 AA.
AC Q8NH7;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Mini-cistron.
GN NHE3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Malakooti J., Ramasamy K.;
RT "Molecular cloning and characterization of the human Na+/H+ exchanger
RT NHE-3 gene promoter region.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282824; AAM53436.1; -.
SQ SEQUENCE 7 AA; 842 MW; 74072DC772D406F0 CRC64;

Query Match 26.2%; Score 11; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VP 3
DB 3 VP 4

RESULT 6
Q8MFV6 PRELIMINARY; PRT; 7 AA.
AC Q8MFV6;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

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DE PsBA (Fragment).
 GN PSBA.
 OS Taraxacum (sect. Dioszegia) sp. 4310Hnew.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae;
 OC Taraxacum.
 OX NCBI_TaxID=154248;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Mes T.H.M.;
 RT "Reconstruction of the evolution of trnF pseudogenes."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY015477; AK021591.1; --
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 1
 SQ SEQUENCE 7 AA; 675 MW; 687451B5A76DDB70 CRC64;
 Query Match 26.2%; Score 11; DB 8; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1e+06;
 Matches 2; Conservative 1; Mismatches 0; Gaps 0;
 Indels 0;
 QY 3 PLTS 6
 Db 3 PSIN 6
 RESULT 7
 P93233 PRELIMINARY; PRT; 7 AA.
 AC P93233;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
 DE (Fragment).
 DE LE-ACSIB
 GN Lycopersicon esculentum (Tomato).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=97351561; PubMed=9207843;
 RA Ostler J.H., Olson D.C., Shiu O.Y., Yang S.F.;
 RT "Differential induction of seven 1-aminocyclopropane-1-carboxylate
 synthase genes by elicitor in suspension cultures of tomato
 (Lycopersicon esculentum)."
 RL Plant Mol. Biol. 34:275-286 (1997).
 DR EMBL; U75692; AAC49682.1; --
 DR GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . . ; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 KW Lyase.
 FT NON TER 1
 SQ SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;
 Query Match 26.2%; Score 11; DB 10; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0;
 QY 3 PL 4
 Db 3 PL 4
 RESULT 8
 P70804 PRELIMINARY; PRT; 7 AA.
 ID P70804
 AC P70804;

DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Algt protein (Fragment).
 GN ALGT.
 OS Azotobacter vinelandii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Azotobacter.
 OX NCBI_TaxID=354;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=E;
 RA MEDLINE=96427318; PubMed=8830682;
 RA Rehm B.H.A., Ertesvag H., Valla S.;
 RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is
 part of an alg gene cluster physically organized in a manner similar
 to that in Pseudomonas aeruginosa."
 RL J. Bacteriol. 178:5884-5889 (1996).
 DR EMBL; X87973; CAA61230.1; --
 FT NON TER 1
 SQ SEQUENCE 7 AA; 684 MW; 71B5A5A5A2D1AED0 CRC64;
 Query Match 23.8%; Score 10; DB 2; Length 7;
 Best Local Similarity 33.3%; Pred. No. 1e+06;
 Matches 2; Conservative 1; Mismatches 0; Gaps 0;
 Indels 0;
 QY 1 CVPLTS 6
 Db 1 CTWSS 6
 RESULT 9
 P72081 PRELIMINARY; PRT; 7 AA.
 ID P72081
 AC P72081;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE 3-methylcephem hydroxylase (Fragment).
 DE CEFF.
 GN Nocardia lactamdurans.
 OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Pseudonocardiaceae; Pseudonocardiaceae; Amycolatopsis.
 OX NCBI_TaxID=1913;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=96009872; PubMed=7557411;
 RA Coque J., Perez-Llarena F.J., Enguita F.J., Fuente J.L., Martin J.F.,
 RA Liras P.;
 RT "Characterization of the cmh genes of Nocardia lactamdurans and
 Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem
 O-carbamoyltransferase for cephamycin biosynthesis."
 RL Gene 162:21-27 (1995).
 DR EMBL; Z21682; CAA79797.1; --
 FT NON TER 1
 SQ SEQUENCE 7 AA; 746 MW; 75A1B2CDD1E681C0 CRC64;
 Query Match 23.8%; Score 10; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1e+06;
 Matches 2; Conservative 1; Mismatches 0; Gaps 0;
 Indels 0;
 QY 4 LTS 6
 Db 5 VTS 7
 RESULT 10
 Q8GL12 PRELIMINARY; PRT; 7 AA.
 ID Q8GL12
 AC Q8GL12;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

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DE PP-50 protein (Fragment).
GN PP-50.
OS Borrelia burgdorferi ( Lyme disease spirochete).
OG Plasmid group cp32-9.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N40;
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
  prophages: conservation amidst diversity.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY142100; AAN17911.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER
SQ SEQUENCE 1 1 849 MW; 6337244330569ED0 CRC64;

Query Match 23.8%; Score 10; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CV 2
Db 1 CM 2

RESULT 11
Q9CSB3 PRELIMINARY; PRT; 7 AA.
ID Q9CSB3
AC Q9CSB3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN DIDI 10A-2b.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root;
RX MEDLINE=21171025; PubMed=11277426;
RA Vercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.;
RT "Arabidopsis thaliana genes expressed in the early compatible
  interaction with root-knot nematodes.";
RL Mol. Plant Microbe Interact. 14:288-299 (2001).
DR EMBL; AJ286350; CAB71014.2; -.
KW Hypothetical protein.
FT NON_TER
FT NON_TER
SQ SEQUENCE 7 AA; 719 MW; 5732C7287EB325D0 CRC64;

Query Match 23.8%; Score 10; DB 10; Length 7;
Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 TSC 7
Db 1 SKC 3

RESULT 12
Q07624 PRELIMINARY; PRT; 7 AA.
ID Q07624
AC Q07624;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE DORFI.

OS Rous sarcoma virus (strain Prague C).
OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=11888;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93010967; PubMed=1327749;
RA Donze O., Spahr P.F.;
RT "role of the open reading frames of Rous sarcoma virus leader RNA in
  translation and genome packaging.";
RL EMBL J. 11:3747-3757 (1992).
DR EMBL; X67587; CAA47862.1; -.
SQ SEQUENCE 7 AA; 672 MW; 776045A7687DD6F0 CRC64;

Query Match 23.8%; Score 10; DB 15; Length 7;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VP 3
Db 6 IP 7

RESULT 13
P83569 PRELIMINARY; PRT; 6 AA.
ID P83569
AC P83569;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sperm attracting peptide SepSAP.
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidae; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP SEQUENCE, FUNCTION, DEVELOPMENTAL STAGE, MASS SPECTROMETRY, AND
  AMIDATION.
RC TISSUE=Egg;
RX PubMed=12207899;
RA Zatylny C., Marvin L., Gagnon J., Henry J.;
RT "Fertilization in Sepia officinalis: the first mollusk sperm-
  attracting peptide.";
RL Biochem. Biophys. Res. Commun. 296:1186-1193 (2002).
CC -!- FUNCTION: ATTRACTS SPERM INCREASING THE CHANCES OF GAMETE
  COLLISION.
CC -!- DEVELOPMENTAL STAGE: FIRST APPEARS IN THE OVARIAN FOLLICLES FURING
  VITELLOGENESIS. ACCUMULATES IN THE OOCYTES BEFORE BEING SECRETED
  DURING FERTILIZATION. EXPRESSION CONTINUES IN THE EMBEDDED OOCYTE.
CC ACCUMULATES IN THE EGG CAPSULE AFTER FERTILIZATION.
CC -!- MASS SPECTROMETRY: MW=596.6; METHOD=MALDI.
KW Amidation.
FT MOD_RES
FT MOD_RES
SQ SEQUENCE 6 AA; 597 MW; 72C8676AA0470000 CRC64;

Query Match 21.4%; Score 9; DB 5; Length 6;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PL 4
Db 1 PI 2

RESULT 14
OS0556 PRELIMINARY; PRT; 7 AA.
ID OS0556
AC OS0556;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE GlyA (Fragment).
GN GlyA.
OS Actinobacillus actinomycetemcomitans (Haemophilus

```

Mon Mar 8 13:10:42 2004

OS actinomycetomycetans).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Actinobacillus.
 OX NCBI_TaxID=714;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33384;
 RX MEDLINE=96355846; PubMed=8751884;
 RA Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,
 RA Kraig E.;
 RT "cis Elements and trans factors are both important in strain-specific
 RT regulation of the leukotoxin gene in Actinobacillus
 PT actinomycetomycetans.";
 RL Infect. Immun. 64:3451-3460(1996).
 DR EMBL; U51862; AAB88721.1; -.
 FT NON TER 1
 SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;
 Query Match 21.4%; Score 9; DB 2; Length 7;
 Best Local Similarity 33.3%; Pred. No. 1e+06;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VPL 4
 Db 3 LRV 5
 RESULT 15
 Q54248
 ID Q54248 PRELIMINARY; PRT; 7 AA.
 AC Q54248;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE RplO protein (fragment).
 GN RPL0.
 OS Streptomyces griseus.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1911;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2-3-11;
 RX MEDLINE=20011291; PubMed=10542330;
 RA Poebling S., Piepersberg W., Wehmeier U.F.;
 RT "Analysis and regulation of the sec Y gene from Streptomyces griseus
 RT N2-3-11 and interaction of the SecY protein with the SecA protein.";
 RL Biochim. Biophys. Acta 1447:298-302(1999).
 DR EMBL; X95915; CAA65160.1; -.
 FT NON TER 1
 SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2A0 CRC64;
 Query Match 21.4%; Score 9; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VPLT 5
 Db 1 VTVT 4

Search completed: March 8, 2004, 12:30:43
 Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:20:28 ; Search time 52 Seconds
(without alignments)
38.035 Million cell updates/sec

Title: US-09-761-636a-11

Perfect score: 42

Sequence: 1 CVPLTSC 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 92273

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_29Jan04.*
- 1: Genesep1980s.*
 - 2: Genesep1990s.*
 - 3: Genesep2000s.*
 - 4: Genesep2001s.*
 - 5: Genesep2002s.*
 - 6: Genesep2003as.*
 - 7: Genesep2003bs.*
 - 8: Genesep2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	100.0	7	AAU04530	AAU04530 VEGF base
2	31	73.8	7	AAW13421	AAW13421 Kidney ho
3	31	73.8	7	AAW12007	AAW12007 Kidney ho
4	31	73.8	7	AAE11813	AAE11813 Phage pep
5	31	73.8	7	AAU10724	AAU10724 Kidney ho
6	31	73.8	7	ABU59533	ABU59533 Kidney re
7	31	73.8	7	ADC33700	ADC33700 Kidney ce
8	31	73.8	7	ADC33699	ADC33699 Kidney ce
9	29	69.0	6	AAU04531	AAU04531 VEGF base
10	28	66.7	7	ABJ00550	ABJ00550 B Lymphoc
11	28	66.7	7	ABG33862	ABG33862 B Lymphoc
12	26	61.9	7	AAV61489	AAV61489 Cadherin-
13	25	59.5	7	AAV62764	AAV62764 PB-cadher
14	25	59.5	7	AAV62007	AAV62007 Cadherin-
15	25	59.5	7	AAV62224	AAV62224 Cadherin-
16	24	57.1	7	AAV85374	AAV85374 IL-2 deri
17	24	57.1	7	AAV64260	AAV64260 Cadherin-
18	23	54.8	6	AAW51449	AAW51449 IGF-1 ana
19	23	54.8	7	AAW85404	AAW85404 IL-2 deri
20	23	54.8	7	AAV61930	AAV61930 Cadherin-
21	23	54.8	7	AAV62758	AAV62758 PB-cadher
22	23	54.8	7	AAV64322	AAV64322 Cadherin-
23	23	54.8	7	AAV61506	AAV61506 Cadherin-
24	23	54.8	7	AAV62489	AAV62489 Cadherin-
25	23	54.8	7	AAV63236	AAV63236 Protocadh

26	23	54.8	7	5	ABB47076	Abb47076 Desmocoll
27	22	52.4	4	2	AAK15772	Aak15772 Farnesyl-
28	22	52.4	4	2	AAK49769	Aak49769 Farnesyl-
29	22	52.4	4	2	AAK77833	Aak77833 Farnesyl
30	22	52.4	4	2	AAW04459	Aaw04459 Farnesyl
31	22	52.4	4	2	AAW67428	Aaw67428 HCV pepti
32	22	52.4	6	6	ABJ37236	Abj37236 Rhodopsin
33	22	52.4	7	2	AAK36871	Aak36871 Insulin-1
34	22	52.4	7	2	AAK43615	Aak43615 Peptide d
35	22	52.4	7	2	AAW67430	Aaw67430 HCV pepti
36	22	52.4	7	3	AAV64307	Aay64307 Cadherin-
37	22	52.4	7	3	AAV64292	Aay64292 Cadherin-
38	22	52.4	7	3	AAV62135	Aay62135 Cadherin-
39	22	52.4	7	3	AAV63266	Aay63266 Protocadh
40	22	52.4	7	5	ABB46174	Abb46174 Desmogiel
41	22	52.4	7	5	ABJ04536	Abj04536 Molt-4 le
42	21	50.0	7	2	AAW60386	Aaw60386 Tumour ho
43	21	50.0	7	2	AAW93712	Aaw93712 Human bre
44	21	50.0	7	3	AAW03612	Aaw03612 Aspergill
45	21	50.0	7	3	AAV64262	Aay64262 Cadherin-

ALIGNMENTS

RESULT 1
AAU04530
ID AAU04530 standard; peptide; 7 AA.
XX
AC AAU04530;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 8.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..7
FT /note= "This bond cyclises the peptide"
XX
PN WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stackler S, Cendron A;
XX
DR WPI; 2001-442248/47.
XX
PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
PS Claim 49; Page 32; 102pp; English.
XX
CC The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the exposed loop of human
CC VEGF (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a

involves administering a phage display library to a subject, and identifying expressed peptides which home to the desired organ or tissue, e.g. brain, kidney, angiogenic vascular tissue or tumour tissue. The isolated peptides (see AAM1312-52, AAM11181-86) can be used to target e.g. drugs, toxins or labels to the selected organ/tissue (claimed) or to identify and/or isolate target molecules (claimed). The peptides can be directly identified *in vivo*, as compared to prior art *in vitro* screening methods, which require further examination to see if they maintain specificity *in vivo*

Sequence 7 AA;

```

Query Match          73.8%; Score 31; DB 2; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

Qy 1 CVPLTSC 7
|:|:|
pb 1 CLPVASC 7

RESULT 3
AAB12007
ID: AAB12007 standard: pentide: 7 AA:

AA
AC

17-000-2000 (first entry)

1 # opitatus sapiens
XX

XX

[illegible]

SO
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FH	Key	Locat:
1	16:16	1
2	16:16	7

ET

XX PN US6068829-A.

XX
30-MAY-2000

XX

XXXX

PR 11-SEP-1997;
PR 10-MAR-1997;

XX
PA (BITN-) BITN

XX

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XX

PT Identifying
PT Planning comp

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PS Example 2; C

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CC

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CC Examples of

XX

THE

Query Match
Best Local Sim

Matches 4;

QY 1 CVM

```

Db      |:|: ||
      1 CLPVASC 7

RESULT 4
AAE11813
ID AAE11813 standard; peptide; 7 AA.
XX
AC AAE11813;
XX
DT 11-SEP-2003 (revised)
DT 18-DEC-2001 (first entry)
XX
DE Phase peptide #21 targetted to kidney.
XX
XX Enriched library fraction; brain; kidney; tumour; panning; diagnostic;
KW molecular medicine; drug delivery; peptidomimetic; pharmaceutical.
XX
XX unidentified bacteriophage.
OS
OS Unidentified.
XX
FN US6296832-B1.
XX
XX 02-OCT-2001.
XX
PF 08-JAN-1999; 99US-00226985.
XX
XX 11-SEP-1995; 95US-00526710.
PR 10-MAR-1997; 97US-00813273.
PR 23-JUN-1997; 97US-00862855.
XX
PA (BURN-) BURNHAM INST.
XX
PI Ruoslahti E, Pasqualini R;
XX
DR WPI; 2001-610691/70.
XX
XX Enriched library fraction comprising molecules recovered by in vivo
PT panning that selectively home to a selected organ or tissue useful for
PT treating disease or in diagnostic methods.
XX
XX Example 2; Col 18; 2lpp; English.
XX
CC The invention relates to an enriched library fraction containing
CC molecules that selectively home to a selected organ or tissue such as
CC brain, kidney or tumour recovered by in vivo panning. The invention
CC generally relates to the field of molecular medicine, drug delivery and
CC to a method of in vivo panning for identifying a molecule that homes to a
CC specific organ. The molecules, e.g., peptides, peptidomimetics, proteins
CC and fragments of proteins contained in an enriched library fraction may
CC be administered to a subject as part of a pharmaceutical composition to
CC treat disease or in diagnostic methods. The present sequence is a peptide
CC from bacteriophage targetted to kidney. (Updated on 11-SEP-2003 to
CC standardise OS field)
XX
SQ Sequence 7 AA;

Query Match 73.8%; Score 31; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
   |:|: ||
Db 1 CLPVASC 7

RESULT 5
AAU10724
ID AAU10724 standard; peptide; 7 AA.
XX
XX AAU10724;
XX
DT 12-MAR-2002 (first entry)
KW Targeting ligand; bioactive agent; polymer matrix; cancer; cytostatic;

```

```

XX DE Kidney homing peptide #1 useful for delivery of target molecules.
XX KW Organ targeting; tissue targeting; cancer; tumour homing molecule;
XX KW delivery of target molecule; kidney homing peptide.
XX OS Synthetic.
XX FN US6306365-B1.
XX PD 23-OCT-2001.
XX PF 08-JAN-1999; 99US-00227906.
XX PR 11-SEP-1995; 95US-00526710.
PR 10-MAR-1997; 97US-00813273.
PR 23-JUN-1997; 97US-00862855.
XX PA (BURN-) BURNHAM INST.
XX PI Ruoslahti E, Pasqualini R;
XX DR WPI; 2002-040196/05.
XX PR Recovering molecules that home to an organ or tissue, useful for
PT identifying molecules that home to a specific organ or tissue, e.g.
PT identifying a tumor homing molecule to identify the presence of cancer,
PT by in vivo panning of a library.
XX
XX Example 2; Col 18; 2lpp; English.
XX
CC The present invention relates to a method of recovering molecules that
CC home to a selected organ or tissue. The method comprises administering to
CC the subject the library of diverse molecules, collecting a sample of the
CC selected organ or tissue (e.g. brain or kidney), and recovering from the
CC sample several molecules that home to the selected organ or tissue. The
CC method is useful for identifying molecules, particularly useful for
CC screening large number of molecules (e.g. peptides), that home to a
CC specific organ. The identified molecule is useful for e.g. raising an
CC antibody specific for a target molecule, targeting a desired moiety (e.g.
CC drug, toxin or detectable label) to the selected organ. Specifically, the
CC method is useful for identifying the presence of cancer in a subject by
CC linking an appropriate moiety to a tumour homing molecules. The present
CC method provides a direct means for identifying molecules that
CC specifically home to a selected organ and, therefore provides a
CC significant advantage over previous methods, which require that a
CC molecule identified using an in vitro screening method subsequently be
CC examined to determine if it maintains its specificity in vivo. AAU10724-
CC AAU10738 represent kidney homing peptides described in the present
CC invention
XX
SQ Sequence 7 AA;

Query Match 73.8%; Score 31; DB 5; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
   |:|: ||
Db 1 CLPVASC 7

RESULT 6
ABU59533
ID ABU59533 standard; peptide; 7 AA.
XX
XX ABU59533;
XX
XX 22-APR-2003 (first entry)
DT
XX
DE Kidney receptor targeting peptide #1.
XX
KW Targeting ligand; bioactive agent; polymer matrix; cancer; cytostatic;

```

KW cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor;
KW fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium;
KW tumour; cationic cancer-targeting peptide.
XX Synthetic.
XX US2002041898-A1.
XX 11-APR-2002.
XX 25-JUL-2001; 2001US-00912609.
XX 05-JAN-2000; 2000US-00478124.
XX 31-OCT-2000; 2000US-00703474.
XX (UNGE/) UNGER E C.
XX (MATS/) MATSUNAGA T O.
XX (RAMA/) RAMASWAMI V.
XX (ROMA/) ROMANOWSKI M J.
XX Unger EC, Matsunaga TO, Ramaswami V, Romanowski MJ;
XX WPI; 2003-208921/20.
XX Targeted delivery system comprising a bioactive agent homogeneously
XX dispersed in a targeted matrix is especially useful in cancer therapy.
XX Claim 25; Page 38; 46pp; English.
XX The invention relates to a composition comprising a bioactive agent
XX homogeneously dispersed in a targeted matrix (polymer and targeting
XX ligand). Also included are a targeted matrix for use as a delivery
XX vehicle comprising a polymer associated with a targeting ligand,
XX enhancing the bioavailability of an agent comprising administration of the
XX composition and treating cancer comprising administration of a drug,
XX novel composition. The method is useful for targeted delivery of a drug,
XX especially in cancer therapy. The targeting ligand may be a peptide.
XX Examples of targeting peptides are disclosed including cathepsin-D
XX substrate peptides, peptides targeting receptors in the brain and kidney,
XX peptides recognising fibronectin- and vitronectin-binding integrins,
XX peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies,
XX peptides targeting the angiogenic endothelium of solid tumours, tissue
XX specific peptides (e.g. of lung, skin, pancreas, intestine, uterus,
XX adrenal gland and retina), and cationic cancer- targeting peptides. The
XX present sequence is a peptide targeting ligand disclosed in the invention
XX Sequence 7 AA;
SQ
Query Match 73.8%; Score 31; DB 6; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CVPLTSC 7
Db 1 CLPVASC 7
RESULT 7
ADC33700
ID ADC33700 standard; peptide; 7 AA.
XX ADC33700;
XX 18-DEC-2003 (first entry)
XX Kidney cell targeted peptide SEQ ID NO:4.
XX chimeric retrovirus envelope protein; ecotropic envelope protein;
KW cytotstatic; gene therapy; cancer.
XX Synthetic.
XX WO2003076596-A2.
FN

KW cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor;
KW fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium;
KW tumour; cationic cancer-targeting peptide.
XX Synthetic.
XX US2002041898-A1.
XX 11-APR-2002.
XX 25-JUL-2001; 2001US-00912609.
XX 05-JAN-2000; 2000US-00478124.
XX 31-OCT-2000; 2000US-00703474.
XX (UNGE/) UNGER E C.
XX (MATS/) MATSUNAGA T O.
XX (RAMA/) RAMASWAMI V.
XX (ROMA/) ROMANOWSKI M J.
XX Unger EC, Matsunaga TO, Ramaswami V, Romanowski MJ;
XX WPI; 2003-208921/20.
XX Targeted delivery system comprising a bioactive agent homogeneously
XX dispersed in a targeted matrix is especially useful in cancer therapy.
XX Claim 25; Page 38; 46pp; English.
XX The invention relates to a composition comprising a bioactive agent
XX homogeneously dispersed in a targeted matrix (polymer and targeting
XX ligand). Also included are a targeted matrix for use as a delivery
XX vehicle comprising a polymer associated with a targeting ligand,
XX enhancing the bioavailability of an agent comprising administration of the
XX composition and treating cancer comprising administration of a drug,
XX novel composition. The method is useful for targeted delivery of a drug,
XX especially in cancer therapy. The targeting ligand may be a peptide.
XX Examples of targeting peptides are disclosed including cathepsin-D
XX substrate peptides, peptides targeting receptors in the brain and kidney,
XX peptides recognising fibronectin- and vitronectin-binding integrins,
XX peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies,
XX peptides targeting the angiogenic endothelium of solid tumours, tissue
XX specific peptides (e.g. of lung, skin, pancreas, intestine, uterus,
XX adrenal gland and retina), and cationic cancer- targeting peptides. The
XX present sequence is a peptide targeting ligand disclosed in the invention
XX Sequence 7 AA;
SQ
Query Match 73.8%; Score 31; DB 6; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CVPLTSC 7
Db 1 CLPVASC 7
RESULT 7
ADC33700
ID ADC33700 standard; peptide; 7 AA.
XX ADC33700;
XX 18-DEC-2003 (first entry)
XX Kidney cell targeted peptide SEQ ID NO:4.
XX chimeric retrovirus envelope protein; ecotropic envelope protein;
KW cytotstatic; gene therapy; cancer.
XX Synthetic.
XX WO2003076596-A2.
FN

XX 18-SEP-2003.
XX 07-MAR-2003; 2003WO-US007323.
XX 08-MAR-2002; 2002US-0362655P.
XX (UYMA-) UNIV MASSACHUSETTS.
XX Green WR, Gollan TJ;
XX WPI; 2003-722332/68.
XX New chimeric retrovirus envelope protein comprising an ecotropic envelope
XX protein and a heterologous short peptide ligand inserted within the
XX ecotropic envelope protein useful for treating cancer.
XX Disclosure; SEQ ID NO 4; 42pp; English.
XX The present invention describes a chimeric retrovirus envelope protein
XX (1) comprising an ecotropic envelope protein and a heterologous short
XX peptide ligand inserted within the ecotropic envelope protein. Also
XX described: (1) a nucleic acid molecule comprising a sequence encoding the
XX recombinant chimeric envelope protein; (2) a vector comprising a nucleic
XX acid sequence encoding the chimeric envelope protein; (3) a recombinant
XX heterologous short peptide ligand; (3) altering the chimeric envelope
XX identifying a nucleic acid sequence encoding the chimeric envelope
XX protein that alters viral tropism; (5) delivering a nucleic acid sequence
XX to a cell; and (6) treating cancer. (1) has cytotstatic activity and can
XX be used in gene therapy. The chimeric retrovirus envelope protein is
XX useful for treating cancer, which comprises providing a cancer cell, e.g.
XX human cancer cell and infecting the cancer cell with a virus, e.g.
XX retrovirus comprising the chimeric envelope protein comprising a
XX heterologous short peptide ligand and a therapeutically useful gene, e.g.
XX encoding thymidine kinase. The present sequence represents a kidney cell
XX targeted peptide, which is given in the exemplification of the present
XX invention.
XX Sequence 7 AA;
SQ
Query Match 73.8%; Score 31; DB 7; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CVPLTSC 7
Db 1 CLPVASC 7
RESULT 8
ADC33699
ID ADC33699 standard; peptide; 7 AA.
XX ADC33699;
XX 18-DEC-2003 (first entry)
XX Kidney cell targeted peptide SEQ ID NO:3.
XX chimeric retrovirus envelope protein; ecotropic envelope protein;
KW cytotstatic; gene therapy; cancer.
XX Synthetic.
XX WO2003076596-A2.
XX 18-SEP-2003.
XX 07-MAR-2003; 2003WO-US007323.
XX 08-MAR-2002; 2002US-0362655P.
XX

Mon Mar 8 13:10:40 2004

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XX FH Key Location/Qualifiers
XX FT Misc-difference 2 /label= Phe, Trp, Tyr
XX FT FT Misc-difference 4
XX FT FT Misc-difference 4 /label= Pro, Tyr
XX FT FT
XX PN WO200216411-A2.
XX XX 28-FEB-2002.
XX XX 17-AUG-2001; 2001WO-US025850.
XX XX 18-AUG-2000; 2000US-0226700P.
XX XX (HUMA-) HUMAN GENOME SCI INC.
XX XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX XX WPI; 2002-499775/53.
XX XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX XX administering B Lymphocyte stimulator binding polypeptide.
XX XX Claim 69; Page 233; 387pp; English.
XX XX The present invention relates to the treatment, prevention or
XX XX amelioration of a disease or disorder associated with: aberrant B
XX XX lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
XX XX of haematopoietic origin; or proliferative disease; and reducing,
XX XX inhibiting or stimulating immunoglobulin production, B cell proliferation
XX XX and graft rejection involving administration of BlyS binding polypeptide.
XX XX The BlyS binding polypeptides are used in the treatment, prevention or
XX XX amelioration of diseases such as immune system diseases, proliferative
XX XX diseases, diseases of cells of haematopoietic origin, graft rejection,
XX XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
XX XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
XX XX neurodegenerative diseases. The present sequence is a B lymphocyte
XX XX stimulator protein binding peptide
XX XX Sequence 7 AA;
XX XX
XX XX Query Match 66.7%; Score 28; DB 5; Length 7;
XX XX Best Local Similarity 57.1%; Pred. No. 1.4e+06;
XX XX Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX XX
XX QY 1 CVPPLTSC 7
XX DB 1 CXPTGTC 7
XX
XX RESULT 11
XX ABG33862
XX ID ABG33862 standard; peptide; 7 AA.
XX XX
XX AC ABG33862;
XX XX
XX DT 15-JUL-2002 (first entry)
XX XX
XX DE B Lymphocyte Stimulator (BlyS) binding peptide #436.
XX XX
XX KW B Lymphocyte Stimulator protein; B Lymphocyte stimulator binding peptide;
XX KW BlyS; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
XX KW synovial fluid; saliva; mucus.
XX XX
XX OS Synthetic.
XX OS
XX PN WO200216412-A2.
XX XX
XX PD 28-FEB-2002.
XX XX
XX XX 17-AUG-2001; 2001WO-US025891.
XX XX
XX XX
XX PR 18-AUG-2000; 2000US-0226489P.
XX XX (DYAX-) DYAX CORP.
XX XX Beltzer JP, Potter MD, Fleming TJ, Ladner RC;
XX XX WPI; 2002-351647/38.
XX XX New B-lymphocyte stimulator binding polypeptide useful in detecting or
XX XX isolating BlyS or BlyS-like polypeptide comprises a specified amino acid
XX XX sequence.
XX XX Disclosure; Page 132; 269pp; English.
XX XX The invention relates to a B Lymphocyte Stimulator (BlyS) binding
XX XX polypeptide. BlyS binding peptides bind BlyS or BlyS-like proteins
XX XX reversibly or irreversibly. The binding peptides are used in detection,
XX XX isolation and/or purification of BlyS in a solution such as water or a
XX XX buffer solution, as well as any fluid and/or cell obtained from an
XX XX individual biological fluid, body tissue, body cell, cell line, tissue
XX XX culture or other source containing BlyS or BlyS-like polypeptides. The
XX XX biological fluids include sera, plasma, lymph, blood, blood fraction,
XX XX urine, synovial fluid, spinal fluid, saliva and mucus. Sequences
XX XX ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and
XX XX ABG33852-33862 represent BlyS binding peptides of the invention
XX XX Sequence 7 AA;
XX XX
XX XX Query Match 66.7%; Score 28; DB 5; Length 7;
XX XX Best Local Similarity 57.1%; Pred. No. 1.4e+06;
XX XX Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX XX
XX QY 1 CVPPLTSC 7
XX DB 1 CXPTGTC 7
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XX RESULT 12
XX AAY61489
XX ID AAY61489 standard; peptide; 7 AA.
XX XX
XX AC AAY61489;
XX XX
XX DT 02-MAR-2000 (first entry)
XX XX
XX DE Cadherin-7 cell adhesion recognition cyclic peptide SEQ ID NO:1375.
XX XX
XX KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
XX KW inhibition; cadherin extracellular domain; cell adhesion recognition;
XX KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
XX KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
XX KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
XX KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
XX KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
XX KW neurological disease; cyclic.
XX XX
XX OS Synthetic.
XX OS Homo sapiens.
XX XX
XX FT Disulfide-bond 1.7
XX FT
XX PN WO957149-A2.
XX XX
XX PD 11-NOV-1999.
XX XX
XX PF 05-MAY-1999; 99WO-CA000363.
XX XX
XX PR 05-MAY-1998; 98US-00073040.
XX PR 06-NOV-1998; 98US-00187859.
XX PR 20-JAN-1999; 99US-00234395.
XX PR 08-MAR-1999; 99US-00264516.
XX XX

```

PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 PI Blaschuk OW, Gour BJ, Byers S;
 XX WPI; 2000-038791/03.
 XX New cadherin modulating agents, used for modulating nonclassical cadherin
 PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX Claim 36; Page 172; 252pp; English.
 XX The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MAs can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC -related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
 CC the exemplification of the present invention
 XX Sequence 7 AA;
 SQ Query Match 61.9%; Score 26; DB 3; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CVPPLTSC 7
 Db 1 CEPKTCG 7
 RESULT 13
 AAY62764
 ID AAY62764 standard; peptide; 7 AA.
 AC AAY62764;
 XX 02-MAR-2000 (first entry)
 DE PB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:4047.
 DE Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; Li-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.
 XX Synthetic.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Disulfide-bond 1..7
 FT WO9957149-A2.
 PN

XX PD 11-NOV-1999.
 XX PF 05-MAY-1999; 99WO-CA000363.
 XX PR 05-MAY-1998; 98US-00073040.
 XX PR 06-NOV-1998; 98US-00187859.
 XX PR 20-JAN-1999; 99US-00234395.
 XX PR 08-MAR-1999; 99US-00264516.
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX Blaschuk OW, Gour BJ, Byers S;
 XX WPI; 2000-038791/03.
 XX New cadherin modulating agents, used for modulating nonclassical cadherin
 PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX Claim 72; Page 193; 252pp; English.
 XX The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MAs can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC -related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
 CC the exemplification of the present invention
 XX Sequence 7 AA;
 SQ Query Match 59.5%; Score 25; DB 3; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CVPPLTSC 7
 Db 1 CDPKTCG 7
 RESULT 14
 AAY62007
 ID AAY62007 standard; peptide; 7 AA.
 AC AAY62007;
 XX 02-MAR-2000 (first entry)
 DE Cadherin-12 cell adhesion recognition cyclic peptide SEQ ID NO:1799.
 DE Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; Li-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;

02-MAR-2000 (first entry)
 Cadherin-14 cell adhesion recognition cyclic peptide SEQ ID NO:3971.
 Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 inhibition; cadherin extracellular domain; cell adhesion recognition;
 OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 cadherin related neuronal receptor; LI-cadherin; protocadherin;
 desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 neurological disease; cyclic.
 Synthetic.
 Homo sapiens.
 Key Location/Qualifiers
 Disulfide-bond 1..7
 MO9957149-A2.
 11-NOV-1999.
 05-MAY-1999; 99WO-CA000363.
 05-MAY-1998; 98US-00073040.
 06-NOV-1998; 98US-00187859.
 20-JAN-1999; 99US-00234395.
 08-MAR-1999; 99US-00264516.
 (ADHE-) ADHEREX TECHNOLOGIES INC.
 Blaschuk OW, Gour BJ, Byers S;
 WPI; 2000-038791/03.
 New cadherin modulating agents, used for modulating nonclassical cadherin
 mediated functions for treating e.g. cancers, obesity, rheumatoid
 arthritis, multiple sclerosis, diabetes or a neurological disease.
 Claim 54; Page 184; 252pp; English.
 The present invention describes cadherin modulating agents (MA)
 comprising peptides which comprise a nonclassical cadherin cell adhesion
 recognition (CAR) sequence. The MAs can be used for modulating
 nonclassical cadherin-mediated functions. They can be used for e.g.
 inhibiting adhesion of nonclassical-cadherin expressing cells in a
 mammal, enhancing delivery of a drug through the skin of a mammal,
 enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 expressing cell, preventing or treating obesity in a mammal, stimulating
 blood vessel regression in a mammal, enhancing drug delivery to the
 central nervous system, treating a demyelinating neurological disease,
 increasing vasopermeability in a mammal, enhancing adhesion of
 nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 a mammal, or preventing pregnancy in a mammal. They can also be used for
 e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 related macular degeneration, multiple sclerosis and diabetes. The
 products can also be used for detection and diagnosis and in bioreactors.
 AAY60592 to AAY64572 represent specifically claimed peptides, and
 AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
 the exemplification of the present invention

rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 neurological disease; cyclic.
 Synthetic.
 Homo sapiens.
 Key Location/Qualifiers
 Disulfide-bond 1..7
 WC9957149-A2.
 11-NOV-1999.
 05-MAY-1999; 99WO-CA000363.
 05-MAY-1998; 98US-00073040.
 06-NOV-1998; 98US-00187859.
 20-JAN-1999; 99US-00234395.
 08-MAR-1999; 99US-00264516.
 (ADHE-) ADHEREX TECHNOLOGIES INC.
 Blaschuk OW, Gour BJ, Byers S;
 WPI; 2000-038791/03.
 New cadherin modulating agents, used for modulating nonclassical cadherin
 mediated functions for treating e.g. cancers, obesity, rheumatoid
 arthritis, multiple sclerosis, diabetes or a neurological disease.
 Claim 48; Page 180; 252pp; English.
 The present invention describes cadherin modulating agents (MA)
 comprising peptides which comprise a nonclassical cadherin cell adhesion
 recognition (CAR) sequence. The MAs can be used for modulating
 nonclassical cadherin-mediated functions. They can be used for e.g.
 inhibiting adhesion of nonclassical-cadherin expressing cells in a
 mammal, enhancing delivery of a drug through the skin of a mammal,
 enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 expressing cell, preventing or treating obesity in a mammal, stimulating
 blood vessel regression in a mammal, enhancing drug delivery to the
 central nervous system, treating a demyelinating neurological disease,
 increasing vasopermeability in a mammal, enhancing adhesion of
 nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 a mammal, or preventing pregnancy in a mammal. They can also be used for
 e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 related macular degeneration, multiple sclerosis and diabetes. The
 products can also be used for detection and diagnosis and in bioreactors.
 AAY60592 to AAY64572 represent specifically claimed peptides, and
 AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
 the exemplification of the present invention

Sequence 7 AA;

Query Match 59.5%; Score 25; DB 3; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
 Db 1 CDPKTCG 7

RESULT 15
 AAY62224
 ID AAY62224 standard; peptide; 7 AA.
 XX
 AC AAY62224;
 XX

Sequence 7 AA;

Query Match 59.5%; Score 25; DB 3; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7

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Mon Mar 8 13:10:40 2004

Db 1 CDEKTC 7

Search completed: March 8, 2004, 12:29:28
Job time : 53 secs

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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:30:49 ; Search time 33 Seconds
(without alignments)
44.790 Million cell updates/sec

Title: US-09-761-636A-11
Perfect score: 42
Sequence: 1 CVPLTSC 7

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Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 21113259 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Published Applications AA.*

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- 13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	26	61.9	7	14	US-10-006-869-1375
6	26	61.9	7	15	US-10-395-032-1375
7	25	59.5	7	14	US-10-006-869-1799
8	25	59.5	7	14	US-10-006-869-3971
9	25	59.5	7	14	US-10-006-869-4047
10	25	59.5	7	15	US-10-395-032-1799
11	25	59.5	7	15	US-10-395-032-3971
12	25	59.5	7	15	US-10-395-032-4047
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14	24	57.1	7	15	US-10-395-032-3574
15	23	54.8	7	14	US-10-006-869-1392

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Sequence 2155, Ap
Sequence 2720, Ap
Sequence 3637, Ap
Sequence 4041, Ap
Sequence 1392, Ap
Sequence 1740, Ap
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Sequence 2720, Ap
Sequence 3637, Ap
Sequence 4041, Ap
Sequence 35, Appl
Sequence 221, Appl
Sequence 225, Appl
Sequence 1888, Ap
Sequence 2750, Ap
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Sequence 1888, Ap
Sequence 2750, Ap
Sequence 3606, Ap
Sequence 3621, Ap
Sequence 184, Appl
Sequence 186, Appl
Sequence 183, Appl
Sequence 185, Appl
Sequence 187, Appl
Sequence 2748, Ap
Sequence 3576, Ap

ALIGNMENTS

RESULT 1
US-09-761-636A-11
; Sequence 11, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-11

Query Match 100.0%; Score 42; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.2e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
Db 1 CVPLTSC 7

RESULT 2
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; Sequence 12, Application US/09761636A
; Patent No. US20020065218A1

Mon Mar 8 13:10:41 2004

us-09-761-636a-11.closed.rapb

GENERAL INFORMATION:
 APPLICANT: ACHEN, Marc
 APPLICANT: STACKER, Steven
 APPLICANT: HUGHES, Richard
 APPLICANT: CENDRON, Angela
 TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
 FILE REFERENCE: 1064/48505 Achen et al
 CURRENT APPLICATION NUMBER: US/09/761,636A
 CURRENT FILING DATE: 2001-01-18
 PRIOR APPLICATION NUMBER: US 60/176,293
 PRIOR FILING DATE: 2000-01-18
 PRIOR APPLICATION NUMBER: US 60/204,590
 PRIOR FILING DATE: 2000-05-16
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 12
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-761-636A-12

Query Match 59.0%; Score 29; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.2e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLT 5
 Db 1 CVPLT 5

RESULT 3
 US-09-932-613-8
 Sequence 8, Application US/09332613
 Publication No. US20030091565A1
 GENERAL INFORMATION:
 APPLICANT: Human Genome Sciences, Inc.
 APPLICANT: Beltzer, James P.
 APPLICANT: Potter, M. Daniel
 APPLICANT: Fleming, Tony J.
 APPLICANT: Rosen, Craig A.
 TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
 FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
 CURRENT APPLICATION NUMBER: US/09/932,613
 CURRENT FILING DATE: 2001-08-17
 NUMBER OF SEQ ID NOS: 458
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 8
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (2)...(2)
 OTHER INFORMATION: X2 is Phe, Trp, or Tyr (preferably Tyr);
 NAME/KEY: MISC FEATURE
 LOCATION: (4)...(4)
 OTHER INFORMATION: X4 is Pro or Tyr (preferably Pro);
 US-09-932-613-8

Query Match 66.7%; Score 28; DB 10; Length 7;
 Best Local Similarity 57.1%; Pred. No. 7.2e+05;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
 Db 1 CXPXTGC 7

RESULT 4
 US-09-932-322-8
 Sequence 8, Application US/09932322
 Publication No. US20030194743A1

GENERAL INFORMATION:
 APPLICANT: Dyx Corp. James P.
 APPLICANT: Beltzer, M. Daniel
 APPLICANT: Potter, M. Daniel
 APPLICANT: Fleming, Tony J.
 APPLICANT: Ladner, Robert Charles
 TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLYS)
 FILE REFERENCE: DYX-018.1 PCT; DYX-018.1 US
 CURRENT APPLICATION NUMBER: US/09/932,322
 CURRENT FILING DATE: 2001-08-17
 NUMBER OF SEQ ID NOS: 458
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 8
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (2)...(2)
 OTHER INFORMATION: X2 is Phe, Trp, or Tyr (preferably Tyr);
 NAME/KEY: MISC FEATURE
 LOCATION: (4)...(4)
 OTHER INFORMATION: X4 is Pro or Tyr (preferably Pro);
 US-09-932-322-8

Query Match 66.7%; Score 28; DB 10; Length 7;
 Best Local Similarity 57.1%; Pred. No. 7.2e+05;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
 Db 1 CXPXTGC 7

RESULT 5
 US-10-006-869-1375
 Sequence 1375, Application US/10006869
 Publication No. US20030082166A1
 GENERAL INFORMATION:
 APPLICANT: Blaschuk, Orest W.
 APPLICANT: Symonds, James Matthew
 APPLICANT: Gour, Barbara J.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
 FILE REFERENCE: 100086.407C7
 CURRENT APPLICATION NUMBER: US/10/006,869
 CURRENT FILING DATE: 2001-12-03
 NUMBER OF SEQ ID NOS: 4052
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1375
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Representative cyclic modulating agent based on
 OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
 US-10-006-869-1375

Query Match 61.9%; Score 26; DB 14; Length 7;
 Best Local Similarity 57.1%; Pred. No. 7.2e+05;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
 Db 1 CEPNTGC 7

RESULT 6
 US-10-395-032-1375
 Sequence 1375, Application US/10395032
 Publication No. US20030229199A1
 GENERAL INFORMATION:

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; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1375
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
; US-10-006-869-1799

Query Match 61.9%; Score 26; DB 15; Length 7;
Best Local Similarity 57.1%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
Db 1 CEPKTGC 7

RESULT 7
US-10-006-869-1799
; Sequence 1799, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1799
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
; US-10-006-869-1799

Query Match 59.5%; Score 25; DB 14; Length 7;
Best Local Similarity 57.1%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
Db 1 CDPKTGC 7

RESULT 8
US-10-006-869-3971
; Sequence 3971, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
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; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3971
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence
; US-10-006-869-3971

Query Match 59.5%; Score 25; DB 14; Length 7;
Best Local Similarity 57.1%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
Db 1 CDPKTGC 7

RESULT 9
US-10-006-869-4047
; Sequence 4047, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4047
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
; US-10-006-869-4047

Query Match 59.5%; Score 25; DB 14; Length 7;
Best Local Similarity 57.1%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
Db 1 CDPKTGC 7

RESULT 10
US-10-395-032-1799
; Sequence 1799, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1799
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
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FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
US-10-395-032-1799

Query Match 59.5%; Score 25; DB 15; Length 7;
Best Local Similarity 57.1%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
| | | | |
Db 1 CDPKTC 7

RESULT 11
US-10-395-032-3971
; Sequence 3971, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C9
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3971
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence
US-10-395-032-3971

Query Match 59.5%; Score 25; DB 15; Length 7;
Best Local Similarity 57.1%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
| | | | |
Db 1 CDPKTC 7

RESULT 12
US-10-395-032-4047
; Sequence 4047, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C9
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4047
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-10-395-032-4047

Query Match 59.5%; Score 25; DB 15; Length 7;
Best Local Similarity 57.1%; Pred. No. 7.2e+05;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CVPLTSC 7
| | | | |
Db 1 CDPKTC 7

RESULT 13
US-10-006-869-3574
; Sequence 3574, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C7
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3574
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-10-006-869-3574

Query Match 57.1%; Score 24; DB 14; Length 7;
Best Local Similarity 42.9%; Pred. No. 7.2e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
| | | | |
Db 1 CDPVSGC 7

RESULT 14
US-10-395-032-3574
; Sequence 3574, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C9
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3574
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-10-395-032-3574

Query Match 57.1%; Score 24; DB 15; Length 7;
Best Local Similarity 42.9%; Pred. No. 7.2e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
| | | | |
Db 1 CDPVSGC 7

Mon Mar 8 13:10:41 2004

RESULT 15
US-10-006-869-1392
; Sequence 1392, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Symonds, James Matthew
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gout, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006.869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1392
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-10-006-869-1392

Query Match 54.8%; Score 23; DB 14; Length 7;
Best Local Similarity 42.9%; Pred. No. 7.2e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CVELTSC 7
|:
Db 1 CIDANSC 7

Search completed: March 8, 2004, 12:36:00
Job time : 33 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:08:26 ; Search time 23 Seconds
(without alignments)
24.691 Million cell updates/sec

Title: US-09-761-636A-7
Perfect score: 61
Sequence: 1 C1SVPLTSVPC 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues
Total number of hits satisfying chosen parameters: 112282

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/prodata/2/iaa/5B COMB. pep.*
3: /cgn2_6/prodata/2/iaa/6A COMB. pep.*
4: /cgn2_6/prodata/2/iaa/6B COMB. pep.*
5: /cgn2_6/prodata/2/iaa/6C COMB. pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	30	49.2	8	1	US-08-189-331-150
2	30	49.2	8	2	US-08-471-068-150
3	27	44.3	10	1	US-08-212-190A-5
4	27	44.3	10	2	US-08-900-321-5
5	27	44.3	10	5	PCT-US95-03610-5
6	26	42.6	6	2	US-08-769-745-15
7	26	42.6	8	1	US-08-189-331-149
8	26	42.6	8	2	US-08-471-068-149
9	25.5	41.8	9	1	US-08-331-383-33
10	25.5	41.8	9	1	US-08-549-008-43
11	25.5	41.8	9	3	US-08-802-981-143
12	25	41.0	8	1	US-08-360-239B-1
13	25	41.0	10	2	US-08-483-077C-26
14	25	41.0	10	2	US-08-519-109B-26
15	25	41.0	10	2	US-08-482-228-108
16	25	41.0	10	3	US-08-482-528-108
17	25	41.0	10	5	PCT-US95-10811-38
18	24	39.3	6	1	US-08-483-434A-21
19	24	39.3	6	3	US-08-476-134A-30
20	24	39.3	6	6	5190920-26
21	24	39.3	6	6	5506208-28
22	24	39.3	7	4	US-09-438-150-1
23	24	39.3	9	2	US-08-340-283-154
24	24	39.3	9	4	US-09-601-729-204
25	24	39.3	10	3	US-08-836-075A-187
26	23.5	38.5	9	1	US-08-331-383-31
27	23.5	38.5	9	1	US-08-549-008-42

Sequence 142, App
Sequence 144, App
Sequence 147, App
Sequence 148, App
Sequence 61, Appl
Sequence 147, App
Sequence 148, App
Sequence 4, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 19, Appl
Sequence 25, Appl
Sequence 3, Appl
Sequence 4, Appl
Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-189-331-150
; Sequence 150, Application US/08189331
; Patent No. 5747334
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; APPLICANT: Fowles, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,331
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mierock, S. Leslie
; REGISTRATION NUMBER: 19,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-189-331-150

Query Match 49.2%; Score 30; DB 1; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 C1SVPLTS 8
|:|:|
Db 1 CVSAPQTS 8

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,190A
FILING DATE: 14-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 15280-204US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-212-190A-5
Query Match 44.3%; Score 27; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 VPLTSPVC 11
Db 1 VPAPVPC 8

RESULT 4
US-08-900-321-5
Sequence 5, Application US/089000321
Patent No. 5981712
GENERAL INFORMATION:
APPLICANT: Kohn, Elise C.
APPLICANT: Liotta, Lance A.
TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,321
FILING DATE: 25-JUL-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,190
FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-204100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,068
FILING DATE:
PRIORITY APPLICATION: 435
PRIOR APPLICATION NUMBER: 08/189,331
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,972
REFERENCE/DOCKET NUMBER: 1101-155
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-068-150
Query Match 49.2%; Score 30; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CISVP LTS 8
Db 1 CV SAPOTS 8

RESULT 3
US-08-212-190A-5
Sequence 5, Application US/08212190A
Patent No. 5652223
GENERAL INFORMATION:
APPLICANT: KOHN, ELISE C.
APPLICANT: LIOTTA, LANCE A.
APPLICANT: KIM, YOUNG SOOK
TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US

```


SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-900-321-5

Query Match 44.3%; Score 27; DB 2; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 VPLTSVPC 11
 |||||
 Db 1 VPPAPVPC 8

RESULT 5
 PCT-US95-03610-5
 ; Sequence 5, Application PC/TUS9503610
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
 ; TITLE OF INVENTION: US5 THEREOF
 ; NUMBER OF SEQUENCES: 10
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/03610
 ; FILING DATE: 14-MAR-1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/212,190
 ; FILING DATE: 14-MAR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Weber, Kenneth A.
 ; REGISTRATION NUMBER: 31,677
 ; REFERENCE/DOCKET NUMBER: 15280-204000PC
 ; REFERENCE/DOCKET NUMBER: DHS Ref. No. E-112-94/0
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 543-9600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; PCT-US95-03610-5

Query Match 44.3%; Score 27; DB 5; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 VPLTSVPC 11
 |||||
 Db 1 VPPAPVPC 8

RESULT 6
 US-08-769-745-15
 ; Sequence 15, Application US/08769745
 ; Patent No. 5955259
 ; GENERAL INFORMATION:
 ; APPLICANT: Holmes, Todd C.
 ; APPLICANT: Levitan, Irwin B.
 ; APPLICANT: Brandeis University
 ; TITLE OF INVENTION: Mechanism for the Regulation of Ion
 ; CHANNEL ACTIVITY

FILE REFERENCE: BRU96-02
 ; CURRENT APPLICATION NUMBER: US/08/769,745
 ; CURRENT FILING DATE: 1996-12-19
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: RastSEQ for Windows Version 3.0
 ; SEQ ID NO 15
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Rat
 ; US-08-769-745-15

Query Match 42.6%; Score 26; DB 2; Length 6;
 Best Local Similarity 83.3%; Pred. No. 3e+05;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLTSVP 10
 |||||
 Db 1 PLTFVP 6

RESULT 7
 US-08-189-331-149
 ; Sequence 149, Application US/08189331
 ; Patent No. 5747334
 ; GENERAL INFORMATION:
 ; APPLICANT: Kay, B. K.
 ; APPLICANT: Fowlkes, D. M.
 ; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
 ; NUMBER OF SEQUENCES: 186
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/189,331
 ; FILING DATE: Concurrently herewith
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 1101-155
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 790-9090
 ; TELEFAX: 212 869-8864/9741
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 149:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; US-08-189-331-149

Query Match 42.6%; Score 26; DB 1; Length 8;
 Best Local Similarity 57.1%; Pred. No. 3e+05;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLT 7
 |:|||
 Db 2 CVSAPQT 8

RESULT 8
 US-08-471-068-149

Mon Mar 8 13:11:03 2004

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; Sequence 149, Application US/08471068
; Patent No. 5948635
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,068
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/189,331
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Lealie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 149:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-471-068-149

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Query Match 42.6%; Score 26; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 CUSVPLT 7
DB 2 CVSAPQT 8

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RESULT 9
US-08-331-383-33
; Sequence 33, Application US/08331383
; Patent No. 5605809
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of
; TITLE OF INVENTION: Proteases in Biological Samples and Use
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,383
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 16865-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-331-383-33

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Query Match 41.8%; Score 25.5; DB 1; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

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QY 3 SVPLTSVPC 11
DB 2 AIPM-SIPC 9

```

```

RESULT 10
US-08-549-008-43
; Sequence 43, Application US/08549008
; Patent No. 5714342
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of
; TITLE OF INVENTION: Protease in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/549,008
; FILING DATE: 27-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,383
; FILING DATE: 28-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 016865-000110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

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MOLECULE TYPE: peptide
US-08-549-008-43

Query Match 41.8%; Score 25.5; DB 1; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05; 0; Indels 1; Gaps 1;
Matches 4; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 3 SVPLTSVPC 11
DB 2 AIPM-SIPC 9

RESULT 11

US-08-802-981-143
Sequence 143, Application US/08802981
Patent No. 6037137
GENERAL INFORMATION:
APPLICANT: Komoriya, Akira
APPLICANT: Packard, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of Enzyme
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 016865-000300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-802-981-143

Query Match 41.8%; Score 25.5; DB 3; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05; 0; Indels 1; Gaps 1;
Matches 4; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 3 SVPLTSVPC 11
DB 2 AIPM-SIPC 9

RESULT 12

US-08-360-239B-1
Sequence 1, Application US/08360239B
Patent No. 5801222
GENERAL INFORMATION:
APPLICANT: Pettit, George R.
APPLICANT: Tan, Rui
TITLE OF INVENTION: Isolation and Structure of
TITLE OF INVENTION: the Human Cancer Cell Growth Inhibitory Cyclic
TITLE OF INVENTION: Octapeptides Phakellistatin 10 and 11

NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Mybeck
STREET: 8010 East Morgan Trail, #10
CITY: Scottsdale
STATE: Arizona
COUNTRY: USA
ZIP: 85258-1234
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM PS/2
OPERATING SYSTEM: DOS 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,239B
FILING DATE: 12/20/94
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Richard R. Mybeck
REGISTRATION NUMBER: 17,886
REFERENCE/DOCKET NUMBER: 4997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (602)-483-1285
TELEFAX: (602)-483-7452
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acid residues
TYPE: amino acid
TOPOLOGY: Cyclic
MOLECULE TYPE:
DESCRIPTION: Cyclooctapeptide
DESCRIPTION: Phakellistatin 10
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: circular
ORIGINAL SOURCE:
ORGANISM: Phakellia sp.
DEVELOPMENTAL STAGE: whole organism
FEATURE:
NAME/KEY: Phakellistatin 10
NAME/KEY: amino acid analysis, high resolution
NAME/KEY: nuclear magnetic resonance and mass
NAME/KEY: spectral MS/MS techniques
OTHER INFORMATION: Phakellistatin 10 is a
OTHER INFORMATION: cell growth inhibitory peptide with
OTHER INFORMATION: activity in murine lymphocytic leukemia
OTHER INFORMATION: cell line of 2.1 mg/ml.
US-08-360-239B-1

Query Match 41.0%; Score 25; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLTSVP 10
DB 1 PLTPIP 6

RESULT 13

US-08-483-077C-26
Sequence 26, Application US/08483077C
Patent No. 5811391
GENERAL INFORMATION:
APPLICANT: Arrhenius, Thomas S.
APPLICANT: Tempczyk, Anna
APPLICANT: Ellices, Mariano J.
APPLICANT: Zheng, Zhong-Li
TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics
TITLE OF INVENTION: Compositions and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700

```

; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA: US/08/483,077C
; APPLICATION NUMBER: US/08/483,077C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
;
; REFERENCE/DOCKET NUMBER: P-CY 1647
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
;
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 10
;
; OTHER INFORMATION: /note= "The carboxy-terminus is a
; carboxamide."
;
; US-08-483-077C-26
;
; Query Match 41.0%; Score 25; DB 2; Length 10;
; Best Local Similarity 44.4%; Pred. No. 3.4e+02;
; Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
;
; QY 2 ISVPLTSPV 10
; : ||: ||
; DB 2 LDVPILDVP 10
;
; RESULT 14
; US-08-519-109B-26
; Sequence 26, Application US/08519109B
; Patent No. 5869448
;
; GENERAL INFORMATION:
; APPLICANT: Arrhenius, Thomas S.
; APPLICANT: Tempczyk, Anna
; APPLICANT: Elices, Mariano J.
; APPLICANT: Zheng, Zhong-Li
; TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
; Compositions and Methods of Using Same
;
; NUMBER OF SEQUENCES: 33
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/519,109B
; FILING DATE: 25-AUG-1995
; CLASSIFICATION: 514
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815

```

```

; REFERENCE/DOCKET NUMBER: P-CY 1795
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
;
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 10
;
; OTHER INFORMATION: /note= "The carboxy-terminus is a
; carboxamide."
;
; US-08-519-109B-26
;
; Query Match 41.0%; Score 25; DB 2; Length 10;
; Best Local Similarity 44.4%; Pred. No. 3.4e+02;
; Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
;
; QY 2 ISVPLTSPV 10
; : ||: ||
; DB 2 LDVPILDVP 10
;
; RESULT 15
; US-08-482-228-108
; Sequence 108, Application US/08482228
; Patent No. 5968753
;
; GENERAL INFORMATION:
; APPLICANT: Teeng-Law, Janet
; APPLICANT: Kobori, Joan A.
; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Guillermo, Roy
; APPLICANT: Helgeson, Sam I.
; APPLICANT: Deans, Robert J.
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
; SELECTION MEDIATED BY PEPTIDE RELEASE
;
; NUMBER OF SEQUENCES: 215
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janice Guthrie, Ph.D.
; STREET: P.O. Box 15210
; CITY: Irvine
; STATE: California
; COUNTRY: USA
; ZIP: 92713-5210
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,228
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Guthrie, Janice
; REGISTRATION NUMBER: 35,170
;
; REFERENCE/DOCKET NUMBER: IT-4630CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 440-5353
; TELEFAX: (714) 553-1952
;
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
;
; US-08-482-228-108
;
; Query Match 41.0%; Score 25; DB 2; Length 10;
; Best Local Similarity 66.7%; Pred. No. 3.4e+02;

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Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 C1SVPLTSV 9

Db 2 CIDVFLTCV 10

Search completed: March 8, 2004, 12:11:49
Job time : 23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2004, 12:15:17 ; Search time 13 Seconds
(without alignments)

66.594 Million cell updates/sec

Title: US-09-761-636A-10

Perfect score: 50

Sequence: 1 CSVPLTSVC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 790

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78.*

1: piri.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	34.0	8	2	G33098
2	16	32.0	9	2	A60356
3	16	32.0	9	2	PT0247
4	15	30.0	5	2	A60521
5	15	30.0	6	2	I65546
6	15	30.0	7	2	PH0932
7	15	30.0	8	2	PH0803
8	14	28.0	5	2	E60274
9	14	28.0	6	2	F41946
10	14	28.0	8	2	A42057
11	14	28.0	8	2	A35180
12	14	28.0	9	2	A60522
13	14	28.0	9	2	B41983
14	14	28.0	9	2	I52974
15	13	26.0	6	2	I49421
16	13	26.0	6	2	S29881
17	13	26.0	7	2	A12016
18	13	26.0	7	2	S42620
19	13	26.0	8	2	S59622
20	13	26.0	8	2	PQ0701
21	13	26.0	9	2	PT0268
22	12	24.0	6	4	A35039
23	12	24.0	7	2	E61491
24	12	24.0	8	2	S71919
25	12	24.0	8	2	S10783
26	12	24.0	9	2	S13636
27	12	24.0	9	2	G58502
28	12	24.0	9	2	S70334
29	11	22.0	4	2	A32039

30 11 22.0 4 2 I54357
31 11 22.0 5 2 B22565
32 11 22.0 6 2 B34835
33 11 22.0 6 2 PT0280
34 11 22.0 7 2 BOMUCR
35 11 22.0 7 2 I48105
36 11 22.0 7 2 I48086
37 11 22.0 7 2 PH1602
38 11 22.0 8 2 S19288
39 11 22.0 8 2 B39745
40 11 22.0 8 2 S68802
41 11 22.0 8 2 S21288
42 11 22.0 8 2 PT0530
43 11 22.0 8 2 I57018
44 11 22.0 8 2 A42689
45 11 22.0 8 4 I54017

ALIGNMENTS

RESULT 1

G33098

205K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)

C:Species: Plasmodium falciparum

C>Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000

C:Accession: G33098

R:Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A:Reference number: A33098

A:Accession: G33098

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <NIC>

Query Match 34.0%; Score 17; DB 2; Length 8;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VPLTSV 8

Db 2 VPLXLV 7

RESULT 2

A60356

118K stomach cancer antigen - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 17-Mar-1999

C:Accession: A60356

R:Shiraishi, Y.

Int. J. Cancer 45, 783-787, 1990

A>Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens

A:Reference number: A60356; MUID:90216080; PMID:2323853

A:Accession: A60356

A:Molecule type: protein

A:Residues: 1-9 <SHI>

C:Keywords: glycoprotein

Query Match 32.0%; Score 16; DB 2; Length 9;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VPLTSV 8

Db 1 IPLKPV 6

RESULT 3

PT0247

IG heavy chain CRD3 region (clone 2-106A) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

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C:Accession: PT0247
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0247
A:Molecule type: DNA
A:Residues: 1-9 <YAM>
A:Experimental source: B lymphocyte
A:Keywords: heterotrimer; immunoglobulin

Query Match 32.0%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SVPLTS 7
Db 2 SAPIDS 7

RESULT 4
A60521
glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N:Alternate names: Glycogen phosphorylase b
C:Species: Liza ramada
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003
C:Accession: A60521
R:Bonamura, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A:Title: Purification and characterization of glycogen phosphorylase B from skeletal mus
A:Reference number: A60521; MUID:190227907; PMID:2109669
A:Accession: A60521
A:Molecule type: protein
A:Residues: 1-5 <BON>
C:Superfamily: glucan phosphorylase
C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F:3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim

Query Match 30.0%; Score 15; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVP 4
Db 3 SVP 5

RESULT 5
I65546
MHC H2-L antigen - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I65546
R:Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
Cell 44, 261-272, 1986
A:Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and their
A:Reference number: I52778; MUID:86106202; PMID:13510743
A:Accession: I65546
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: GB:M12483; NID:gl199565; PIDN:AAA39663.1; PID:g554234

Query Match 30.0%; Score 15; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 VPCT 6
Db 2 VPCT 5

RESULT 6
PH0932
T-cell receptor beta chain V-D-J region (clone 3) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0932
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental aller
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0932
A:Molecule type: mRNA
A:Residues: 1-7 <GOL>
A:Experimental source: complete Freund's adjuvant-immunized lymph node
A:Keywords: T-cell receptor

Query Match 30.0%; Score 15; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSVP 4
Db 1 CASP 4

RESULT 7
PH0803
T-cell receptor alpha chain (J2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0803
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0803
A:Molecule type: mRNA
A:Residues: 1-8 <CAS>
A:Cross-references: EMBL:X60912
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 30.0%; Score 15; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPILT 6
Db 1 CAAGIT 6

RESULT 8
E60274
major protein antigen MP763 - Mycobacterium tuberculosis (fragment)
C:Species: Mycobacterium tuberculosis
C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C:Accession: E60274
R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A:Title: Isolation and partial characterization of major protein antigens in the cultu
A:Reference number: A60274; MUID:91099989; PMID:1898899
A:Accession: E60274
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <NAG>

Query Match 28.0%; Score 14; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PLT 6
Db 3 PIT 5

```

```

RESULT 9
F41946
T-cell receptor gamma chain (1a.27) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: F41946
R:Whetsell, M.; Mowley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A>Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A:Reference number: A41946; MUID:92049316; PMID:1658619
A:Accession: F41946
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <WHE>
C:Keywords: T-cell receptor

Query Match      28.0%; Score 14; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSV 3
   | |
   | |
Db 2 CAV 4

RESULT 10
A42057
fibroblast growth factor receptor 1, secreted - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C:Accession: A42057
R:Werner, S.; Duan, D.S.R.; de Vries, C.; Peters, K.G.; Johnson, D.E.; Williams, L.T.
Mol. Cell. Biol. 12, 82-88, 1992
A>Title: Differential splicing in the extracellular region of fibroblast growth factor r
A:Reference number: A42057; MUID:92107200; PMID:1309595
A:Accession: A42057
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <WER>
A:Cross-references: GB:M80363
C:Keywords: growth factor receptor

Query Match      28.0%; Score 14; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 VPLTS 7
   | | |
   | | |
   | | |
Db 1 VLLTS 5

RESULT 11
A35180
neutral proteinase (EC 3.4.21.-), calcium-activated - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 21-Mar-1996
C:Accession: A35180
R:Yoshihara, Y.; Ueda, H.; Fujii, N.; Shide, A.; Yajima, H.; Satoh, M.
J. Biol. Chem. 265, 5809-5815, 1990
A>Title: Purification of a novel type of calcium-activated neutral protease from rat bra
A:Reference number: A35180; MUID:90202830; PMID:2318836
A:Accession: A35180
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <YOS>
C:Keywords: hydrolase

Query Match      28.0%; Score 14; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 12
A60522
sperm-activating peptide SAP-IV - sea urchin (Diadema setosum)
C:Species: Diadema setosum
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C:Accession: A60522
R:Yoshino, K.I.; Kurita, M.; Yamaguchi, M.; Nomura, K.; Takao, T.; Shimonishi, Y.; Suz
Comp. Biochem. Physiol. B 95, 423-429, 1990
A>Title: A species-specific sperm-activating peptide from the egg jelly of the sea urch
A:Reference number: A60522; MUID:90227916; PMID:2158412
A:Accession: A60522
A:Molecule type: protein
A:Residues: 1-9 <YOS>
C:Superfamily: unassigned animal peptides
F;2-9/Disulfide bonds: #status experimental

Query Match      28.0%; Score 14; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 SVC 9
   | |
   | |
   | |
Db 7 AVC 9

RESULT 13
B41983
orf downstream to bacterioferritin - Azotobacter vinelandii (fragment)
C:Species: Azotobacter vinelandii
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: B41983
R:Grossman, M.J.; Hinton, S.M.; Minak-Bernero, V.; Slaughter, C.; Stiefel, B.I.
Proc. Natl. Acad. Sci. U.S.A. 89, 2419-2423, 1992
A>Title: Unification of the ferritin family of proteins.
A:Reference number: A41983; MUID:92196129; PMID:1549605
A:Accession: B41983
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-9 <GRO>
A:Cross-references: GB:M83692; NID:gl42297; PIDN:AAA22122.1; PID:gl42299
A:Note: sequence extracted from NCBI backbone (NCBIP:88442)

Query Match      28.0%; Score 14; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PLTS 7
   | |
   | |
   | |
Db 4 PRTS 7

RESULT 14
I52974
seminal vesicle protein IV - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I52974
R:Teng, C.T.; Harris, S.E.
DNA 2, 105-111, 1983
A>Title: The seminal vesicle secretion IV gene: detection of S1 nuclease-sensitive sit
A:Reference number: I52974; MUID:83261204; PMID:6307619
A:Accession: I52974
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-9 <RES>
A:Cross-references: GB:M27324; NID:G207124; PIDN:AAA63501.1; PID:G207125
C:Genetics:
A:Gene: SVSIV

```


Query Match 28.0%; Score 14; DB 2; Length 9;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LTVS 8
 Db 3 LTSL 6

RESULT 15

I49421
 Laminin B1 - western wild mouse (fragment)
 C;Species: Mus spretus (western wild mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C;Accession: I49421
 R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
 Mamm. Genome 5, 349-355, 1994
 A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
 A;Reference number: I48934; MUID:94319082; PMID:8043949
 A;Accession: I49421
 A;Status: preliminary; translated from GH/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-6 <RES>
 A;Cross-references: EMBL:U05736; NID:9497073; PIDN:AAB60477.1; PID:9642829

Query Match 26.0%; Score 13; DB 2; Length 6;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 SVC 9
 Db 3 STC 5

Search completed: March 8, 2004, 12:20:24
 Job time : 13 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:11:57 ; Search time 10 Seconds
(without alignments)
46.863 Million cell updates/sec

Title: US-09-761-636A-10
Perfect score: 50
Sequence: 1 CSVPLTSVC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 251

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	38.0	9	1 MGMT_BOVIN	P29177 bos taurus
2	14	28.0	8	1 ACT_CARMA	P80709 carcinus ma
3	14	28.0	9	1 YBFR_AZOVI	P25825 azotobacter
4	13	26.0	6	1 E101_LITRU	P82096 litoria rub
5	12	24.0	8	1 ALL6_CYDFO	P82157 cydia pomon
6	12	24.0	8	1 FUSS_FUSSO	P81010 fusarium so
7	12	24.0	8	1 UPAL_HUMAN	P30087 homo sapien
8	12	24.0	9	1 FAR5_PENMO	P83320 penaeus mon
9	12	24.0	9	1 FLA2_TREHY	P80159 treponema h
10	12	24.0	9	1 OXYA_SCYCA	P42396 scyllorhinu
11	12	24.0	9	1 OXYF_SCYCA	P42397 scyllorhinu
12	12	24.0	9	1 OXYT_BUPRE	P42995 bufo regula
13	12	24.0	9	1 OXYV_SQUAC	P43000 squalus aca
14	11	22.0	6	1 VP19_HSVIK	P23210 herpes simp
15	11	22.0	7	1 CARP_MYTED	P10420 mytilus edu
16	11	22.0	7	1 MNP1_LEPDE	P42984 leptinotars
17	11	22.0	7	1 TEPY_PACDA	P83455 pachymedusa
18	11	22.0	8	1 PKP3_PERAM	P82618 periplaneta
19	11	22.0	8	1 VGLG_HSV2B	P81780 herpes simp
20	11	22.0	9	1 COXE_THUOB	P80975 thunnus obe
21	11	22.0	9	1 FAR9_ASCSU	P43172 ascaris suu
22	11	22.0	9	1 ISOT_CYPCA	P42993 cyprinus ca
23	11	22.0	9	1 LMT3_LOCOMI	P41489 locusta mig
24	11	22.0	9	1 OXYA_SQUAC	P42999 squalus aca
25	11	22.0	9	1 OXYT_EISFO	P42998 eisenia foe
26	11	22.0	9	1 OXYT_OCTVU	P80027 octopus vul
27	11	22.0	9	1 OXYT_RABIT	P32878 oryctolagus
28	11	22.0	9	1 RU33_BOVIN	P82926 bos taurus
29	11	22.0	9	1 TAL3_PICJA	P17441 pichia jadi
30	11	22.0	9	1 UPAT3_HUMAN	P30089 homo sapien
31	11	22.0	9	1 UPAT7_HUMAN	P30093 homo sapien
32	10	20.0	7	1 TV51_LITRU	P82065 litoria rub
33	10	20.0	8	1 UPAA_HUMAN	P30096 homo sapien

34	10	20.0	9	1 CCAP_CARMA	P38556 carcinus ma
35	10	20.0	9	1 CONO_CONGE	P05486 conus geogr
36	10	20.0	9	1 CONO_CONST	P05487 conus stria
37	10	20.0	9	1 DNF1_LOCOMI	P16339 locusta mig
38	10	20.0	9	1 OXYT_CYPCA	P23879 cyprinus ca
39	10	20.0	9	1 OXYT_RAJCL	P42994 raja clavata
40	10	20.0	9	1 PPK1_PERAM	P82891 periplaneta
41	10	20.0	9	1 TAL1_PICJA	P17440 pichia jadi
42	9	18.0	5	1 E103_LITRU	P82099 litoria rub
43	9	18.0	6	1 CIP1_MYTED	P13736 mytilus edu
44	9	18.0	6	1 CIP2_MYTED	P13737 mytilus edu
45	9	18.0	7	1 BRHP_CONIM	P58803 conus imper

ALIGNMENTS

RESULT 1
MGMT_BOVIN
ID MGMT_BOVIN STANDARD; PRT; 9 AA.
AC P29177;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE Methylated-DNA-protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-methylguanine-DNA methyltransferase) (Fragment).
GN MGMT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.

RC TISSUE=Thymus;
RX MEDLINE=90174912; PubMed=2308822;
RA Rydberg B., Hall J., Karran P.;
RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA methyltransferase.";
RL Nucleic Acids Res. 18:17-21(1990).
CC -!- FUNCTION: Repair of alkylated guanine in DNA by stoichiometrically transferring the alkyl group at the O-6 position to a cysteine residue in the enzyme. This is a suicide reaction: the enzyme is irreversibly inactivated.
CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) + protein [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein S-methyl-L-cysteine.
CC -!- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OCT METHYLTRANSFERASE WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
DR InterPro; IPR001497; Methyltransf_1.
DR PROSITE; PS00374; MGMT; PARTIAL.
KW DNA repair; Transferase; Methyltransferase.
FT NON TER 1 1
FT ACT SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
FT NON TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 38.0%; Score 19; DB 1; Length 9;
Best Local Similarity 28.6%; Pred. No. 1.4e+05;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY	3	VPLTSVC	9
Db	3	IPILTPC	9

RESULT 2
ACT_CARMA
ID ACT_CARMA STANDARD; PRT; 8 AA.
AC P80709;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Actin (Fragment).
 OS Carinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunioidea; Portunidae; Carinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
 RA Baghdassarian D.;
 RT "A" transaldolase. An enzyme implicated in crab steroidogenesis.";
 RL Endocrine 5:23-32(1996).
 CC -1- FUNCTION: Actins are highly conserved proteins that are involved
 CC in various types of cell motility and are ubiquitously expressed
 CC in all eukaryotic cells.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
 CC 6.8, ITS MW IS: 46 kDa.
 CC -1- SIMILARITY: Belongs to the actin family.
 CC InterPro: IPR004001; Actin.
 DR InterPro: IPR004000; Actin like.
 DR PROSITE: PS00406; ACTINS 1; PARTIAL.
 DR PROSITE: PS00432; ACTINS 2; PARTIAL.
 DR PROSITE: PS01132; ACTINS_ACT LIKE; PARTIAL.
 KW Structural protein.
 FT NON TER 1 1
 FT NON TER 8 8
 FT NON TER 1 1
 SQ SEQUENCE 8 AA; 976 MW; 1424005AB2CAEB3 CRC64;
 Query Match 28.0%; Score 14; DB 1; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CSVPL 5
 DB 2 CDVDI 6
 RESULT 3
 YBFR AZOVI
 ID YBFR AZOVI STANDARD; PRT; 9 AA.
 AC P25825;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein in bfr 3' region (Fragment).
 OS Azotobacter vinelandii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Azotobacter.
 OX NCBI_TaxID=354;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92196129; PubMed=1549605;
 RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,
 RA Stiefel E.J.;
 RT "Unification of the ferritin family of proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL; M81692; AAA22122.1;
 DR PIR; B41983; B41983.
 KW Hypothetical protein.
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B41776D CRC64;
 Query Match 28.0%; Score 14; DB 1; Length 9;

Best Local Similarity 75.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 PLTS 7
 DB 4 PRTS 7
 RESULT 4
 EI01 LITRU
 ID EI01 LITRU STANDARD; PRT; 6 AA.
 AC P82036;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Electrin 1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella.";
 RL Aust. J. Chem. 52:639-645(1999).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Skin.
 KW Amphibian defense peptide; Amidation.
 FT MOD RES 6 6
 FT MOD RES 6 6
 SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;
 Query Match 26.0%; Score 13; DB 1; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 VPL 5
 DB 2 VPI 4
 RESULT 5
 ALL6 CYDPO
 ID ALL6 CYDPO STANDARD; PRT; 8 AA.
 AC P82157;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiaastatin 6.
 OS Cydia pomonella (Codling moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997).
 CC -1- SIMILARITY: Belongs to the allatostatin family.
 KW Neuropeptide; Amidation.
 FT MOD RES 8 8
 FT MOD RES 8 8
 SQ SEQUENCE 8 AA; 936 MW; 0E2879C45B573767 CRC64;
 Query Match 24.0%; Score 12; DB 1; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VPL 5
Db :|||
1 LPL 3

RESULT 6

FUSS FUSSO STANDARD; PRT; 8 AA.
AC P81010;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Allergen Fus s I3596* (Fragment)
OS Fusarium solani (subsp. pisi) (Nectria haematococca).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=70791;
RN [1]
RP SEQUENCE.
RC STRAIN=IARI 3596; TISSUE=Mycelium;
RA Verma J., Gangal S.V.;
RL Submitted (JUL-1997) to Swiss-Prot.
KW -!- ALLERGEN: Causes an allergic reaction in human.
CC Allergen.
FT NON TER
SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 24.0%; Score 12; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVP 4
Db :|||
6 NVP 8

RESULT 7

UPA1 HUMAN STANDARD; PRT; 8 AA.
AC P30087;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing."
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 4.9, its MW is: 65 kDa.
DR SWISS-2DPAGE; P30087; HUMAN.
FT NON TER
FT UNSURE
FT NON TER
SQ SEQUENCE 8 AA; 944 MW; C01772C455B806DA CRC64;

Query Match 24.0%; Score 12; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVP 4
Db :|||
5 NVP 7

RESULT 8
FARS PENMO STANDARD; PRT; 9 AA.
AC P83320;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP5 (SMPSLRLF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eviscalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
RA Chaivuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1121.1; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1106 MW; B60B07340735A766 CRC64;

Query Match 24.0%; Score 12; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVP 4
Db :|||
1 SMP 3

RESULT 9

FLA2 TREHY STANDARD; PRT; 9 AA.
AC P80159;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Flagellar filament outer layer protein flaa2 (35 kDa sheath protein)
DE (Fragment).
GN FLA2.
OS Treponema hyodysenteriae (Serpulina hyodysenteriae).
OC Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspira.
OX NCBI_TaxID=159;
RN [1]
RP SEQUENCE.
RC STRAIN=CS;
RX MEDLINE=93139764; PubMed=1487733;
RA Koopman M.B.H., Baats B., van Vorstenbosch C.J.A.H.V.,
RA van der Zeijst B.A.M., Kusters J.G.;
RT "The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are
composed of two sheath proteins and three core proteins.";
RL J. Gen. Microbiol. 138:2697-2706(1992).
CC -!- SUBUNIT: Component of the outer layer of the flagella.
CC -!- FUNCTION: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO
CC SHEATH PROTEINS, FLA1 (44 kDa) AND FLA2 (35 kDa) AROUND A CORE
CC THAT CONTAINS THREE PROTEINS FLA1 (37 kDa), FLA2 (34 kDa) AND
CC FLA3 (32 kDa).
CC -!- SUBCELLULAR LOCATION: Periplasmic flagellum.
KW Flagellum; Periplasmic.
FT UNSURE 2
FT UNSURE 8 9

```

RT isolated from the spotted dogfish (Scyliorhinus caniculus).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 1 9
SQ SEQUENCE 9 AA; 1016 MW; 17EDD76B44449DB CRC64;

Query Match 24.0%; Score 12; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CSV 3
| |
Db 6 CPV 8

RESULT 12
OXYT_BUFRE STANDARD; PRT; 9 AA.
AC P42395;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Seritocin ([Ser5,Ile8]-oxytocin).
OS Bufo regularis (Leopard toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Bufonidae; Bufo.
OC NCBI_TaxID=8390;
[1] _SEQUENCE.
RP TISSUE=Pituitary neurointermediate lobe;
RC MEDLINE=36059313; PubMed=7591488;
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;
RT "A new neurohypophyseal peptide, seritocin ([Ser5,Ile8]-oxytocin),
RT identified in a dryness-resistant African toad, Bufo regularis.";
RL Int. J. Pept. Protein Res. 45:482-487(1995).
CC -!- FUNCTION: Devoid of oxytocic activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 1 9
SQ SEQUENCE 9 AA; 983 MW; 17FF476EA54ED04B CRC64;

Query Match 24.0%; Score 12; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SVPL 5
| |
Db 5 SCPI 8

RESULT 13
OXYT_SQUAC STANDARD; PRT; 9 AA.
AC P43000;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Valitocin.
OS Squalus canthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidea; Squalidae; Squalus.
OC NCBI_TaxID=7797;

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RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RL isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 23:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-
RT oxytocin) and apatocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4.1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 996 MW; 17EDD76EB456D04B CRC64;

Query Match 24.0%; Score 12; DB 1; Length 9;
Best Local Similarity 56.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSV 3
|
|
DB 6 CPV 8

RESULT 14
VP19 HSV1K STANDARD; PRT; 6 AA.
ID AC P23210;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Capsid assembly and DNA maturation protein (Varion protein UL38)
DE (Capsid protein VP19C) (Fragment).
GN UL38.
OS Herpes simplex virus (type 1 / strain KOS).
OC Viruses; GEDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91101287; PubMed=1846198;
RA Flanagan W.M., Papavasiliou A.G., Rice M., Hecht L.B.,
RA Silverstein S., Wagner E.K.;
RT "Analysis of the herpes simplex virus type 1 promoter controlling the
RT expression of UL38, a true late gene involved in capsid assembly.";
RL J. Virol. 65:769-786(1991).
CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
CC EMBEDDED. BINDS DNA.
CC -!- SIMILARITY: Belongs to the herpesviruses VP19C family.
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-----
DB EMBL; M57646; AAA45830.1;
KW Capsid assembly; Coat protein; DNA-binding.
FT NON TER 6
SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;

Query Match 22.0%; Score 11; DB 1; Length 6;
Best Local Similarity 25.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVPL 5
|
|
DB 1 AMPM 4

Search completed: March 8, 2004, 12:18:23
Job time : 10 secs

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Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PL 5
|
|
DB 5 PL 6

RESULT 15
CARP MYTED STANDARD; PRT; 7 AA.
ID AC P10420;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Catch-relaxing peptide (CARP).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RX MEDLINE=88052022; PubMed=3676797;
RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
RA Muneoka Y.;
RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
RL Brain Res. 422:374-376(1987).
CC -!- FUNCTION: This peptide exhibits both potentiating (contraction)
CC and inhibitory (relaxation) effects on the anterior byssus
CC retractor muscle.
DR PIR; A29342; ECMUCR.
KW Hormone; Amidation.
FT MOD RES 7 7
SQ SEQUENCE 7 AA; 831 MW; 6734072687669DE0 CRC64;

Query Match 22.0%; Score 11; DB 1; Length 7;
Best Local Similarity 25.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVPL 5
|
|
DB 1 AMPM 4

Search completed: March 8, 2004, 12:18:23
Job time : 10 secs

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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:14:57 ; Search time 34.5 Seconds
(without alignments)
82.309 Million cell updates/sec

Title: US-09-761-636A-10
Perfect score: 50
Sequence: 1 CSVPLTSVC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 840

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	40.0	8	2 Q8GMM5	Q8GMM5 acinetobact
2	18	36.0	9	10 Q9FXL0	Q9FXL0 lilium long
3	17	34.0	7	13 Q8J20	Q8J20 gallus gall
4	17	34.0	7	13 Q42564	Q42564 fugu rubrip
5	17	34.0	8	15 Q85562	Q85562 moloney mur
6	17	34.0	9	11 Q8CG13	Q8CG13 mus musc
7	16	32.0	8	2 Q8KPY4	Q8KPY4 microcystis
8	16	32.0	8	2 Q849P4	Q849P4 salmone
9	16	32.0	8	4 Q9Y4X6	Q9Y4X6 homo sapien
10	16	32.0	8	4 Q16468	Q16468 homo sapien
11	16	32.0	8	10 Q8L802	Q8L802 zea mays (m
12	16	32.0	9	6 Q9TRU7	Q9TRU7 bos taurus
13	16	32.0	9	11 Q35953	Q35953 mus musc
14	15	30.0	8	2 Q56140	Q56140 streptococ
15	15	30.0	8	8 Q9TKES	Q9TKES leptospermu
16	15	30.0	8	8 Q9MD43	Q9MD43 rattus norv

17	15	30.0	8	10 Q9SAY7	Q9SAY7 dioscorea t
18	15	30.0	9	8 Q9TKF2	Q9TKF2 asteromyrtu
19	15	30.0	9	8 Q9TKG1	Q9TKG1 calothamius
20	14	28.0	7	2 P70804	P70804 azotobacter
21	14	28.0	7	15 Q07624	Q07624 rous sarcom
22	14	28.0	7	13 Q9P868	Q9P868 gallus gall
23	13	26.0	7	12 Q67113	Q67113 influenzavi
24	13	26.0	8	4 Q15890	Q15890 homo sapien
25	13	26.0	8	4 Q15898	Q15898 homo sapien
26	13	26.0	9	2 Q31363	Q31363 borrelia ga
27	13	26.0	9	2 Q9K4M6	Q9K4M6 staphylococ
28	13	26.0	9	2 Q15999	Q15999 homo sapien
29	13	26.0	9	8 Q9TKD9	Q9TKD9 pericalymma
30	13	26.0	9	11 Q99JF4	Q99JF4 mus musc
31	13	26.0	9	12 Q90350	Q90350 hepatitis g
32	13	26.0	9	12 Q9E1U7	Q9E1U7 hepatitis b
33	13	26.0	9	12 Q71069	Q71069 canine dist
34	13	26.0	9	15 Q64972	Q64972 avian rous-
35	12	24.0	5	13 P83308	P83308 gallus gall
36	12	24.0	7	10 P93233	P93233 lycopersico
37	12	24.0	7	10 Q9CSB3	Q9CSB3 arabidopsis
38	12	24.0	7	11 Q55184	Q55184 rattus norv
39	12	24.0	8	2 Q45615	Q45615 bacillus su
40	12	24.0	8	2 Q32560	Q32560 escherichia
41	12	24.0	8	2 Q9X3K1	Q9X3K1 prochloroco
42	12	24.0	8	2 P83152	P83152 anabaena sp
43	12	24.0	8	2 Q7K4Q5	Q7K4Q5 nodularia s
44	12	24.0	8	4 Q8IV87	Q8IV87 homo sapien
45	12	24.0	8	5 Q02032	Q02032 lytechinus

ALIGNMENTS

RESULT 1

Q8GMM5 PRELIMINARY; PRT; 8 AA.

AC Q8GMM5; DT 01-MAR-2003 (TRENBLrel. 23, Created)

DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE Transposase (Fragment).

GN TNP17.

OS Acinetobacter sp. BW3.

OG Plasmid pKUH207.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Moraxellaceae; Acinetobacter.

OX NCBI_TaxID=106395;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BW3; PLASMID=pKUH207;

RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,

RA Nikiforov V.G.;

RT "pKUH2-like aberrant transposons and possible mechanisms of their

RT dissemination.";

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BW3; PLASMID=pKUH207;

RA Kholodii G.Y., Mindlin S.Z., Gorlenko Z.M., Yurieva O.V.,

RA Petrova M.A., Nikiforov V.G.;

RT "A young family of transposable adaptive DNA segments identified in

RT the Acinetobacter genus.";

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ250234; CAC80784.1; -;

DR EMBL; AJ486856; CAD31078.1; -;

DR GO; GO:0046821; C:extrachromosomal DNA; IEA.

KW Plasmid.

FT NON_TER 1 1

SQ SEQUENCE 8 AA; 911 MW; 2D71B2D6C1A73774 CRC64;

Query Match 40.0%; Score 20; DB 2; Length 8;

Best Local Similarity 80.0%; Pred. No. 1e+06;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PLTSV 8

Db 2 PLTVQ 6

RESULT 2

Q9FXLO PRELIMINARY; PRT; 9 AA.
 ID Q9FXLO; AC Q9FXLO;
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
 DE LIM8 protein (Fragment).
 GN LIM8.
 OS Lilium longiflorum (Trumpet Lily).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.
 OX NCBI_TaxID=4690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Hinomoto;
 RA Uefuji H., Takase H., Hiratsuka K.;
 RT "Lilium longiflorum LIM8 gene, promoter region and partial sequence.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB050987; BAB17856.1; -.
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 1021 MW; 6F8BD76685A6C2CB CRC64;

Query Match 36.0%; Score 18; DB 10; Length 9;

Best Local Similarity 60.0%; Pred. No. 1e+06;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVPLT 6

Db 5 SVPVT 9

RESULT 3

Q8JU20 PRELIMINARY; PRT; 7 AA.
 ID Q8JU20; AC Q8JU20;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE Extracellular fatty acid binding protein (Fragment).
 GN EXPABP.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Wang Q., Li H., Li H.;
 RT "Cloning and sequencing of 3' UTR of EXPABP gene in chicken.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF487519; AA196665.1; -.
 FT NON TER 1 1
 SQ SEQUENCE 7 AA; 780 MW; 72CB1AB2D5BEBB70 CRC64;

Query Match 34.0%; Score 17; DB 13; Length 7;

Best Local Similarity 100.0%; Pred. No. 1e+06;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSV 3

Db 2 CSV 4

RESULT 4

Q42564 PRELIMINARY; PRT; 7 AA.
 ID Q42564; AC Q42564;
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
 GN SCN8A.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97442476; PubMed=9295353;
 RA Plummer N.W., McBurney M.W., Meisler M.H.;
 RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
 RT two-domain protein in fetal brain and non-neuronal cells.";
 RL J. Biol. Chem. 272:24008-24015(1997).
 DR EMBL; U97673; AAB80916.1; -.
 DR GO; GO:0005216; F:ion channel activity; IEA.
 KW Ionic channel.
 FT NON TER 1 1
 SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 34.0%; Score 17; DB 13; Length 7;

Best Local Similarity 71.4%; Pred. No. 1e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 3 VPITSVC 9

Db 1 VPL--VC 5

RESULT 5

Q85562 PRELIMINARY; PRT; 8 AA.
 ID Q85562; AC Q85562;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Truncated env protein (Fragment).
 OS Moloney murine leukemia virus.
 OC Viruses; Retroviruses; Retroviridae; Gammaretrovirus.
 OX NCBI_TaxID=11801;
 RN [1]
 RP SEQUENCE OF 4-8 FROM N.A.
 RX MEDLINE=82196891; PubMed=6281735;
 RA Donoghue D.J., Hunter T.;
 RT "A generalized method of subcloning DNA fragments by restriction site
 RT reconstruction: Application to sequencing the amino-terminal region of
 RT the transforming gene of Gazdar murine sarcoma virus.";
 RL Nucleic Acids Res. 10:2549-2564(1982).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83164305; PubMed=6300424;
 RA Donoghue D.J., Hunter T.;
 RT "Recombination junctions of variants of Moloney murine sarcoma virus:
 RT Generation and divergence of a mammalian transforming gene.";
 RL J. Virol. 45:607-617(1983).
 DR EMBL; K03105; AAA46490.1; -.
 FT NON TER 1 1
 SQ SEQUENCE 8 AA; 732 MW; 98C2D5EB84DC76D CRC64;

Query Match 34.0%; Score 17; DB 15; Length 8;

Best Local Similarity 100.0%; Pred. No. 1e+06;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSV 3

Db 5 CSV 7


```

RESULT 6
Q8CG13 ID Q8CG13 PRELIMINARY; PRT; 9 AA.
AC Q8CG13;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Glutamate receptor ionotropic N-methyl D-aspartate-like 1A
DE (Fragment).
DE GRIN1A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Wyther K.S., Mohan Raj B.K., Sciorra L.J., Roginski R.S.;
RT "The mouse orthologue of the human ionotropic glutamate receptor-like
RT gene (GRIN1A) maps to mouse chromosome 9."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF462417; AA015648.1; -.
DR EMBL; AF462416; AA015648.1; JOINED.
DR MGD; MGI:107282; Grin1a.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 1 1
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1091 MW; 6A91233EB059C33B CRC64;

Query Match 34.0%; Score 17; DB 11; Length 9;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSVP 4
Db 6 CKLP 9

RESULT 7
Q8KXP4 ID Q8KXP4 PRELIMINARY; PRT; 8 AA.
AC Q8KXP4;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Phycocyanin alpha subunit (Fragment).
GN PCa.
OS Microcystis sp. T96-1.
OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
OX NCBI_TaxID=198099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=bloom water sample T96-1;
RA Baker J.A., Ensch B., Neilan B.A., McKay D.B.;
RT "Monitoring changing toxigenicity of a cyanobacterial bloom using
RT molecular methods."
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY117046; AAM54719.1; -.
FT NON TER 8 8
SQ SEQUENCE 8 AA; 890 MW; F4DB01A73771A336 CRC64;

Query Match 32.0%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PLT 6
Db 4 PLT 6

RESULT 8
Q849P4 ID Q849P4 PRELIMINARY; PRT; 8 AA.
AC Q849P4;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE PipB (fragment).
DE Salmonella deby.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=28144;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9813031;
RA Markham P.F., Amavisit P., Lightfoot D., Browning G.F.;
RT "Variation between pathogenic serovars within Salmonella pathogenicity
RT islands."
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY144492; AAO49836.1; -.
FT NON TER 8 8
SQ SEQUENCE 8 AA; 861 MW; EFCSBDD451A04766 CRC64;

Query Match 32.0%; Score 16; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 1e+06;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 VPLTS 7
Db 1 MPITN 5

RESULT 9
Q9Y4X6 ID Q9Y4X6 PRELIMINARY; PRT; 8 AA.
AC Q9Y4X6;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Nuclear LIM interactor (Fragment).
GN NLI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20108806; PubMed=10640831;
RA Drechsler M., Schumacher V., Friedrich S., Wildhardt G., Giesler S.,
RA Schroth A., Bodem J., Royer-Pokora B.;
RT "Genomic structure, alternative transcripts and chromosome location of
RT the human LIM domain binding protein gene LDB1."
RL Cytogenet. Cell Genet. 87:119-124 (1999).
DR EMBL; AJ243097; CAB45408.1; -.
FT NON TER 8 8
SQ SEQUENCE 8 AA; 767 MW; EE6EBDEB862D5B6 CRC64;

Query Match 32.0%; Score 16; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSVP 4
Db 5 CACP 8

RESULT 10
Q16468 ID Q16468 PRELIMINARY; PRT; 8 AA.
AC Q16468;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

```

```

DE DNA for cosmid cCl3-1134 PCR primer 1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96435920; PubMed=8838806;
RA James L.A., Ogilvie D.J., Yamakawa K., Nakamura Y., Stirling C.J.,
RA Anand R.;
RT "Walking, cloning and mapping with YACs in 3q27. Localisation of 5
RT ERTs including 3 members of the Cystatin gene family and
RT identification of CoG islands.";
RL Genomics 32:425-430(1996).
DR EMBL; X88976; CAA6407.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 925 MW; FD5411A7376871B6 CRC64;

Query Match 32.0%; Score 16; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PLS 6
DB 4 PLS 6

RESULT 11
ID Q8L802 PRELIMINARY; PRT; 8 AA.
AC Q8L802;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Pat (Fragment).
GN PAT.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Ronning S.B., Berald K.G., Vaitilingom M.M., Holst-Jensen A.;
RT "Transformation event-specific quantitative real-time PCR for
RT genetically modified Bt1 maize (Zea mays) and estimation of the
RT impact of exogenous DNA on the limit of quantification.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY123624; AAM89275.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 909 MW; 6046C1B2D77412D7 CRC64;

Query Match 32.0%; Score 16; DB 10; Length 8;
Best Local Similarity 40.0%; Pred. No. 1e+06;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 PLSV 8
DB 4 PLSV 8

RESULT 12
OYTRU7
ID Q9TRU7 PRELIMINARY; PRT; 9 AA.
AC Q9TRU7;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE GAP-3. GTPase-activating protein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.

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OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=92112868; PubMed=1309786;
RA Nice E.C., Fabri L., Hammacher A., Holden J., Simpson R.J.,
RA Burgess A.W.;
RT "The purification of a Rap1 GTPase-activating protein from bovine
RT brain cytosol.";
RL J. Biol. Chem. 267:1546-1553(1992).
FT NON TER 1
FT NON TER 9
SQ SEQUENCE 9 AA; 1063 MW; 89EDA77B47604B5A CRC64;

Query Match 32.0%; Score 16; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 VPLTSV 8
DB 4 IPYPSV 9

RESULT 13
O35953
ID O35953 PRELIMINARY; PRT; 9 AA.
AC O35953;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
GN SCN8A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RL11;
RX MEDLINE=97442476; PubMed=9295353;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
RT two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97672; AAB80914.1; -.
DR MGD; MGI:103169; Scn8a.
DR GO; GO:0007628; P:adult walking behavior; IMP.
KW Ionic channel.
FT NON TER 1
SQ SEQUENCE 9 AA; 898 MW; 22D92865B735B737 CRC64;

Query Match 32.0%; Score 16; DB 11; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 VPLT 6
DB 1 VPLS 4

RESULT 14
Q56140
ID Q56140 PRELIMINARY; PRT; 8 AA.
AC Q56140;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE STP6 protein (Fragment).
GN STP6.
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1308;
RN [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN-ST11;
RX MEDLINE=95047254; PubMed=7958782;
RA Constable A., Mollet B.;
RT "Isolation and characterisation of promoter regions from Streptococcus
thermophilus.";
RL FEMS Microbiol. Lett. 122:85-90(1994).
DR EMBL; X78210; CAA55045.1; --
FT NON TER 8
SQ SEQUENCE 8 AA; 846 MW; ED086772D5B045B6 CRC64;

Query Match 30.0%; Score 15; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVP 4
|
|
|
Db 4 SVP 6

RESULT 15
Q9TKES PRELIMINARY; PRT; 8 AA.
AC Q9TKES;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE AtpB (fragment).
GN ATPB.
OS Leptospermum erubescens.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Leptospermum.
OX NCBI_TaxID=106049;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:0-0(2000).
DR EMBL; AF184690; AAF03860.1; --
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 8
SQ SEQUENCE 8 AA; 876 MW; ECA1B1B764405056 CRC64;

Query Match 30.0%; Score 15; DB 8; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PLTS 7
|
|
|
Db 5 PTTS 8

Search completed: March 8, 2004, 12:19:46
Job time : 35.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:11:17 ; Search time 48.5 Seconds
(without alignments)
52.431 Million cell updates/sec

Title: US-09-761-636A-10

Perfect score: 50

Sequence: 1 CSVPPLTVC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 231240

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	9	4	AAU04529
2	37	74.0	9	5	ABJ04424
3	32	64.0	9	5	ABG34948
4	30	60.0	7	6	ABJ37356
5	30	60.0	7	6	ABJ37436
6	30	60.0	9	5	ABG05266
7	28	56.0	9	7	ADC44660
8	27	54.0	9	2	AAW45666
9	27	54.0	9	2	AAW46691
10	27	54.0	9	5	ABP54842
11	26	52.0	7	7	ADB79677
12	26	52.0	9	4	AAU03756
13	26	52.0	9	5	ABP54826
14	26	52.0	9	5	ABP54835
15	26	52.0	9	5	ABP54823
16	26	52.0	9	6	ABR75294
17	25	50.0	7	3	ABR51972
18	25	50.0	8	5	ABJ04484
19	25	50.0	9	2	AAW48844
20	25	50.0	9	3	AAW64300
21	25	50.0	9	4	AAU03747
22	25	50.0	9	5	ABJ04620
23	25	50.0	9	5	ABJ04630
24	25	50.0	9	5	ABJ04417
25	25	50.0	9	7	ADC44658

26	25	50.0	9	7	ADP78117	Ade78117 Synthetic
27	25	50.0	9	7	ADP78037	Ade78037 Synthetic
28	25	50.0	9	7	ADP78097	Ade78097 Synthetic
29	25	50.0	9	7	ADP77841	Ade77841 Synthetic
30	24	48.0	6	4	AAE05003	Aae05003 Human rel
31	24	48.0	6	4	AAE06020	Aab60620 Human MUM
32	24	48.0	7	3	AAW84175	Aay84175 Amino aci
33	24	48.0	7	4	AAU04530	Aau04530 VEGF base
34	24	48.0	9	2	AAE36888	Aar36888 Insulin-1
35	24	48.0	9	2	AAE36882	Aar36882 Peptide d
36	24	48.0	9	2	AAE36832	Aar36832 Peptide d
37	24	48.0	9	4	AAU03758	Aau03758 Cyclic pe
38	24	48.0	9	4	AAU03731	Aau03731 Cyclic pe
39	24	48.0	9	4	AAU03770	Aau03770 Cyclic pe
40	24	48.0	9	4	AAU03739	Aau03739 Cyclic pe
41	24	48.0	9	4	AAU03760	Aau03760 Cyclic pe
42	24	48.0	9	5	ABG35053	Abg35053 Endostati
43	24	48.0	9	5	ABG68159	Abg68159 Optimised
44	24	48.0	9	5	ABJ04372	Abj04372 Human uro
45	24	48.0	9	5	ABP54841	Abp54841 Alpha-IIB
						Abp54837 Alpha-IIB

ALIGNMENTS

RESULT 1
AAU04529
ID AAU04529 standard; peptide; 9 AA.
XX
AC AAU04529;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 7.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..9
FT /note= "This bond cyclises the peptide"
XX
DN WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stackers S, Cendron A;
XX
PF 2001-442248/47.
XX
PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
PS Claim 49; Page 32; 102pp; English.
XX
CC The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the expose loop of human
CC VEGF (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain). The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 CC
 CC Sequence 9 AA;

Query Match 100.0%; Score 50; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSVPLTNSVC 9
 |||||
 Db 1 CSVPLTNSVC 9

RESULT 2
 ABJ04424
 ID ABJ04424 standard; peptide; 9 AA.
 XX
 AC ABJ04424;
 XX
 XX 24-OCT-2002 (first entry)
 XX
 XX Stem cell (mesenchymal) targeting peptide 13.
 XX
 KW BRASIL; targeting peptide; bacterial infection;
 KW Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;
 KW inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;
 KW viral infection; cardiovascular disease; degenerative disease.
 XX
 OS Unidentified.
 XX
 XX WO200220822-A2.
 XX
 XX 14-MAR-2002.
 XX
 XX 07-SEP-2001; 2001WO-US028124.
 XX
 XX 08-SEP-2000; 2000US-0231266P.
 XX
 XX 17-JAN-2001; 2001US-00765101.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX
 XX Arap W, Pasqualini R;
 XX
 XX WPI; 2002-404697/43.
 XX
 XX Identification of targeting peptides that can be used to treat diseases
 XX e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis
 XX of Selective Ligands) method comprises a single differential
 XX centrifugation step.
 XX
 XX Example 5; Page 75; 167pp; English.

CC The invention comprises a method (BRASIL - Biopanning and Rapid Analysis
 CC of Selective Interactive Ligands) to obtain a targeting peptide. The
 CC BRASIL method of the invention involves: exposing a target to a phage
 CC display library in a first phase; exposing the first phase to a second
 CC phase; and separating the phage bound to the target from unbound phage.
 CC The BRASIL method of the invention allows cell phages to be separated
 CC from the remaining unbound phage in a single differential centrifugation
 CC step. When compared to conventional cell panning methods, the BRASIL
 CC method shows a significant increase in recovery of specific phage and a
 CC substantial decrease in background. The BRASIL method is useful for
 CC identifying targeting peptides. The targeting peptides identified by the
 CC method of the invention are useful for treating disease states, such as:
 CC diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune
 CC disease; bacterial infection; viral infection; cardiovascular disease and
 CC degenerative disease. The present amino acid sequence represents a
 CC targeting peptide of the invention
 CC
 CC Sequence 9 AA;

Query Match 74.0%; Score 37; DB 5; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CSVPLTNSVC 9
 |||||
 Db 1 CSVPLTNSVC 9

RESULT 3
 ABG34948
 ID ABG34948 standard; peptide; 9 AA.

XX
 AC ABG34948;
 XX
 XX 15-JUL-2002 (first entry)
 XX
 XX Human bone marrow targeting peptide #20.
 XX
 KW Targeting peptide; cancer; Hodgkin's disease; cytostatic;
 KW immunosuppressive; anti-inflammatory; antiarthritic; antiviral;
 KW antiatherosclerotic; antidiabetic; antibacterial; diabetes mellitus;
 KW inflammatory disease; arthritis; atherosclerosis; cancer;
 KW autoimmune disease; bacterial infection; viral infection.
 XX
 OS Homo sapiens.
 XX
 XX WO200220722-A2.
 XX
 XX 14-MAR-2002.
 XX
 XX 07-SEP-2001; 2001WO-US027702.
 XX
 XX 08-SEP-2000; 2000US-0231266P.
 XX
 XX 17-JAN-2001; 2001US-00765101.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX
 XX Arap W, Pasqualini R;
 XX
 XX WPI; 2002-383050/41.
 XX
 XX Identifying targeting peptides useful for treating e.g. diabetes
 XX mellitus, inflammatory diseases, cancer, or autoimmune diseases,
 XX comprises exposing a sample to a phage display library and recovering
 XX phage bound to the sample.
 XX
 XX Claim 56; Page 207; 298pp; English.
 XX
 XX This invention relates to a novel method for identifying disease
 XX targeting peptides. The method comprises exposing a sample from an organ,
 XX tissue or cell type of interest, to a phage display library and
 XX recovering phage bound to the sample (the phage expresses targeting
 XX peptides). The peptides identified by the method of the invention may

CC have cytostatic, immunosuppressive, anti-inflammatory, antiarthritic,
 CC antiatherosclerotic, antidiabetic, antibacterial and antiviral
 CC activities. The methods and composition are useful for identifying
 CC targeting peptides and one or more receptors for a targeting peptide. The
 CC targeting peptides are used for selective delivery of therapeutic agents,
 CC including gene therapy vectors and fusion proteins, to specific organs,
 CC tissues, or cell types in subject. The targeting peptide may also be used
 CC for treating diseases such as diabetes mellitus, inflammatory diseases,
 CC arthritis, atherosclerosis, cancer, autoimmune diseases, bacterial and
 CC viral infections and Hodgkin's disease. The present sequence represents a
 CC targeting peptide of the invention
 XX
 SQ Sequence 9 AA;

Query Match 64.0%; Score 32; DB 5; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSVPPLTVC 9
 |||||
 Db 1 CSPPLTRWC 9

RESULT 4
 ABB37356
 ID ABB37356 standard; peptide; 7 AA.

XX AC ABB37356;
 XX DT 08-MAY-2003 (first entry)
 XX DE G-protein coupled receptor peptide region #68.
 XX KW Compound library; microenvironment; G-protein Coupled Receptor; GPCR.
 XX OS Unidentified.

XX PN WO2003004147-A2.

XX PD 16-JAN-2003.

XX PF 05-JUL-2002; 2002WO-GB003094.

XX PR 06-JUL-2001; 2001GB-00016570.

XX PS (BIOF-) BIOFOCUS PLC.

XX PI Crossley R, Rose VS, Stevens AP;

XX XX WPI; 2003-221549/21.

XX PT Producing compound library, by generating biological target model using
 PT target sequence information, defining microenvironments interacting with
 PT ligand and motifs interacting with microenvironment, and assembling
 PT motifs.

XX PS Disclosure; Fig 3; 39pp; English.

XX CC The invention relates to a novel method for producing a compound library.
 CC The novel method involves reducing a biological target into a group of
 CC one or more amino acids required for interaction with a ligand, to
 CC generate a model of the biological target, using the model to define a
 CC microenvironment in the biological target capable of interacting with the
 CC ligand, defining motifs which interact with the microenvironment, and
 CC assembling the motifs to generate a compound library for screening.
 CC The novel method is useful to produce compound libraries for screening
 CC natural ligands such as peptides and proteins or for producing chemical
 CC compounds based on drug motifs for screening. This sequence represents a
 CC peptide of a G-protein Coupled Receptor (GPCR), which relates to the
 CC novel compound library production method of the invention
 XX

SQ Sequence 7 AA;

Query Match 60.0%; Score 30; DB 6; Length 7;
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSVPPLT 6
 |||||
 Db 1 CSLPLT 6

RESULT 5
 ABB37436
 ID ABB37436 standard; peptide; 7 AA.

XX AC ABB37436;

XX DT 08-MAY-2003 (first entry)

XX DE G-protein coupled receptor endothelin ET-A receptor peptide #68.

XX KW Compound library; microenvironment; G-protein Coupled Receptor; GPCR.

XX OS Unidentified.

XX PN WO2003004147-A2.

XX PD 16-JAN-2003.

XX PF 05-JUL-2002; 2002WO-GB003094.

XX PR 06-JUL-2001; 2001GB-00016570.

XX PS (BIOF-) BIOFOCUS PLC.

XX PI Crossley R, Rose VS, Stevens AP;

XX XX WPI; 2003-221549/21.

XX PT Producing compound library, by generating biological target model using
 PT target sequence information, defining microenvironments interacting with
 PT ligand and motifs interacting with microenvironment, and assembling
 PT motifs.

XX PS Disclosure; Fig 7; 39pp; English.

XX CC The invention relates to a novel method for producing a compound library.
 CC The novel method involves reducing a biological target into a group of
 CC one or more amino acids required for interaction with a ligand, to
 CC generate a model of the biological target, using the model to define a
 CC microenvironment in the biological target capable of interacting with the
 CC ligand, defining motifs which interact with the microenvironment, and
 CC assembling the motifs to generate a compound library for screening.
 CC The novel method is useful to produce compound libraries for screening
 CC natural ligands such as peptides and proteins or for producing chemical
 CC compounds based on drug motifs for screening. This sequence represents a
 CC peptide of a G-protein Coupled Receptor (GPCR) including Endothelin ET-A
 CC receptor, which relates to the novel compound library production method
 CC of the invention
 XX

SQ Sequence 7 AA;

Query Match 60.0%; Score 30; DB 6; Length 7;
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSVPPLT 6
 |||||
 Db 1 CSLPLT 6

RESULT 6
 ABB05266
 ID ABB05266 standard; peptide; 9 AA.

XX

AC ABB05266;
 XX
 DT 29-AUG-2003 (revised)
 DT 04-APR-2002 (first entry)
 DE
 DE Vascular endothelial growth factor binding peptide V-20 SEQ ID NO:98.
 XX
 XX Human; tumour necrosis factor alpha; TNF-alpha; VEGF; detergent; stain;
 KW bacteriophage; phage library; vascular endothelial growth factor;
 KW collar soil; polyurethane; egg; tea; hair; skin; cleaning composition.
 XX
 OS unidentified bacteriophage.
 OS Unidentified.
 XX
 XX WO200179479-A2.
 FN
 XX
 XX 25-OCT-2001.
 PD
 XX
 XX 11-APR-2001; 2001WO-US011811.
 PF
 XX
 XX 14-APR-2000; 2000US-0197259P.
 PR
 XX
 XX (GENV) GENENCOR INT INC.
 PA
 XX
 XX Estell DA, Murray CJ, Tijerina P, Chen Y;
 PI
 XX
 XX WPI; 2002-139323/18.
 DR
 XX
 XX Screening ligand library comprises allowing binding of ligand with anti-
 PT target, contacting unbound ligands with selected target to form target-
 PT bound ligand complex and identifying target bound ligands on the complex.
 PT
 XX
 PS Claim 22; Page 28; 51pp; English.
 XX
 XX The present invention describes a method for screening a ligand library
 CC (LL). The method comprises: (a) contacting the LL with an anti-target
 CC (AT) to allow the ligands to bind to the AT; (b) separating unbound
 CC ligands; (c) contacting the unbound ligands with a selected target (T) to
 CC allow binding of unbound ligands to (T) to form a (T)-bound ligand
 CC complex (C); (d) separating (C) from ligands which do not bind (T); and
 CC (e) identifying (T)-bound ligands on (C). The method can be used for
 CC screening a ligand library, e.g., a library of peptides, polypeptides,
 CC non-polypeptides or oligonucleotides. A ligand (f) identified by the
 CC method can be used in a cleaning, therapeutic or personal care
 CC application. The method is preferably useful for identifying peptides
 CC useful in cleaning compositions, which involves contacting peptide
 CC library with AT such as fabric, ceramic, glass, stainless steel or
 CC plastic; separating unbound AT peptides; contacting unbound AT peptides
 CC with a target which is a stain such as porphyrin derived stain, tannin
 CC derived stain, carotenoid pigment derived stain, anthocyanin pigment
 CC derived stain, soil-based derived stain, oil-based derived stain, and
 CC human body stain, to allow unbound peptide to bind with the stain to form
 CC a stain-bound peptide complex and identifying the stain-bound peptide on
 CC the stain-bound peptide complex. A selective targeting method for
 CC screening a library of ligands that bind to a target may be used to
 CC identify ligands that bind to a target under harsh conditions. The
 CC selective targeting method may be used to screen and identify a ligand
 CC useful for therapeutic intervention, e.g., a library of ligands may be
 CC screened to identify a tumour-bound ligand. The selective targeting
 CC method may be used to identify cell type specific surface molecules.
 CC Preferred anti-targets include one or more different cell types, cells in
 CC different states, or cells that do not display the surface molecule.
 CC ABB05232 to ABB05346 represent phage-peptides ligands which are used in
 CC the exemplification of the present invention. (Updated on 29-AUG-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 9 AA;
 Query Match 60.0%; Score 30; DB 5; Length 9;
 Best Local Similarity 44.4%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 OY 1 CSVPITSVVC 9

Db 1 CSVPITSVVC 9
 RESULT 7
 ADC44660
 ID ADC44660 standard; peptide; 9 AA.
 XX
 AC ADC44660;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Endothelial cell binding peptide SEQ ID NO:389.
 XX
 XX endothelial cell binding protein; EGBP; anti-tumour; cytostatic;
 KW vasotrophic; antipsoriatic; dermatological; ophthalmological;
 KW antidiabetic; antiarthritic; vulnerary; antiulcer; antiinflammatory;
 KW antibacterial; gynaecological; angiogenesis.
 XX
 OS Synthetic.
 XX
 XX WO2003037172-A2.
 FN
 XX
 XX 08-MAY-2003.
 PD
 XX
 XX 01-NOV-2002; 2002WO-US035258.
 PF
 XX
 XX 01-NOV-2001; 2001US-0334822P.
 PR
 XX
 XX (GPCB-) GPC BIOTECH INC.
 PA
 XX
 XX Gyuris J, Lamphere L, Morris AJ, Tsaioun K;
 PI
 XX
 XX WPI; 2003-482072/45.
 DR
 XX
 XX Novel synthetic or recombinant polypeptide useful for promoting, reducing
 PT proliferation and/or migration of endothelial cells, and for modulating
 PT angiogenesis, has endothelial cell binding protein sequences.
 PT
 XX
 PS Claim 3; SEQ ID NO 389; 126pp; English.
 XX
 XX The invention relates to a novel isolated, synthetic or recombinant
 CC peptide or polypeptide which includes one or more endothelial cell
 CC binding protein (ECBP) sequences. A peptide of the invention has anti-
 CC tumour, cytostatic, vasotrophic, antipsoriatic, dermatological,
 CC ophthalmological, antidiabetic, antiarthritic, vulnerary, antiulcer,
 CC antiinflammatory, antibacterial, and gynaecological activity. The peptide
 CC is useful for promoting, reducing the proliferation and/or migration of
 CC endothelial cells, by treating the cells with an ECBP agonist, which is
 CC preferably the peptide, to promote proliferation and/or migration of the
 CC treated cells, and for reducing or promoting angiogenesis, by treating
 CC the cells with an ECBP antagonist, which is preferably the peptide of the
 CC invention. A peptide of the invention is also useful for manufacturing a
 CC medicament for promoting angiogenesis, by admixing an ECBP agonist or
 CC ECBP antagonist to promote or reduce angiogenesis at one or more sites in
 CC a treated mammal. The medicament is useful for promoting or reducing
 CC angiogenesis. ECBP sequences are useful to alter the infectivity spectrum
 CC of a viral particle. The present sequence represents an ECBP of the
 CC invention.
 XX
 SQ Sequence 9 AA;
 Query Match 56.0%; Score 28; DB 7; Length 9;
 Best Local Similarity 33.3%; Pred. No. 1.4e+06;
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 OY 1 CSVPITSVVC 9
 Db 1 CDLPITSRIC 9
 RESULT 8
 AAW45666

ID AAW45666 standard; peptide; 9 AA.
 AC AAW45666;
 XX
 XX
 XX 27-AUG-2003 (revised)
 DT 09-JUN-1998 (first entry)
 XX
 XX
 XX HBV X 69 peptide with binding affinity for HLA-A3-like molecules.
 XX
 XX HLA molecule; cytotoxic T cell; immunogenic peptide; binding affinity;
 KW HLA-A3 supermotif; tumour; infection; parasite; CTL; antigen; HIV pol;
 KW HBV; hepatitis B virus.
 XX
 XX Synthetic.
 OS Hepatitis B virus.
 OS
 XX WO97333602-A1.
 PN
 XX
 XX 18-SEP-1997.
 PD
 XX
 XX 10-MAR-1997; 97WO-US003778.
 PF
 XX
 XX 11-MAR-1996; 96US-0013113P.
 PR
 XX
 XX (CYTE-) CYTEL CORP.
 PA
 XX Sette A, Chestnut RW, Sidney J;
 PI
 XX WPI, 1997-470637/43.
 DR
 XX
 XX Inducing cytotoxic T cell response against specific antigen - using
 PT immunogenic peptide with binding affinity for HLA-A3-like molecules, to
 PT treat or prevent tumours and infections by virus, parasites etc.
 PT
 XX
 XX Example 1; Page 37; 79pp; English.
 PS
 XX
 XX This sequence represents an immunogenic peptide with binding affinity for
 CC HLA-A3-like molecules. A cytotoxic T cell (CTL) response against a
 CC particular antigen (Ag) is induced in a patient by contacting a CTL with
 CC an immunogenic peptide of 9-15 amino acids which binds to at least two
 CC HLA-A3-like molecules with dissociation constant less than 500 nM and
 CC induces a cytotoxic T cell response. The immunogenic peptide has a
 CC sequence of 9 amino acids, comprising a binding motif, with from the N-to
 CC C-terminal: primary anchor sites (PAR) at positions 2 (selected from Ala,
 CC Leu, Ile, Val, Met, Ser or Thr) and 9 (Arg or Lys) and at least one
 CC secondary anchor sites (SAR), i.e. Tyr, Phe or Trp at positions 3, 6 or
 CC 7, and/or Pro at position 8. The immunogenic peptides are used in peptide
 CC based vaccines and therapeutic compositions, for treating viral,
 CC parasitic or fungal diseases or cancer, e.g. prostatic cancer, hepatitis
 CC B or C, renal or cervical carcinoma, lymphoma, cytomegalovirus infection
 CC or condyloma acuminatum. They can also be used to elicit a CTL response
 CC in vitro for subsequent return of the cells to the patient, e.g. where
 CC the patient does not respond to peptide vaccines or other therapies.
 CC Selection of specific residues for PAR and SAR results in higher binding
 CC affinity and thus increased immunogenicity. (Updated on 27-AUG-2003 to
 CC correct OS field.)
 XX
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 54.0%; Score 27; DB 2; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CSVPLTS 7
 Db 1 CALPFTS 7
 RESULT 9
 AAY46691
 ID AAY46691 standard; peptide; 9 AA.
 XX
 XX
 AC AAY46691;

XX 01-DEC-1999 (first entry)
 DT
 XX
 XX Immunogenic peptide having a human leukocyte antigen binding motif #1302.
 DE
 XX
 XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX
 XX Synthetic.
 OS
 OS Homo sapiens.
 XX
 XX WO9945954-A1.
 PN
 XX
 XX 16-SEP-1999.
 PD
 XX
 XX 13-MAR-1998; 98WO-US005039.
 PF
 XX
 XX 13-MAR-1998; 98WO-US005039.
 PR
 XX
 XX (EPIM-) EPIMUNE INC.
 PA
 XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
 PI
 XX WPI, 1999-551214/46.
 DR
 XX
 XX New immunogenic peptides with HLA binding motif, useful in treatment and
 PT diagnosis of cancers and viral diseases.
 PT
 XX
 XX Claim 1; Page 81; 150pp; English.
 PS
 XX
 XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also known
 CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
 CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
 CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
 CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
 CC (CTLs) which destroy antigen-bearing cells are normally induced by an
 CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
 CC than the intact foreign antigen itself, and are particularly important in
 CC tumour rejection and in fighting viral infections. The peptides are
 CC therefore useful therapeutically to treat or prevent viral infections and
 CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
 CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
 CC elicit an immune response in individuals susceptible or otherwise at risk
 CC of viral infection or cancer, or used to treat chronic or acute
 CC conditions. They are also useful diagnostically, and can be used to
 CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
 CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
 CC patient. The polynucleotides encoding the immunogenic peptides are also
 CC useful therapeutically and for immunisation as above
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 54.0%; Score 27; DB 2; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CSVPLTS 7
 Db 1 CALPFTS 7
 RESULT 10
 ABP54842
 ID ABP54842 standard; peptide; 9 AA.
 XX
 XX ABP54842;
 XX
 XX 08-JAN-2003 (first entry)
 DT
 XX

DE Alpha-IIB beta-3 integrin activating peptide.
 XX
 KW Alpha-IIB beta-3 integrin activator; integrin; CD41; CD61;
 KW glycoprotein IIB/IIIA; von Willebrand disease; coagulant; vulnery;
 KW cyclic.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Disulfide-bond 1. .9
 FT Region 3. .5
 FT /note= "binding motif, region specifically described in
 FT Claim 1"
 XX
 PN WO200272619-A1.
 PD 19-SEP-2002.
 XX
 PF 12-MAR-2002; 2002WO-FI000193.
 XX
 PR 12-MAR-2001; 2001FI-00000492.
 XX
 PA (CTTC-) CTT CANCER TARGETING TECHNOLOGIES OY.
 XX
 PI Koivunen E, Gahmberg CG;
 XX
 DR WPI; 2002-750482/81.
 XX
 PT New alphaIIB beta3 integrin activating peptides useful for manufacturing
 PT a composition for treating or preventing thrombotic or bleeding
 PT disorders, e.g. von Willebrand disease, and in wound healing and tissue
 PT regeneration.
 XX
 PS Disclosure; Page 12; 34pp; English.
 XX
 CC The present sequence is that of a novel alpha-IIB beta-3 integrin
 CC (glycoprotein IIB/IIIA or CD41/CD61) activating peptide. This cyclic
 CC peptide comprises a consensus binding motif (Val-Pro-Trp) and was
 CC identified by focusing a phage library screening on integrin ligands
 CC which are not blocked by a GRGDs peptide. The VW motif is present in the
 CC A3-domain of von Willebrand factor (vWF), suggesting that vWF is an
 CC interaction. The invention relates to the use of novel peptides (see
 CC APP4823-25) comprising the consensus binding motif as pharmaceuticals
 CC for the treatment of thrombotic diseases and bleeding disorders,
 CC including von Willebrand disease, and in artificial tissue transplants to
 CC aid in wound healing and tissue regeneration (all claimed)
 XX
 XX Sequence 9 AA;
 XX
 Query Match 54.0%; Score 27; DB 5; Length 9;
 Best Local Similarity 44.4%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CSVPPLNSVC 9
 Db 1 CDVPELDLC 9
 XX
 RESULT 11
 ADB79677
 ID ADB79677 standard; peptide; 7 AA.
 XX
 AC ADB79677;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Parapoxvirus ORF 100 C-terminal peptide.
 XX
 KW virucide; anti-HIV; hepatotropic; antiinflammatory; cytostatic;
 KW vulnery; antiasthmatic; antiallergic; dermatological; antidiabetic;
 KW immunosuppressive; antirheumatic; antiarthritic; thyromimetic;
 KW protozoacide; amoebicide; antibacterial; gene therapy; virus;

KW viral infections; non-viral infections; proliferative disease;
 KW inflammatory disease; allergic disease; autoimmune disease.
 XX
 OS Parapoxvirus.
 XX
 PN WO2003006654-A2.
 XX
 PD 23-JAN-2003.
 XX
 PF 12-JUN-2002; 2002WO-EP006440.
 XX
 PR 13-JUN-2001; 2001INZ-00512341.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Weber O, Friederichs SM, Siegling A, Schlapp T, Mercer AA;
 PI Fleming SB;
 XX
 DR WPI; 2003-221750/21.
 XX
 PT New polynucleotide and recombinant proteins of Parapoxvirus ovis, useful
 PT for manufacturing a medicament for treating virus related disease, viral
 PT infections, non-viral infections, proliferative disease or inflammatory
 PT disease.
 XX
 PS Example 4; Page 37; 51pp; English.
 XX
 CC The invention relates to a novel purified and isolated polynucleotide
 CC (NI) of Parapoxvirus ovis (PPVO) comprising a nucleotide sequence (S1,
 CC not defined in the specification), or its complementary sequence,
 CC fragment or functional variant. A polynucleotide of the invention has
 CC virucide, anti-HIV, hepatotropic, antiinflammatory, cytostatic,
 CC vulnery, antiasthmatic, antiallergic, dermatological, antidiabetic,
 CC immunosuppressive, antirheumatic, antiarthritic, thyromimetic,
 CC protozoacide, amoebicide, and antibacterial activity. The polynucleotides
 CC may have a use in gene therapy. The recombinant proteins encoded by the
 CC polynucleotides, or recombinant viruses comprising a Vaccinia virus
 CC genome and fragments of a PPVO genome are useful for manufacturing
 CC pharmaceutical compositions for treating virus related disease (e.g.
 CC hepatitis, papillomatosis, herpes virus infections, liver fibrosis, HIV
 CC infections or influenza), viral infections, non-viral infections (e.g.
 CC infections with mycobacteria, mycoplasma, amoeba or plasmodia),
 CC proliferative disease (e.g. cancer, leukaemia, warts or other skin
 CC neoplasms), inflammatory disease (e.g. Crohn's disease, COPD, asthma or
 CC conditions related to healing of wounds), allergic disease, and/or
 CC autoimmune diseases (systemic lupus erythematosus, Sjogren's disease,
 CC Hashimoto's thyroiditis, rheumatoid arthritis or diabetes mellitus). The
 CC present sequence is used in the exemplification of the invention.
 XX
 XX Sequence 7 AA;
 XX
 Query Match 52.0%; Score 26; DB 7; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 4 PLTSVC 9
 Db 1 PLTGWC 6
 XX
 RESULT 12
 AAU03756
 ID AAU03756 standard; peptide; 9 AA.
 XX
 AC AAU03756;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE Cyclic peptide inhibitor of LFA-1/ICAM-1 interaction #33.
 XX
 KW Cyclic; lymphocyte function associated antigen-1; LFA-1; asthma;
 KW intracellular adhesion molecule; ICAM-1; inhibitor; leukaemia;
 KW haematopoietic neoplastic disease; myocardial infarction;

KW radiation injury; rheumatoid arthritis; lymphoma metastasis;
 KW retinoic acid syndrome; all-trans retinoic acid.

XX Synthetic.

XX WO200151508-A1.

XX PD 19-JUL-2001.

XX PF 16-JAN-2001; 2001WO-US001382.

XX PR 14-JAN-2000; 2000US-00483550.

XX PR 16-JAN-2001; 2001US-00760599.

XX PA (SCTE-) SCI & TECHNOLOGY CORP @UNM.

XX PI Larson RS;

XX DR WPI; 2001-432906/46.

XX Composition comprising a cyclic peptide inhibitor of lymphocyte function
 PT associated antigen-1 and intracellular adhesion molecule 1 interaction,
 PT for treating e.g. asthma and myocardial infarction.

XX Example 2; Page 23; 59pp; English.

XX The sequence represents the amino acid sequence of cyclic peptide
 CC inhibitor #33 of lymphocyte function associated antigen-1 and
 CC intracellular adhesion molecule (LFA-1/ICAM-1) interaction. A composition
 CC comprising a cyclic peptide inhibitor of LFA-1/ICAM-1 interaction is
 CC useful for treating haematopoietic neoplastic disease, myocardial
 CC infarction, radiation injury, asthma, rheumatoid arthritis or lymphoma
 CC metastasis. The composition is also useful for inhibiting in a subject
 CC the interaction between LFA-1 expressed on a leukocyte and ICAM-1
 CC expressed on another cell, preventing retinoic acid syndrome in a subject
 CC receiving all-trans retinoic acid, inhibiting growth of leukaemia cells,
 CC inhibiting emigration of leukocytes from blood into tissue and screening
 CC a candidate compound for binding to ICAM-1

XX SQ Sequence 9 AA;

Query Match 52.0%; Score 26; DB 4; Length 9;

Best Local Similarity 33.3%; Pred. No. 1.4e+06;

Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CSVPLTSVC 9

Db 1 CALRMSIC 9

RESULT 13

ABP54826

ID ABP54826 standard; peptide; 9 AA.

XX AC ABP54826;

XX DT 08-JAN-2003 (first entry)

XX DE Alpha-IIB beta-3 integrin activating peptide.

XX KW Alpha-IIB beta-3 integrin activator; integrin; CD41; CD61;

XX KW glycoprotein IIB/IIIA; von Willebrand disease; coagulant; vulnerary;

XX KW cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Disulfide-bond 1. .9

FT Region 3. .5

FT /note= "binding motif, region specifically described in
 FT Claim 1"

XX PN WO200272619-A1.

XX PD 19-SEP-2002.

XX PF 12-MAR-2002; 2002WO-FI000193.

XX PR 12-MAR-2001; 2001FI-00000492.

XX PA (CTTC-) CTT CANCER TARGETING TECHNOLOGIES OY.

XX PI Koivunen E, Gahmberg CG;

XX DR WPI; 2002-750482/81.

XX New alphaIIB beta3 integrin activating peptides useful for manufacturing
 PT a composition for treating or preventing thrombotic or bleeding
 PT disorders, e.g. von Willebrand disease, and in wound healing and tissue
 PT regeneration.

XX Disclosure; Page 13; 34pp; English.

XX The present sequence is that of a novel alpha-IIB beta-3 integrin
 CC (glycoprotein IIB/IIIA or CD41/CD61) activating peptide. This cyclic
 CC peptide comprises a consensus binding motif (Val-Pro-Trp) that was
 CC identified by focusing a phage library screening on integrin ligands, A3-
 CC which are not blocked by a GRGDSP peptide. The motif is present in the A3-
 CC domain of von Willebrand factor (vWf), suggesting that vWf is an
 CC activator of the alpha-IIB beta-3 complex, enabling stable platelet-vWf
 CC interaction. The invention relates to the use of novel peptides
 CC comprising the consensus binding motif as pharmaceuticals for the
 CC treatment of thrombotic diseases and bleeding disorders, including von
 CC Willebrand disease, and in artificial tissue transplants to aid in wound
 CC healing and tissue regeneration (all claimed)

XX SQ Sequence 9 AA;

Query Match 52.0%; Score 26; DB 5; Length 9;

Best Local Similarity 44.4%; Pred. No. 1.4e+06;

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CSVPLTSVC 9

Db 1 CAPEWARYC 9

RESULT 14

ABP54835

ID ABP54835 standard; peptide; 9 AA.

XX AC ABP54835;

XX DT 08-JAN-2003 (first entry)

XX DE Alpha-IIB beta-3 integrin activating peptide.

XX KW Alpha-IIB beta-3 integrin activator; integrin; CD41; CD61;

XX KW glycoprotein IIB/IIIA; von Willebrand disease; coagulant; vulnerary;

XX KW cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Disulfide-bond 1. .9

FT Region 3. .5

FT /note= "binding motif, region specifically described in
 FT Claim 1"

XX PN WO200272619-A1.

XX PD 19-SEP-2002.

XX PF 12-MAR-2002; 2002WO-FI000193.

XX PR 12-MAR-2001; 2001FI-00000492.

XX (CTTC-) CTT CANCER TARGETING TECHNOLOGIES OY.
 XX PA Koivunen E, Gahmberg CG;
 XX PI WPI; 2002-750482/81.
 XX DR New alphaIIb beta3 integrin activating peptides useful for manufacturing
 XX PT a composition for treating or preventing thrombotic or bleeding
 XX PT disorders, e.g. von Willebrand disease, and in wound healing and tissue
 XX PT regeneration.
 XX PS Disclosure; Page 12; 34pp; English.
 XX CC The present sequence is that of a novel alpha-IIb beta-3 integrin
 XX CC (glycoprotein IIb/IIIa or CD41/CD61) activating peptide. This cyclic
 XX CC peptide comprises a consensus binding motif (Val-Pro-Trip) and was
 XX CC identified by focusing a phage library screening on integrin ligands
 XX CC which are not blocked by a GRGDS peptide. The motif is present in the A3-
 XX CC domain of von Willebrand factor (vWF), suggesting that vWF is an
 XX CC activator of the alpha-IIb beta-3 complex, enabling stable platelet-vWF
 XX CC interaction. The invention relates to the use of novel peptides (see
 XX CC ABP54823-25) comprising the consensus binding motif as pharmaceuticals
 XX CC for the treatment of thrombotic diseases and bleeding disorders,
 XX CC including von Willebrand disease, and in artificial tissue transplants to
 XX CC aid in wound healing and tissue regeneration (all claimed)
 XX SQ Sequence 9 AA;
 XX Query Match 52.0%; Score 26; DB 5; Length 9;
 XX Best Local Similarity 44.4%; Pred. No. 1.4e+06;
 XX Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CSVPPLTSVC 9
 Db 1 CAVPWGRIC 9
 RESULT 15
 ABP54823
 ID ABP54823 standard; peptide; 9 AA.
 XX AC ABP54823;
 XX DT 08-JAN-2003 (first entry)
 XX DE Alpha-IIb beta-3 integrin activating peptide.
 XX KW Alpha-IIb beta-3 integrin activator; integrin; CD41; CD61;
 XX KW glycoprotein IIb/IIIa; von Willebrand disease; coagulant; vulnerary;
 XX KW cyclic.
 XX OS Synthetic.
 XX EH Key Location/Qualifiers
 FT Disulfide-bond 1..9
 FT FT Misc-difference 2
 FT /note= "any amino acid residue"
 FT Region 3..5
 FT /note= "Binding motif, region specifically described in
 FT Claim 1"
 FT Misc-difference 6
 FT /note= "any amino acid residue"
 FT FT Misc-difference 7
 FT /note= "any amino acid residue"
 FT FT Misc-difference 8
 FT /note= "any amino acid residue"
 XX WO200272619-A1.
 XX PD 19-SEP-2002.
 XX PF 12-MAR-2002; 2002WO-FI000193.

XX 12-MAR-2001; 2001FI-00000492.
 XX (CTTC-) CTT CANCER TARGETING TECHNOLOGIES OY.
 XX PI Koivunen E, Gahmberg CG;
 XX DR WPI; 2002-750482/81.
 XX PT New alphaIIb beta3 integrin activating peptides useful for manufacturing
 XX PT a composition for treating or preventing thrombotic or bleeding
 XX PT disorders, e.g. von Willebrand disease, and in wound healing and tissue
 XX PT regeneration.
 XX PS Claim 2; Page 19; 34pp; English.
 XX CC The present sequence is that of a novel alpha-IIb beta-3 integrin
 XX CC (glycoprotein IIb/IIIa or CD41/CD61) activating peptide. This cyclic
 XX CC peptide comprises a consensus binding motif (Val-Pro-Trip) that was
 XX CC identified by focusing a phage library screening on integrin ligands,
 XX CC which are not blocked by a GRGDS peptide. The motif is present in the A3-
 XX CC domain of von Willebrand factor (vWF), suggesting that vWF is an
 XX CC activator of the alpha-IIb beta-3 complex, enabling stable platelet-vWF
 XX CC interaction. The invention relates to the use of novel peptides
 XX CC comprising the consensus binding motif as pharmaceuticals for the
 XX CC treatment of thrombotic diseases and bleeding disorders, including von
 XX CC Willebrand disease, and in artificial tissue transplants to aid in wound
 XX CC healing and tissue regeneration (all claimed)
 XX SQ Sequence 9 AA;
 XX Query Match 52.0%; Score 26; DB 5; Length 9;
 XX Best Local Similarity 44.4%; Pred. No. 1.4e+06;
 XX Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CSVPPLTSVC 9
 Db 1 CXVFWXXXC 9
 Search completed: March 8, 2004, 12:17:51
 Job time : 49.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2004, 12:19:53 ; Search time 26 Seconds
(without alignments)
73.092 Million cell updates/sec

Title: US-09-761-636A-10
Perfect score: 50
Sequence: 1 CSVPLTSVC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 90760

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pcp:
3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pcp:
4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pcp:
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11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pcp:
12: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pcp:
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15: /cgn2_6/prodata/2/pubpaa/US10D_PUBCOMB.pcp:
16: /cgn2_6/prodata/2/pubpaa/US10E_PUBCOMB.pcp:
17: /cgn2_6/prodata/2/pubpaa/US10F_PUBCOMB.pcp:
18: /cgn2_6/prodata/2/pubpaa/US10G_PUBCOMB.pcp:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	9	9	US-09-761-636A-10
2	30	60.0	9	9	US-09-832-723-98
3	30	60.0	9	14	US-10-303-331-98
4	28	56.0	9	14	US-10-286-457-389
5	26	52.0	9	9	US-09-760-599-34
6	26	52.0	9	14	US-10-254-446A-147
7	25	50.0	9	9	US-09-760-599-25
8	25	50.0	9	14	US-10-006-869-3614
9	25	50.0	9	14	US-10-286-457-387
10	25	50.0	9	15	US-10-395-032-3614
11	24	48.0	7	9	US-09-761-636A-11
12	24	48.0	9	8	US-08-344-824-293
13	24	48.0	9	9	US-09-760-599-9
14	24	48.0	9	9	US-09-760-599-17
15	24	48.0	9	9	US-09-760-599-36

16	24	48.0	9	9	US-09-760-599-38	Sequence 38, Appl
17	24	48.0	9	9	US-09-760-599-48	Sequence 48, Appl
18	24	48.0	9	10	US-09-747-802-6	Sequence 6, Appl
19	24	48.0	9	10	US-09-932-165-284	Sequence 284, App
20	24	48.0	9	14	US-10-277-292-249	Sequence 249, App
21	24	48.0	9	14	US-10-277-292-322	Sequence 322, App
22	24	48.0	9	14	US-10-277-292-349	Sequence 349, App
23	24	48.0	9	14	US-10-277-292-464	Sequence 464, App
24	24	48.0	9	15	US-10-280-340-249	Sequence 249, App
25	24	48.0	9	15	US-10-280-340-322	Sequence 322, App
26	24	48.0	9	15	US-10-280-340-349	Sequence 349, App
27	24	48.0	9	15	US-10-280-340-464	Sequence 464, App
28	24	48.0	9	15	US-10-107-532-250	Sequence 250, App
29	24	48.0	9	15	US-10-107-532-256	Sequence 256, App
30	24	48.0	9	15	US-10-107-532-257	Sequence 257, App
31	24	48.0	9	15	US-10-107-532-278	Sequence 278, App
32	24	48.0	9	15	US-10-107-532-792	Sequence 792, App
33	24	48.0	9	15	US-10-107-532-809	Sequence 809, App
34	24	48.0	9	15	US-10-107-532-1314	Sequence 1314, Ap
35	24	48.0	9	15	US-10-107-532-1319	Sequence 1319, Ap
36	24	48.0	9	15	US-10-107-532-1344	Sequence 1344, Ap
37	24	48.0	9	15	US-10-107-532-1857	Sequence 1857, Ap
38	24	48.0	9	15	US-10-107-532-1864	Sequence 1864, Ap
39	24	48.0	9	15	US-10-107-532-1882	Sequence 1882, Ap
40	24	48.0	9	15	US-10-107-532-2382	Sequence 2382, Ap
41	24	48.0	9	15	US-10-107-532-2409	Sequence 2409, Ap
42	24	48.0	9	15	US-10-107-532-2411	Sequence 2411, Ap
43	24	48.0	9	15	US-10-107-532-2917	Sequence 2917, Ap
44	24	48.0	9	15	US-10-107-532-2943	Sequence 2943, Ap
45	24	48.0	9	15	US-10-107-532-2948	Sequence 2948, Ap

ALIGNMENTS

RESULT 1
US-09-761-636A-10
; Sequence 10, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-10

Query Match 100.0%; Score 50; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSVPLTSVC 9
Db 1 CSVPLTSVC 9

RESULT 2
US-09-832-723-98
; Sequence 98, Application US/09832723
; Patent No. US20020098524A1

```

; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Chen, Yiyou
; APPLICANT: Murray, Christopher J.
; APPLICANT: Tijerina, Pilar
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-2
; CURRENT APPLICATION NUMBER: US/09/832,723
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,259
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptides screened from a phage display random
; OTHER INFORMATION: peptide library
US-09-832-723-98

Query Match 60.0%; Score 30; DB 9; Length 9;
Best Local Similarity 44.4%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
DB 1 CKMPTSKVC 9

RESULT 3
US-10-303-331-98
; Sequence 98, Application US/10303331
; Publication No. US20030152976A1
; GENERAL INFORMATION:
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Winetzkv, Deborah S.
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-3
; CURRENT APPLICATION NUMBER: US/10/303,331
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: US 09/832,723
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,259
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptides screened from a phage display random
; OTHER INFORMATION: peptide library
US-10-303-331-98

Query Match 60.0%; Score 30; DB 14; Length 9;
Best Local Similarity 44.4%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
DB 1 CKMPTSKVC 9

RESULT 4
US-10-286-457-389
; Sequence 389, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; APPLICANT: Larson Mr., Richard S.
; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
; FILE REFERENCE: SCI200/4-1CIP
; CURRENT APPLICATION NUMBER: US/09/760,599
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION:
US-09-760-599-34

Query Match 52.0%; Score 26; DB 9; Length 9;
Best Local Similarity 33.3%; Pred. No. 7.2e+05;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
DB 1 CALEMRISC 9

RESULT 5
US-09-760-599-34
; Sequence 34, Application US/09760599
; Patent No. US20010034326A1
; GENERAL INFORMATION:
; APPLICANT: Larson Mr., Richard S.
; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
; FILE REFERENCE: SCI200/4-1CIP
; CURRENT APPLICATION NUMBER: US/09/760,599
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 389
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, base
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-389

Query Match 56.0%; Score 28; DB 14; Length 9;
Best Local Similarity 33.3%; Pred. No. 7.2e+05;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
DB 1 CDLPTSRIC 9

RESULT 6
US-10-254-446A-147
; Sequence 147, Application US/10254446A
; Publication No. US20030113714A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M
; APPLICANT: Smalley, Richard E.
; APPLICANT: Ryan, Esther
; APPLICANT: Lee, Seung-Wuk
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES
; FILE REFERENCE: 119927-1066
; CURRENT APPLICATION NUMBER: US/10/254,446A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/325,664
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 147
; APPLICANT: JENO GYURIS et al.
```

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; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopan
US-10-254-446A-147

Query Match      52.0%; Score 25; DB 14; Length 9;
Best Local Similarity 44.4%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CSVPLTSVC 9
Db 1 CKLQLTNQC 9

RESULT 7
US-09-760-599-25
; Sequence 25, Application US/09760599
; Patent No. US20010034326A1
; GENERAL INFORMATION:
; APPLICANT: Larson Mr., Richard S.
; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
; FILE REFERENCE: SCI200/4-1CIP
; CURRENT APPLICATION NUMBER: US/09/760,599
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-760-599-25

Query Match      50.0%; Score 25; DB 9; Length 9;
Best Local Similarity 33.3%; Pred. No. 7.2e+05;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CSVPLTSVC 9
Db 1 CMLRWNSIC 9

RESULT 8
US-10-006-869-3614
; Sequence 3614, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 3614
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-10-006-869-3614

Query Match      50.0%; Score 25; DB 14; Length 9;
Best Local Similarity 44.4%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CSVPLTSVC 9
Db 1 CTFHIDSVC 9

RESULT 9
US-10-286-457-387
; Sequence 387, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 387
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, base
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-387

Query Match      50.0%; Score 25; DB 14; Length 9;
Best Local Similarity 44.4%; Pred. No. 7.2e+05;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CSVPLTSVC 9
Db 1 CPDPTTRIC 9

RESULT 10
US-10-395-032-3614
; Sequence 3614, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 3614
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-10-395-032-3614

Query Match      50.0%; Score 25; DB 15; Length 9;
Best Local Similarity 44.4%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CSVPLTSVC 9
Db 1 CTFHIDSVC 9

RESULT 11
```

```
US-09-761-636A-11
; Sequence 11, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; TYPE: PRT
; LENGTH: 7
; ORGANISM: Homo sapiens
US-09-761-636A-11

Query Match          48.0%; Score 24; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VPLTSS 7
Db 2 VPLTSS 6

RESULT 12
US-08-344-824-293
; Sequence 293, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 293:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
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STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-344-824-293

Query Match          48.0%; Score 24; DB 8; Length 9;
Best Local Similarity 57.1%; Pred. No. 7.2e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 VPLTSVC 9
Db 1 VPASQVC 7

RESULT 13
US-09-760-599-9
; Sequence 9, Application US/09760599
; Patent No. US20010034326A1
; GENERAL INFORMATION:
; APPLICANT: Larson Mr., Richard S.
; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
; FILE REFERENCE: SC1200/4-1CIP
; CURRENT APPLICATION NUMBER: US/09/760,599
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-760-599-9

Query Match          48.0%; Score 24; DB 9; Length 9;
Best Local Similarity 33.3%; Pred. No. 7.2e+05;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CSVPLTSVC 9
Db 1 CLLRMNSIC 9

RESULT 14
US-09-760-599-17
; Sequence 17, Application US/09760599
; Patent No. US20010034326A1
; GENERAL INFORMATION:
; APPLICANT: Larson Mr., Richard S.
; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
; FILE REFERENCE: SC1200/4-1CIP
; CURRENT APPLICATION NUMBER: US/09/760,599
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-760-599-17

Query Match          48.0%; Score 24; DB 9; Length 9;
Best Local Similarity 33.3%; Pred. No. 7.2e+05;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CSVPLTSVC 9
Db 1 CLLRMNSIC 9

RESULT 15
US-09-760-599-17
; Sequence 17, Application US/09760599
; Patent No. US20010034326A1
; GENERAL INFORMATION:
; APPLICANT: Larson Mr., Richard S.
; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
; FILE REFERENCE: SC1200/4-1CIP
; CURRENT APPLICATION NUMBER: US/09/760,599
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-760-599-17

Query Match          48.0%; Score 24; DB 9; Length 9;
Best Local Similarity 33.3%; Pred. No. 7.2e+05;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CSVPLTSVC 9
Db 1 CLLRMNSIC 9

RESULT 15
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US-09-760-599-36
; Sequence 36, Application US/09760599
; Patent No. US20010034326A1
; GENERAL INFORMATION:
; APPLICANT: Larson Mr., Richard S.
; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
; FILE REFERENCE: SCI200/4-1CIP
; CURRENT APPLICATION NUMBER: US/09/760,599
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-760-599-36

Query Match 48.0%; Score 24; DB 9; Length 9;
Best Local Similarity 33.3%; Pred. NO. 7.2e+05;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CSVPLTSVC 9
| : : |
Db 1 CLLAMRSIC 9

Search completed: March 8, 2004, 12:28:22
Job time : 26 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:00:45 ; Search time 22 Seconds
(without alignments)
18.773 Million cell updates/sec

Title: US-09-761-636A-6
Perfect score: 46
Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 71086

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTCUS COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	65.2	8	3	US-09-100-409A-27
2	26	56.5	8	4	US-09-089-878-3
3	25	54.3	8	1	US-08-397-633A-100
4	25	54.3	8	3	US-09-258-754-49
5	25	54.3	8	3	US-09-042-107-49
6	25	54.3	8	4	US-09-722-250D-49
7	23	50.0	7	3	US-08-973-551-14
8	23	50.0	8	2	US-08-520-535-3
9	23	50.0	8	3	US-09-079-432-3
10	23	50.0	8	3	US-09-258-754-33
11	23	50.0	8	3	US-09-258-754-42
12	23	50.0	8	3	US-09-258-754-214
13	23	50.0	8	3	US-09-042-107-33
14	23	50.0	8	3	US-09-042-107-42
15	23	50.0	8	3	US-09-042-107-214
16	23	50.0	8	3	US-08-160-604-79
17	23	50.0	8	3	US-08-160-604-80
18	23	50.0	8	4	US-09-722-250D-33
19	23	50.0	8	4	US-09-722-250D-42
20	23	50.0	8	4	US-09-722-250D-214
21	23	50.0	8	4	US-09-428-082B-457
22	22	47.8	6	4	US-09-187-859-3664
23	22	47.8	6	4	US-09-839-542B-3664
24	22	47.8	7	4	US-09-187-859-3665
25	22	47.8	7	4	US-09-839-542B-3665
26	22	47.8	8	3	US-09-258-754-36
27	22	47.8	8	3	US-09-258-754-48

28	22	47.8	8	3	US-09-258-754-256
29	22	47.8	8	3	US-09-042-107-36
30	22	47.8	8	3	US-09-042-107-48
31	22	47.8	8	3	US-09-042-107-256
32	22	47.8	8	4	US-09-187-859-1071
33	22	47.8	8	4	US-09-187-859-3624
34	22	47.8	8	4	US-09-839-542B-1071
35	22	47.8	8	4	US-09-839-542B-3624
36	22	47.8	8	4	US-09-722-250D-36
37	22	47.8	8	4	US-09-722-250D-48
38	22	47.8	8	4	US-09-722-250D-256
39	22	47.8	8	4	US-09-446-423-11
40	21	45.7	5	4	US-09-187-859-3663
41	21	45.7	6	4	US-09-839-542B-3663
42	21	45.7	6	4	US-09-187-859-985
43	21	45.7	6	4	US-09-187-859-2242
44	21	45.7	6	4	US-09-839-542B-985
45	21	45.7	6	4	US-09-839-542B-2242

ALIGNMENTS

RESULT 1
US-09-100-409A-27
; Sequence 27, Application US/09100409A
; Patent No. 6090388
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION FOR PREVENTION AND TREATMENT OF HIV INFECTION AND IMMUNE DISORDERS
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF HIV INFECTION AND IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,409A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 1151-4154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-409A-27

Query Match 65.2%; Score 30; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 36+05; 2; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 2

Cy 1 CNEESLIC 8
Db 1 CNOGSFLC 8

RESULT 2

US-09-089-878-3
; Sequence 3, Application US/09089878
; Patent No. 6458528
; GENERAL INFORMATION:
; APPLICANT: Groat, Randall G.
; APPLICANT: O'Connor, Thomas P.
; APPLICANT: Mermer, Brian
; TITLE OF INVENTION: DIAGNOSIS OF FELINE IMMUNODEFICIENCY VIRUS INFECTION
; FILE REFERENCE: 00088/111001
; CURRENT APPLICATION NUMBER: US/09/089,878
; CURRENT FILING DATE: 1998-06-03
; EARLIER APPLICATION NUMBER: US 60/085,615
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Feline immunodeficiency virus
US-09-089-878-3

Query Match 56.5%; Score 26; DB 4; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
||:
DB 1 CNOQOFFC 8

RESULT 3

US-08-397-633A-100
; Sequence 100, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; TITLE OF INVENTION: OF ENZYMIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOERBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-397-633A-100

Query Match 54.3%; Score 25; DB 1; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
||:
DB 1 CQOSKVIC 8

RESULT 4

US-09-258-754-49
; Sequence 49, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-49

Query Match 54.3%; Score 25; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
||:
DB 1 CGNETLRC 8

RESULT 5

US-09-042-107-49
; Sequence 49, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-49

Query Match 54.3%; Score 25; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
||:
DB 1 CGNETLRC 8

Db 1 CNETLRC 8

RESULT 6

US-09-722-250D-49
; Sequence 49, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; FILE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-49

Query Match 54.3%; Score 25; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 1 CNETLRC 8

RESULT 7

US-08-973-551-14
; Sequence 14, Application US/08973551
; Patent No. 6113902
; GENERAL INFORMATION:
; APPLICANT: Chermann, Jean-Claude
; APPLICANT: Le Contel, Carole
; APPLICANT: Galea, Pascale
; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING
; TITLE OF INVENTION: AN INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND
; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF
; TITLE OF INVENTION: DIAGNOSIS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,551
; FILING DATE: 30-DEC-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/01006
; FILING DATE: 28-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9507914
; FILING DATE: 30-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Granados, Patricia D.

; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 65691/130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-973-551-14

Query Match 50.0%; Score 23; DB 3; Length 7;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEES 5
Db 2 CNPES 6

RESULT 8

US-08-520-535-3
; Sequence 3, Application US/08520535
; Patent No. 5817750
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,535
; FILING DATE: 28-AUG-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-08-520-535-3

Query Match 50.0%; Score 23; DB 2; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 1 CWDGLMC 8

RESULT 9

US-09-079-432-3
; Sequence 3, Application US/09079432
; Patent No. 5955572
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,432
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/520,535
; FILING DATE: 28-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-09-079-432-3

Query Match 50.0%; Score 23; DB 2; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
| : : | :
DB 1 CWDDGLMC 8

RESULT 10
US-09-258-754-33
; Sequence 33, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT FILING DATE: 1999-02-26
; CURRENT APPLICATION NUMBER: US/09/258,754
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-079-432-3

US-09-258-754-33

Query Match 50.0%; Score 23; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CNEESLIC 8
| : : | :
DB 1 CRHESSC 8

RESULT 11
US-09-258-754-42
; Sequence 42, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-42

Query Match 50.0%; Score 23; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
| : : | :
DB 1 CHEGYLTC 8

RESULT 12
US-09-258-754-214
; Sequence 214, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 214
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-214

Query Match 50.0%; Score 23; DB 3; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CNEESLIC 8
| : : : |
Db 1 CFKSTLLC 8

RESULT 13

US-09-042-107-33
; Sequence 33, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-33

Query Match 50.0%; Score 23; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CNEESLIC 8
| : : : |
Db 1 CRHSSC 8

RESULT 14

US-09-042-107-42
; Sequence 42, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-42

Query Match 50.0%; Score 23; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CNEESLIC 8
| : : : |
Db 1 CHEGYLTC 8

RESULT 15

US-09-042-107-214
; Sequence 214, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:

; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 214
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-214

Query Match 50.0%; Score 23; DB 3; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CNEESLIC 8
| : : : |
Db 1 CFKSTLLC 8

Search completed: March 8, 2004, 12:04:10
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:07:41 ; Search time 20 Seconds
(without alignments)
52.905 Million cell updates/sec

Title: US-09-761-636A-7
Perfect score: 61
Sequence: 1 C1SVPLTSVPC 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1327

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	22	36.1	11	2 D57789	Gallbladder stone
2	20	32.8	16	2 I65546	MHC H2-L antigen
3	19	31.1	5	2 A60521	glycogen phosphory
4	18	29.5	10	2 C39191	hypothetical prote
5	17	27.9	8	2 G33098	205K exoantigen
6	17	27.9	10	2 C39111	Ig heavy chain C r
7	17	27.9	10	2 PH0944	T-cell receptor be
8	17	27.9	11	2 S21727	gamma-interferon-i
9	17	27.9	11	2 PH0929	T-cell receptor be
10	16	26.2	4	2 I51049	metallothionein-A
11	16	26.2	9	2 A60356	118K stomach cance
12	16	26.2	9	2 PT0247	Ig heavy chain CRD
13	16	26.2	10	2 S62880	polygalacturonase
14	16	26.2	10	2 A61622	vitellogenin, 190k
15	16	26.2	10	2 PH0926	T-cell receptor be
16	16	26.2	10	2 PH0926	T-cell receptor be
17	16	26.2	10	2 A32195	Na+/K+-exchanging
18	16	26.2	11	1 ECLQ2M	tachykinin II - mi
19	15	24.6	10	2 B59272	parapsoral crystal
20	15	24.6	10	2 PH1584	peptide-N4-(N-acet
21	15	24.6	11	2 PH1584	Ig H chain V-D-J r
22	15	24.6	11	2 PH0042	stathmin - mouse (
23	15	24.6	11	2 PH0941	T-cell receptor be
24	14	23.0	6	4 A35039	major protein anti
25	14	23.0	7	2 PC1316	hypothetical colla
26	14	23.0	8	2 S08996	large granule L3 c
27	14	23.0	8	2 B49823	hypertrehalosemic
28	14	23.0	8	2 B49823	adipokinetic hormo
29	14	23.0	8	2 A33995	neuropeptide Led-C
					adipokinetic hormo

30 14 23.0 8 2 PL0184 capsid protein VP-
31 14 23.0 8 2 A42057 fibroblast growth
32 14 23.0 8 2 A35180 neutral proteinase
33 14 23.0 9 2 B41983 orf downstream to b
34 14 23.0 9 2 A29477 diuretic neuropept
35 14 23.0 9 2 I52974 seminal vesicle pr
36 14 23.0 10 1 XAVI6B angiotensin-conver
37 14 23.0 10 2 JCL1416 hypertrehalosemic
38 14 23.0 10 2 S09138 hypertrehalosemic
39 14 23.0 10 2 B33995 hypertrehalosemic
40 14 23.0 10 2 PC2171 triacylglycerol li
41 14 23.0 10 2 PA0050 protein Q410052 -
42 14 23.0 10 2 B61218 alpha-gliadin 6Ha
43 14 23.0 10 2 B61218 alpha-gliadin 6Ha
44 14 23.0 11 1 XASNEA bradykinin-potent
45 14 23.0 11 2 S58244 pyrroloquinoline q

ALIGNMENTS

RESULT 1
D57789
Gallbladder stone matrix protein, 14.5K - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 23-Feb-1996
C:Accession: D57789
R:Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, February 1996
A:Description: The proteins of gallbladder stones.
A:Reference number: A57789
A:Accession: D57789
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <BIN>

Query Match 36.1%; Score 22; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
DB 1 PATSAP 6

RESULT 2
I65546
MHC H2-L antigen - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I65546
R:Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
Cell 44, 261-272, 1986
A:Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and the
A:Reference number: I52778; MUID:86106202; PMID:3510743
A:Accession: I65546
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: GB:M12483; NID:G199565; PIDN:AAA39663.1; PID:G554234

Query Match 32.8%; Score 20; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VPC 11
DB 2 VPC 4

RESULT 3
A60521
Glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)

```

N;Alternate names: glycogen phosphorylase b
C;Species: Liza ramada
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003
C;Accession: A60521
R;Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A;Title: Purification and characterization of glycogen phosphorylase B from skeletal muscle
A;Reference number: A60521; PMID:2109669
A;Accession: A60521
A;Molecule type: protein
A;Residues: 1-5 <BON>
C;Superfamily: glucan phosphorylase
C;Keywords: glycyltransferase; hexosyltransferase; phosphoprotein
P;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experiment

Query Match 31.1%; Score 19; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVP 5
DB 2 ISVP 5

RESULT 4
C39191
hypothetical protein 1 (Tetx 5' region) - Bacteroides fragilis
C;Species: Bacteroides fragilis
C;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 30-Sep-1993
C;Accession: C39191
R;Speer, B.S.; Bedzyk, L.; Salvers, A.A.
J. Bacteriol. 173, 176-183, 1991
A;Title: Evidence that a novel tetracycline resistance gene found on two Bacteroides tra
A;Reference number: A39191; PMID:91100280; PMID:1846135
A;Accession: C39191
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-10 <SPE>
A;Cross-references: GB:M37699

Query Match 29.5%; Score 18; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 3.8e+03; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SVPLTSV 9
DB 4 SREWTSI 10

RESULT 5
G33098
205K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falciparum
C;Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C;Accession: G33098
R;Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A;Reference number: A33098
A;Accession: G33098
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <NIC>

Query Match 27.9%; Score 17; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 VPLTSV 9
DB 2 VPLXLV 7

RESULT 6
C39191
Ig heavy chain C region - Pacific hagfish (fragment)
C;Species: Eptatretus stoutii (Pacific hagfish)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C;Accession: C39191
R;Varner, J.; Neame, P.; Litman, G.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991
A;Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural simi
A;Reference number: A39191; PMID:91156684; PMID:2000382
A;Accession: C39191
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <VAR>
C;Keywords: heterotetramer; immunoglobulin

Query Match 27.9%; Score 17; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 5.6e+03; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISVPL 6
DB 4 ISSPL 8

RESULT 7
PH0944
T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0944
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenberg, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
A;Reference number: PH0944; PMID:92078857; PMID:1836012
A;Accession: PH0944
A;Molecule type: mRNA
A;Residues: 1-10 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
A;Note: the authors translated the codon GAC for residue 9 as Glu
C;Keywords: T-cell receptor

Query Match 27.9%; Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 5.6e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVP 5
DB 1 CASSP 5

RESULT 8
S21727
gamma-interferon-induced protein IP-30 precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S21727
R;Wei, M.L.; Cresswell, P.
Nature 356, 443-446, 1992
A;Title: HLA-A2 molecules in an antigen-processing mutant cell contain signal sequence-
A;Reference number: S21727; PMID:92212461; PMID:11557127
A;Accession: S21727
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <WEI>

Query Match 27.9%; Score 17; DB 2; Length 11;
Best Local Similarity 37.5%; Pred. No. 6.2e+03; Indels 0; Gaps 0;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISVPLTSV 9
DB 3 LDVPTAAV 10

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RESULT 9

PH0929
 T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 C:Accession: PH0929
 R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenberg, A.A.; Wilson, D.B.
 J. Exp. Med. 174, 1467-1476, 1991
 A>Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
 A:Reference number: PH0929; MUID:92078857; PMID:1836012
 A:Accession: PH0929
 A:Molecule type: mRNA
 A:Residues: 1-11 <GOL>
 A:Experimental source: concanavalin A-activated lymphoblast
 C:Keywords: T-cell receptor

Query Match 27.9%; Score 17; DB 2; Length 11;
 Best Local Similarity 57.1%; Pred. No. 6.2e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTSVPLT 7
 | | | | |
 DB 1 CASRFGT 7

RESULT 10

IS1049
 metallothionein-A - rainbow trout (fragment)
 C:Species: Oncorhynchus mykiss (rainbow trout)
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C:Accession: IS1049
 R:Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.
 Eur. J. Biochem. 230, 344-349, 1995
 A>Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) me
 A:Reference number: IS1049; MUID:95324545; PMID:7601121
 A:Accession: IS1049
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-4 <OLS>
 A:Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 26.2%; Score 16; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PC 11
 | |
 DB 3 PC 4

RESULT 11

A60356
 118K stomach cancer antigen - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 17-Mar-1999
 C:Accession: A60356
 R:Shiraishi, Y.
 Int. J. Cancer 45, 783-787, 1990
 A>Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens fr
 A:Reference number: A60356; MUID:90216080; PMID:2323853
 A:Accession: A60356
 A:Molecule type: protein
 A:Residues: 1-9 <SHI>
 C:Keywords: glycoprotein

Query Match 26.2%; Score 16; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 VPLTSV 9
 : | | |
 DB 1 IPLKPV 6

RESULT 12

PT0247
 Ig heavy chain CDR3 region (clone 2-106A) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0247
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A:Reference number: PT0222; MUID:91108337; PMID:1899102
 A:Accession: PT0247
 A:Molecule type: DNA
 A:Residues: 1-9 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 26.2%; Score 16; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SVPLTS 8
 | | | |
 DB 2 SAPIDS 7

RESULT 13

S62880
 polygalacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)
 C:Species: Aspergillus sp.
 C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
 C:Accession: S62880
 R:Stratilova, E.; Dzuova, M.; Markovic, O.; Joernvall, H.
 FEBS Lett. 382, 164-166, 1996
 A>Title: An essential tyrosine residue of Aspergillus polygalacturonase.
 A:Reference number: S62880; MUID:96196586; PMID:8612742
 A:Accession: S62880
 A:Molecule type: protein
 A:Residues: 1-10 <STR>
 C:Keywords: glycosidase; hydrolase
 F:/Active site: Tyr #status predicted

Query Match 26.2%; Score 16; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PC 11
 | |
 DB 9 PC 10

RESULT 14

A61622
 vitellogenin, 190k chain - gypsy moth (fragment)
 N:Contains: vitellin
 C:Species: Lymantria dispar (gypsy moth)
 C>Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 15-Oct-1999
 C:Accession: A61622
 R:Hiremath, S.; Eshita, S.
 Insect Biochem. Mol. Biol. 22, 605-611, 1992
 A>Title: Purification and characterization of vitellogenin from the gypsy moth, Lymantr
 A:Reference number: A61622
 A:Accession: A61622
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <HIR>
 C:Keywords: egg yolk; hemolymph

Query Match 26.2%; Score 16; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLT 7
| | |
Db 2 PLT 4

RESULT 15

PH0926

T-cell receptor beta chain V-D-J region (isolate 12) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0926

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic

A;Reference number: PH0891; MUID:32078857; PMID:1836012

A;Accession: PH0926

A;Molecule type: mRNA

A;Residues: 1-10 <GOL>

A;Experimental source: concanavalin A-activated lymphoblast

A;Note: the authors translated the codon AGA for residue 4 as Thr

C;Keywords: T-cell receptor

Query Match 26.2%; Score 16; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CUSVP 5
| | |
Db 1 CASRP 5

Search completed: March 8, 2004, 12:11:14
Job time : 21 secs


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RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerins: novel antimicrobial peptides from the Indian frog Rana
RT tigrina."
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
CC S.aureus, M.luteus, P.putida and S.cerevisiae.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1342; METHOD=WALDI.
KW Amphibian defense peptide; Antibiotic; Fungicide; Amidation.
FT DISULFID 2 10
FT MOD RES 11 11
FT SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;
SQ SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;

Query Match 31.1%; Score 19; DB 1; Length 11;
Best Local Similarity 33.3%; Pred. No. 9.7e+02;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 C1SVPL 6
Db 2 C2MIP1 7

RESULT 3
COW2_CONFU STANDARD; PRT; 8 AA.
AC P58785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu-contryphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC STRAIN=Clipperton Island; TISSUE=Venom;
RX MEDLINE=9938839; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
RA Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contryphan family."
RL J. Pept. Res. 54:93-99(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
CC -!- SIMILARITY: Belongs to the contryphan family.
KW Toxin; Hydroxylation; D-amino acid.
FT DISULFID 2 8
FT MOD RES 4 4
FT SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 29.5%; Score 18; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 C1SVPL 5
Db 2 C2VLLP 6

RESULT 4
MGMT_BOVIN
ID MGMT_BOVIN STANDARD; PRT; 9 AA.
AC P23177;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Methylated-DNA-protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-
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DE methylguanine-DNA methyltransferase) (Fragment).
GN MGMT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=90174912; PubMed=2308822;
RA Rydberg B., Hall J., Karran P.;
RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA
RT methyltransferase."
RL Nucleic Acids Res. 18:17-21(1990).
CC -!- FUNCTION: Repair of alkylated guanine in DNA by stoichiometrically
CC transferring the alkyl group at the O-6 position to a cysteine
CC residue in the enzyme. This is a suicide reaction: the enzyme is
CC irreversibly inactivated.
CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) +
CC [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein
CC S-methyl-L-cysteine.
CC -!- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OGT METHYLTRANSFERASE
CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
DR InterPro; IPR001497; Methyltransf_1.
DR PROSITE; PS00374; MGMT; PARTIAL.
KW DNA repair; Transferase; Methyltransferase.
FT ACT_SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
FT NON_TER 1 1
FT NON_TER 9 9
FT SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 28.7%; Score 17.5; DB 1; Length 9;
Best Local Similarity 37.5%; Pred. No. 1.4e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 4 VPLTSPVC 11
Db 3 IPILT-PC 9

RESULT 5
UPA4_HUMAN
ID UPA4_HUMAN STANDARD; PRT; 10 AA.
AC P30090;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 12) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing."
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 4.8, its MW is: 40.5 kDa.
CC -!- MISCELLANEOUS: This spot is on a position thought to be that of
CC Zn-alpha-2 glycoprotein, but it does not correspond to that
CC protein.
DR SWISS-2DPAGE; P30090; HUMAN.
FT NON_TER 1 1
FT UNSURE 4 4
FT NON_TER 10 10
FT SEQUENCE 10 AA; 1067 MW; 269492EB05A1A457 CRC64;
SQ SEQUENCE 10 AA; 1067 MW; 269492EB05A1A457 CRC64;
```

Mon Mar 8 13:11:04 2004

Query Match 27.9%; Score 17; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPLTS 8

DB 2 VPNTS 6

RESULT 6

CXLL1 CONMR STANDARD; PRT; 11 AA.
AC P5807; (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lambda-conotoxin CMrVIA.
OS Conus marmoreus (Marble cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=42752;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=20564325; PubMed=1098292;
RA Balaji R.A., Ontake A., Sato K., Gopalakrishnakone P., Kini R.M.,
RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide
pattern and protein folding. Isolation and characterization from the
venom of Conus marmoreus".
RL J. Biol. Chem. 275:39516-39522 (2000).
CC -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1237.93; MW ERR=0.21; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
KW Neurotoxin; Toxin; Hydroxylation.
FT DISULFID 2 11
FT MOD RES 10 10 HYDROXYLATION.
SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B7323B58 CRC64;

Query Match 26.2%; Score 16; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PC 11

DB 10 PC 11

RESULT 7

LPK2 LOCM1 STANDARD; PRT; 10 AA.
AC P41486;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Locustapyrokinin 2 (LOW-PK-2) (FXPRL-amide).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94094539; PubMed=7903606;
RA Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,
RT "Isolation, identification and synthesis of locustapyrokinin II from
Locusta migratoria, another member of the FXPRL-amide peptide

family.";
RL Comp. Biochem. Physiol. 106C:103-109 (1993).
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
activity).
CC -!- SIMILARITY: Belongs to the pyrokinin family.
DR InterPro: IPR001484; Pyrokinin.
DR PROSITE: PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1145 MW; CFAF4271A9D1B772 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVP 5

DB 2 SVP 4

RESULT 8

AKH TABAT STANDARD; PRT; 8 AA.
AC P14595;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
DE (DCC 1).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC Tabanus.
OX NCBI_TaxID=7207;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RT Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
hypotrehalosemic activity isolated from the corpora cardiaca of horse
flies (Diptera)".
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164 (1989).
CC -!- FUNCTION: This hormone, released from cells in the corpora
cardiaca after the beginning of flight, causes release of
diglycerides from the fat body and then stimulates the flight
muscles to use these diglycerides as an energy source.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HETH / RPCH family.
DR PIR: A33995; A33995.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 LTSVP 10

DB 2 LTFTP 6

RESULT 9

HTF2 PERAM STANDARD; PRT; 8 AA.
ID HTF2 PERAM
AC P04549;
RT 13-AUG-1987 (Rel. 05, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosemic factor II (Neuropeptide M-II) (Periplaneta CC-2)
DE (Pea-CAH-II) (Jeb-CC-II) (Hypertrehalosemic neuropeptide II).
OS Periplaneta americana (American cockroach),
OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blattella orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OK NCBI_TaxID=6978, 7539, 6976;
RN [1]
RN SEQUENCE.
RP SPECIES=P.americana;
RC MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L., Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RN SEQUENCE.
RP SPECIES=P.americana;
RC MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RN SEQUENCE.
RP SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RC MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
RT beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN [4]
RN SEQUENCE.
RP SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RC MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L., Jr.;
RT "Primary structures of hypertrehalosemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gryphodrhina portentosus, Blattella germanica and Blattella orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -!- FUNCTION: Hypertrehalosemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; B44960; B44960.
DR PIR; B49823; B49823.
DR PIR; S08996; S08996.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1006 MW; 867457771A9D1A736 CRC64;
Query Match 23.0%; Score 14; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 LTSVP 10
Db 2 LTFTP 6

RESULT 10
UPAA HUMAN STANDARD; PRT; 8 AA.
ID UPAA_HUMAN STANDARD; PRT; 8 AA.
AC P30096;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OK NCBI_TaxID=9606;
RN [1]
RN SEQUENCE.
RP TISSUE=Plasma;
RC MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 7, its MW is: 12 kDa.
DR SWISS-2DPAGE; P30096; HUMAN.
DT NON_TER 1 1 F->P.
FT VARIANT 5 5 /FTID=VAR_000004.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;
Query Match 23.0%; Score 14; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 VPLTSP 10
Db 1 VLTFTP 7

RESULT 11
DNFI LOCM1 STANDARD; PRT; 9 AA.
ID DNFI_LOCM1 STANDARD; PRT; 9 AA.
AC P16339;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Locupressin (Diuretic neuropeptide Fl/F2).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OK NCBI_TaxID=7004;
RN [1]
RN SEQUENCE.
RP TISSUE=Suboesophageal ganglion, and Thoracic ganglion;
RC MEDLINE=88077077; PubMed=3689410;
RA Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
RA Delaage M., Schooley D.A.;
RT "Identification of an arginine vasopressin-like diuretic hormone from
RT Locusta migratoria.";
RL Biochem. Biophys. Res. Commun. 149:180-186(1987).
CC -!- FUNCTION: DIURETIC HORMONE.
CC -!- SUBUNIT: Monomer (Fl) and homodimer (F2); disulfide-linked.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR PIR; A29477; A29477.
DR InterPro; IPR000981; Neurhyp horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS HORM; 1.
KW Hormone; Neuropeptide; Amidation.
FT DISULFID 1 6 IN FL.
FT DISULFID 1 1 INTERCHAIN (WITH C-6) (IN F2).
FT DISULFID 6 6 INTERCHAIN (WITH C-1) (IN F2).
FT MOD_RES 9 9 AMIDATION.

SQ SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 LTSVP 10
: : :
Dd 3 ITNCP 7

RESULT 12

YBPR_AZOV1 STANDARD; PRT; 9 AA.

AC P25825;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in bfr 3'region (Fragment).
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
CX NCBI_TaxID=354;
RN [1]
PP SEQUENCE FROM N.A.
RX MEDLINE=92196129; PubMed=1549605;
RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,
RA Stiefel E.I.;
RT "Unification of the ferritin family of proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423 (1992).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M83692; AAA22122.1; -;
DR PIR; B41983; B41983.
KW Hypothetical protein.
FT NON TER 9
SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B417776D CRC64;

Query Match 23.0%; Score 14; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLTS 8
: : :
Dd 4 PRTS 7

RESULT 13

BPP2_BOTJA STANDARD; PRT; 10 AA.

AC P01022;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme
DE inhibitor V-6-II).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
CX NCBI_TaxID=8724;
RN [1]
PP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,

RA Kocy O.;
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
RT jararaca. Isolation, elucidation of structure, and synthesis.";
RL Biochemistry 10:4033-4039 (1971).
CC -1- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01255; XAVI6B.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1
SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 7.1e+03;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PLTSVP 10
: : :
Dd 4 PRQIP 9

RESULT 14

HTF2_CARMO STANDARD; PRT; 10 AA.

AC P11385;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic factor II (HTF-II) (HRTH-II) (Hypertrehalosaemic
DE neuropeptide II).
OS Carausius morosus (Indian stick insect), and
OS Extatosoma tiaratum (Stick insect).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatodea;
OC Heteronemidae; Carausius.
CX NCBI_TaxID=7022, 7024;
RN [1]
PP SEQUENCE.
RC SPECIES=C.morosus; TISSUE=Corpora cardiaca;
RX MEDLINE=87157103; PubMed=3828078;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structure of the hypertrehalosaemic factor II from the
RT corpus cardiaca of the Indian stick insect, Carausius morosus,
RT determined by fast atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 368:67-75 (1987).
RN [2]
PP SEQUENCE.
RC SPECIES=E.tiaratum; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354 (1990).
RN [3]
PP CARBOHYDRATE-LINKAGE SITE.
RC SPECIES=C.morosus; TISSUE=Corpora cardiaca;
RX MEDLINE=93129188; PubMed=1482345;
RA Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;
RT "A tryptophan-substituted member of the AKH/RPCH family isolated from
RT a stick insect corpus cardiaca.";
RL Biochem. Biophys. Res. Commun. 189:1303-1309 (1992).
CC -1- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1308.61; METHOD=FAB.
CC -1- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; JCI416; JCI416.
DR PIR; S09138; S09138.

DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Glycoprotein; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT CARBOHYD 8 8 C-LINKED (MAN) (PROBABLE).
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1164 MW; 9B9036745771A9D1 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 LTSVP 10
Db 2 LTFTP 6

RESULT 15
HTF_TABAT STANDARD; PRT; 10 AA.
AC P14596;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic factor (HOTH) (Dipteran corpora cardiaca factor II) (DCC II).
DE (DCC II).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC Tabanus.
OX NCBI_taxid=7207;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RFCH family.
DR PIR; B33995; B33995.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1169 MW; 916036786771A9D1 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LTSVP 10
Db 2 LTFTP 6

Search completed: March 8, 2004, 12:09:49
Job time : 11 secs

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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:07:16 ; Search time 38 Seconds
(without alignments)
91.334 Million cell updates/sec

Title: US-09-761-636A-7
Perfect score: 61
Sequence: 1 C1SVPLTSVPC 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues 1903
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	34.4	11	6	Q9TQSO
2	20	32.8	8	2	Q8GM5
3	20	32.8	10	15	Q85598
4	20	32.8	10	15	Q85563
5	20	32.8	10	15	Q85619
6	19	31.1	8	2	Q56140
7	19	31.1	10	8	Q9TKF7
8	19	31.1	10	8	Q9TKF9
9	19	31.1	10	8	Q9TKG2
10	19	31.1	10	8	Q9TKF1
11	19	31.1	10	8	Q9TKF8
12	19	31.1	10	8	Q9TKF4
13	19	31.1	10	8	Q9TKF3
14	19	31.1	10	8	Q9TKEO
15	19	31.1	10	8	Q9TKF0
16	19	31.1	10	8	Q9TKF6

Q9thm7 leptospermu
Q8ke2 leptospermu
Q9tk3 leptospermu
Q9tk7 kunzea pulc
Q9thm6 leptospermu
Q9tk6 leptospermu
Q9tk8 kunzea eric
Q9tk9 kunzea baxt
Q9tkel neofabricia
Q9tk4 leptospermu
Q9tk9 lophostemon
P83092 spinacia ol
Q9fx10 lilium long
Q9ny38 homo sapien
Q99nd1 mus musculu
Q8kpx4 microcystis
Q9k4m6 staphylococ
Q7x6a3 zea mays su
Q96041 oenothera b
Q7y018 zea mays su
Q39957 hepatitis g
Q77872 oreochromis
Q77873 oreochromis
Q77871 oreochromis
Q91y49 mus musculu
Q849p4 salmonella
Q16468 homo sapien
Q02831 oryctolagus
Q9try3 sus sp. ins

ALIGNMENTS

RESULT 1
Q9TQSO ID Q9TQSO PRELIMINARY; PRT; 11 AA.
AC Q9TQSO; AC Q9TQSO; 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DE C-KIT (Fragment).
GN KIT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Olsen H.G., Vage D.I., Lien S., Klungland H.;
RT "A polymorphism in the bovine c-kit gene".
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL; AJ243424; CAB60775.1; -.
DR ENBL; AJ243060; CAB60774.1; -.
FT NON TER 1 1
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1126 MW; DD785FF8A2D2D772 CRC64;
Query Match 34.4%; Score 21; DB 6; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.6e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 3 SVPLTSV 9
Db 3 AVPVSV 9
RESULT 2
Q8GM5 ID Q8GM5 PRELIMINARY; PRT; 8 AA.
AC Q8GM5;
DT 01-MAR-2003 (TREMELrel. 23, Created)


```

DT 01-JUN-2003 (TrEMBLrel. 23, Last sequence update)
DE Transposase (Fragment).
GN TNPI7.
OS Acinetobacter sp. BW3.
OC Plasmid pKLH207.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=106395;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BW3; PLASMID=pKLH207;
RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
RA Nikiforov V.G.;
RT "pKLH2-like aberrant transposons and possible mechanisms of their
RT dissemination.";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BW3; PLASMID=pKLH207;
RA Kholodii G.Y., Mindlin S.Z., Gorlenko Z.M., Yurieva O.V.,
RA Petrova M.A., Nikiforov V.G.;
RT "A young family of transposable adaptive DNA segments identified in
RT the Acinetobacter genus.";
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250234; CAC80784.1; -.
DR EMBL; AJ486856; CAD31078.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON TER 1
SQ SEQUENCE 8 AA; 911 MW; 2D71B2D6C1A73774 CRC64;

Query Match 32.8%; Score 20; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLTSV 9
DB 2 PLTQV 6

RESULT 3
Q85598 PRELIMINARY; PRT; 10 AA.
AC Q85598;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Moloney murine sarcoma virus (Strain HT1) env/mos 5' junction
DE (Fragment).
OS Moloney murine leukemia virus.
OC Viruses; Retrovirdae; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=83164305; PubMed=6300424;
RA Donoghue D.J., Hunter T.;
RT "Recombination junctions of variants of Moloney murine sarcom virus:
RT Generation and divergence of a mammalian transforming gene.";
RL J. Virol. 45:607-617(1983).
DR EMBL; K03106; AAA46492.1; -.
FT NON TER 10
SQ SEQUENCE 10 AA; 1081 MW; 7BECFCBEA771B5A4 CRC64;

Query Match 32.8%; Score 20; DB 15; Length 10;
Best Local Similarity 75.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 SVPC 11
DB 4 STPC 7

RESULT 4
Q85563 PRELIMINARY; PRT; 10 AA.
AC Q85563;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Env-mos fusion protein (Fragment).
OS Moloney murine leukemia virus.
OC Viruses; Retrovirdae; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=82196891; PubMed=6281735;
RA Donoghue D.J., Hunter T.;
RT "A generalized method of subcloning DNA fragments by restriction site
RT reconstruction: Application to sequencing the amino-terminal region of
RT the transforming gene of Gazdar murine sarcoma virus.";
RL Nucleic Acids Res. 10:2549-2564(1982).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=83164305; PubMed=6300424;
RA Donoghue D.J., Hunter T.;
RT "Recombination junctions of variants of Moloney murine sarcom virus:
RT Generation and divergence of a mammalian transforming gene.";
RL J. Virol. 45:607-617(1983).
DR EMBL; K03105; AAA46491.1; -.
FT NON TER 10
SQ SEQUENCE 10 AA; 1062 MW; F9ECFCBEA771B5B1 CRC64;

Query Match 32.8%; Score 20; DB 15; Length 10;
Best Local Similarity 75.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 SVPC 11
DB 4 STPC 7

RESULT 5
Q85619 PRELIMINARY; PRT; 10 AA.
AC Q85619;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Moloney murine sarcoma virus (Strain ml) env/mos 5' junction
DE (Fragment).
OS Moloney murine leukemia virus.
OC Viruses; Retrovirdae; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=83164305; PubMed=6300424;
RA Donoghue D.J., Hunter T.;
RT "Recombination junctions of variants of Moloney murine sarcom virus:
RT Generation and divergence of a mammalian transforming gene.";
RL J. Virol. 45:607-617(1983).
DR EMBL; K03108; AAA46494.1; -.
FT NON TER 10
SQ SEQUENCE 10 AA; 1081 MW; 7BECFCBEA771B5A4 CRC64;

Query Match 32.8%; Score 20; DB 15; Length 10;
Best Local Similarity 75.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 SVPC 11
DB 4 STPC 7

RESULT 6
Q56140

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ID Q56140 PRELIMINARY; PRT; 8 AA.
AC Q56140;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE STP6 protein (Fragment).
GN STP6.
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ST11;
RX MEDLINE=95047254; PubMed=7958782;
RA Constable A., Mollet B.;
RT "Isolation and characterisation of promoter regions from Streptococcus
thermophilus."; Lett. 122:85-90(1994).
RL FEMS Microbiol. Lett. 122:85-90(1994).
DR EMBL; X78210; CAA55045.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 846 MW; ED086772DSB045B6 CRC64;

Query Match 31.1%; Score 19; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 2 ISVP 5
Db 3 ISVP 6

RESULT 7
Q9TKF7 PRELIMINARY; PRT; 10 AA.
ID Q9TKF7;
AC Q9TKF7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE AtPB (Fragment).
GN AtPB.
OS Agonis grandiflora.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Agonis.
OX NCBI_TaxID=106028;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:0-0(2000).
DR EMBL; AF184675; AAF03845.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 10
SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

Query Match 31.1%; Score 19; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
Db 5 PTTSRP 10

RESULT 8
Q9TKF9 PRELIMINARY; PRT; 10 AA.
ID Q9TKF9;
AC Q9TKF9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE AtPB (Fragment).
GN AtPB.

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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE AtPB (Fragment).
GN AtPB.
OS Melaleuca viridiflora.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Melaleuca.
OX NCBI_TaxID=106062;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:0-0(2000).
DR EMBL; AF184670; AAF03840.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 10
SQ SEQUENCE 10 AA; 1144 MW; 028C2CA1B1B76440 CRC64;

Query Match 31.1%; Score 19; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
Db 5 PTTSRP 10

RESULT 9
Q9TKG2 PRELIMINARY; PRT; 10 AA.
ID Q9TKG2;
AC Q9TKG2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE AtPB (Fragment).
GN AtPB.
OS Callistemon polandii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Callistemon.
OX NCBI_TaxID=73732;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:0-0(2000).
DR EMBL; AF184666; AAF03836.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 10
SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

Query Match 31.1%; Score 19; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
Db 5 PTTSRP 10

RESULT 10
Q9TKF1 PRELIMINARY; PRT; 10 AA.
ID Q9TKF1;
AC Q9TKF1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE AtPB (Fragment).
GN AtPB.

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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Myrtaceae; Angiosperms;
 RN NCBI_TaxID=106039;
 [1]
 RP SEQUENCE FROM N.A.
 RA O'Brien M.M., Quinn C.J., Wilson P.G.;
 RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
 RL Aust. J. Bot. 48:0-0(2000).
 DR EMBL; AF184678; AAF03848.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

OS Homalospermum firmum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Myrtaceae; Homalospermum.
 RN NCBI_TaxID=106039;
 [1]
 RP SEQUENCE FROM N.A.
 RA O'Brien M.M., Quinn C.J., Wilson P.G.;
 RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
 RL Aust. J. Bot. 48:0-0(2000).
 DR EMBL; AF184682; AAF03852.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

Query Match 31.1%; Score 19; DB 8; Length 10;
 Best Local Similarity 66.7%; Pred. No. 7.6e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 31.1%; Score 19; DB 8; Length 10;
 Best Local Similarity 66.7%; Pred. No. 7.6e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
 DB 5 PTTSRP 10

QY 5 PLTSVP 10
 DB 5 PTTSRP 10

RESULT 11

RESULT 13

Q9TKF8 PRELIMINARY; PRT; 10 AA.

Q9TKF3 PRELIMINARY; PRT; 10 AA.

AC Q9TKF8; 01-MAY-2000 (TrEMBLrel. 13, Created)

AC Q9TKF3; 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE AtPB (Fragment).

DE AtPB (Fragment).

GN AtPB.

GN AtPB.

OS Tristaniopsis laurina.

OS Asteromyrtus brassii.

OG Chloroplast.

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC Myrtales; Myrtaceae; Tristaniopsis.

OC Myrtales; Myrtaceae; Asteromyrtus.

OX NCBI_TaxID=106073;

OX NCBI_TaxID=106034;

RN SEQUENCE FROM N.A.

RN SEQUENCE FROM N.A.

RA O'Brien M.M., Quinn C.J., Wilson P.G.;

RA O'Brien M.M., Quinn C.J., Wilson P.G.;

RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";

RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";

RL Aust. J. Bot. 48:0-0(2000).

RL Aust. J. Bot. 48:621-628(2000).

DR EMBL; AF184672; AAF03842.1; -.

DR EMBL; AF184679; AAF03849.2; -.

DR GO; GO:0009507; C:chloroplast; IEA.

DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.

KW Chloroplast.

FT NON TER 10 10

FT NON TER 10 10

SQ SEQUENCE 10 AA; 1126 MW; 15132CA1B1B76440 CRC64;

SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

Query Match 31.1%; Score 19; DB 8; Length 10;

Query Match 31.1%; Score 19; DB 8; Length 10;

Best Local Similarity 66.7%; Pred. No. 7.6e+03;

Best Local Similarity 66.7%; Pred. No. 7.6e+03;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10

QY 5 PLTSVP 10

DB 5 PTTSRP 10

DB 5 PTTSRP 10

RESULT 12

RESULT 14

Q9TKF4 PRELIMINARY; PRT; 10 AA.

Q9TKF3 PRELIMINARY; PRT; 10 AA.

AC Q9TKF4; 01-MAY-2000 (TrEMBLrel. 13, Created)

AC Q9TKF0; 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE AtPB (Fragment).

DE AtPB (Fragment).

GN Angiosperms salina.

GN Angiosperms salina.

OS Chloroplast.

OS Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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DE AtPB (Fragment).
GN ATPB.
OS Neofabricia sericispala.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Neofabricia.
OX NCBI_TaxID=106065;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:0-0(2000).
DR EMBL; AF184700; AAF03869.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

Query Match 31.1%; Score 19; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
DB 5 PTTSRP 10

RESULT 15
QNTKFO
ID Q9TKF0 PRELIMINARY; PRT; 10 AA.
AC Q9TKF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE AtPB (fragment).
GN ATPB.
OS Kunzea ambigua (Tick bush).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Kunzea.
OX NCBI_TaxID=106041;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:0-0(2000).
DR EMBL; AF184683; AAF03853.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

Query Match 31.1%; Score 19; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
DB 5 PTTSRP 10

Search completed: March 8, 2004, 12:10:42
Job time : 40 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:03:40 ; Search time 52 Seconds
(without alignments)
59.770 Million cell updates/sec

Title: US-09-761-636A-7
Perfect score: 61
Sequence: 1 C1SVPLTSVPC 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 348779

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Genesecp_29Jan04:*
1: Genesecp1980s:*
2: Genesecp1990s:*
3: Genesecp2000s:*
4: Genesecp2001s:*
5: Genesecp2002s:*
6: Genesecp2003as:*
7: Genesecp2003bs:*
8: Genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	61	100.0	11	4	AAU04526 VEGF base
2	59	96.7	11	4	AAU04542 VEGF base
3	57	93.4	11	4	AAU04545 VEGF base
4	54	88.5	11	4	AAU04543 VEGF base
5	52	85.2	11	4	AAU04544 VEGF base
6	45.5	74.6	10	4	AAU04532 VEGF base
7	41	67.2	9	4	AAU04533 VEGF base
8	32	52.5	9	4	AAU04529 VEGF base
9	30	49.2	8	2	AAU04528 Partial p
10	30	49.2	8	2	AAU04529 Partial p
11	30	49.2	10	6	AAU04529 Partial p
12	30	49.2	10	6	AAU04529 Partial p
13	29	47.5	11	5	AAU04529 Partial p
14	29	47.5	11	5	AAU04529 Partial p
15	27	44.3	10	2	AAU04529 Partial p
16	27	44.3	11	5	AAU04529 Partial p
17	26	42.6	6	2	AAU04529 Partial p
18	26	42.6	8	2	AAU04529 Partial p
19	26	42.6	9	2	AAU04529 Partial p
20	26	42.6	9	6	AAU04529 Partial p
21	26	42.6	10	4	AAU04529 Partial p
22	26	42.6	10	5	AAU04529 Partial p
23	25.5	41.8	9	2	AAU04529 Partial p
24	25.5	41.8	9	2	AAU04529 Partial p
25	25.5	41.8	9	2	AAU04529 Partial p

26	25	41.0	9	2	AAV26264	Isolated
27	25	41.0	9	4	AAE01112	Human leu
28	25	41.0	9	6	ABR24203	Human can
29	25	41.0	9	6	AAE29971	Human air
30	25	41.0	10	2	AAW01720	Inhibitor
31	25	41.0	10	2	AAW01720	Inhibitor
32	25	41.0	10	2	AAW8078	Inhibitor
33	25	41.0	10	2	AAV55214	Anti CD34
34	25	41.0	10	3	AAV86960	Human hae
35	25	41.0	10	3	AAV77429	Fibronect
36	25	41.0	10	4	AAW95853	Human com
37	25	41.0	10	6	ABR24101	Human can
38	25	41.0	10	6	ABR24325	Human can
39	25	41.0	11	4	AAU00642	Human mem
40	25	41.0	11	4	AAU00642	Human mem
41	25	41.0	11	7	ADB88785	Membrane
42	24	39.3	6	2	AAU03869	Hypotensi
43	24	39.3	6	4	AAU05003	Human rel
44	24	39.3	6	4	AAU06020	Human Mm
45	24	39.3	7	4	AAU04530	VEGF base

ALIGNMENTS

RESULT 1
AAU04526
ID AAU04526 standard; peptide; 11 AA.
XX
AC AAU04526;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 3.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..11
FT /note= "This bond cyclises the peptide"
XX
PN W0200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
XX
PR 16-MAY-2000; 2000US-0204590P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR WPI; 2001-442248/47.
XX
PT Novel monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
PS Claim 49; Page 32; 102pp; English.
XX
CC The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the exposed loop of human
CC VEGF (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTSVPLTSVPC 11
 |||||
 Db 1 CTSVPLTSVPC 11

RESULT 2
 AAU04542
 ID AAU04542 standard; peptide; 11 AA.

XX AAU04542;

DT 26-SEP-2001 (first entry)

XX VEGF based monocyclic peptide 20.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 XX neovascularisation; lymphangiogenesis; psoriasis; tumour;
 XX diabetes induced neovascular sequelae; rheumatoid arthritis;
 XX diabetic retinopathy; chronic inflammation; cyclic.

XX Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 1..11 /note= "This bond cyclises the peptide"

FN WO200152875-A1.

PD 26-JUL-2001.

PF 18-JAN-2001; 2001WO-US001533.

PR 18-JAN-2000; 2000US-0176293P.

PR 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine

PT residues.

XX Example 25; Page 47; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the exposed loop of human
 CC VEGF (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 11 AA;

Query Match 96.7%; Score 59; DB 4; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.0034;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTSVPLTSVPC 11
 |||||
 Db 1 CTSVPLTSVPC 11

RESULT 3

AAU04545

ID AAU04545 standard; peptide; 11 AA.

XX AAU04545;

DT 26-SEP-2001 (first entry)

XX VEGF based monocyclic peptide 23.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 XX neovascularisation; lymphangiogenesis; psoriasis; tumour;
 XX diabetes induced neovascular sequelae; rheumatoid arthritis;
 XX diabetic retinopathy; chronic inflammation; cyclic.

XX Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 1..11 /note= "This bond cyclises the peptide"

FN WO200152875-A1.

PD 26-JUL-2001.

PF 18-JAN-2001; 2001WO-US001533.

PR 18-JAN-2000; 2000US-0176293P.

PR 16-MAY-2000; 2000US-0204590P.

PA (LUDW-) LUDWIG INST CANCER RES.
XX Achen MG, Hughes RA, Stacker S, Cendron A;
PI WPI; 2001-442248/47.
XX
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
XX Example 25; Page 47; 102pp; English.
PS
XX The sequence represents a monomeric monocyclic peptide of the invention,
XX whose 3-dimensional structure is modelled on the exposed loop of human
CC VEGF (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a
CC peptide loop fragment from an exposed loop of a growth factor protein and
CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC peptides) and a cyclic peptide with at least one amino acid deleted prior
CC to cyclisation are used to interfere with angiogenesis,
CC neovascularisation or lymphangiogenesis in a mammal with a condition
CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC The condition is diabetic retinopathy, psoriasis, arthropathy,
CC hemangioma, vascularised malignant or benign tumour, post-recovery
CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC trauma, substance-induced neovascularisation of the liver, excessive
CC hormone-related angiogenic dysfunction, diabetes induced neovascular
CC sequelae, hypertension induced neovascular sequelae, or chronic liver
CC infection. The peptides are also used to modulate vascular permeability
CC in a mammal (the mammal has a condition characterised by fluid
CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC or brain. The peptides are used to image blood vessels and lymphatic
CC vasculature. The monomeric and bicyclic peptides are used to interfere
CC with at least one biological activity induced by VEGF, VEGF-C or -D and
CC are also used in combination with an anti-inflammatory agent, to treat a
CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC diabetic retinopathy
XX
XX Sequence 11 AA;
SQ
Query Match 93.4%; Score 57; DB 4; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.0072;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTSVPLTSPVC 11
Db 1 CTSVPLTSPVC 11
RESULT 4
AAU04543
ID AAU04543 standard; peptide; 11 AA.
XX AAU04543;
AC
XX 26-SEP-2001 (first entry)
DT
XX VEGF based monocyclic peptide 21.
DE
XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
XX Synthetic.
OS
XX Key Location/Qualifiers
FH Disulfide-bond 1. .11
FT /note= "This bond cyclises the peptide"
FT
XX

PN W0200152875-A1.
XX 26-JUL-2001.
XX
XX 18-JAN-2001; 2001WO-US001533.
XX
XX 18-JAN-2000; 2000US-0176293P.
XX 16-MAY-2000; 2000US-0204590P.
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Achen MG, Hughes RA, Stacker S, Cendron A;
XX WPI; 2001-442248/47.
XX
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
XX Example 25; Page 47; 102pp; English.
PS
XX The sequence represents a monomeric monocyclic peptide of the invention,
XX whose 3-dimensional structure is modelled on the exposed loop of human
CC VEGF (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a
CC peptide loop fragment from an exposed loop of a growth factor protein and
CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC peptides) and a cyclic peptide with at least one amino acid deleted prior
CC to cyclisation are used to interfere with angiogenesis,
CC neovascularisation or lymphangiogenesis in a mammal with a condition
CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC The condition is diabetic retinopathy, psoriasis, arthropathy,
CC hemangioma, vascularised malignant or benign tumour, post-recovery
CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC trauma, substance-induced neovascularisation of the liver, excessive
CC hormone-related angiogenic dysfunction, diabetes induced neovascular
CC sequelae, hypertension induced neovascular sequelae, or chronic liver
CC infection. The peptides are also used to modulate vascular permeability
CC in a mammal (the mammal has a condition characterised by fluid
CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC or brain. The peptides are used to image blood vessels and lymphatic
CC vasculature. The monomeric and bicyclic peptides are used to interfere
CC with at least one biological activity induced by VEGF, VEGF-C or -D and
CC are also used in combination with an anti-inflammatory agent, to treat a
CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC diabetic retinopathy
XX
XX Sequence 11 AA;
SQ
Query Match 88.5%; Score 54; DB 4; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.023;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTSVPLTSPVC 11
Db 1 CTSVPLTSPVC 11
RESULT 5
AAU04544
ID AAU04544 standard; peptide; 11 AA.
XX AAU04544;
AC
XX 26-SEP-2001 (first entry)
DT
XX VEGF based monocyclic peptide 22.
DE
XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW

Mon Mar 8 13:11:03 2004

XX diabetes induced neovascular sequelae; rheumatoid arthritis;
XX diabetic retinopathy; chronic inflammation; cyclic.

XX Synthetic.

XX Key Location/Qualifiers

XX Disulfide-bond 1..11 /note= "This bond cyclises the peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

XX 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stackler S, Cendron A;

XX WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
XX from an exposed loop of a growth factor protein by oxidizing the cysteine
XX residues.

XX Example 25; Page 47; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,
XX whose 3-dimensional structure is modelled on the expose loop of human
XX VEGF (vascular endothelial growth factor). The invention relates to a
XX method of producing a monomeric monocyclic peptide by a measuring beta-
XX beta carbon separation distances on opposite antiparallel strands of a
XX peptide loop fragment from an exposed loop of a growth factor protein and
XX cyclising the peptide by oxidising the cysteine residues. The monocyclic
XX peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
XX peptides) and a cyclic peptide with at least one amino acid deleted prior
XX to cyclisation are used to interfere with angiogenesis,
XX neovascularisation or lymphangiogenesis in a mammal with a condition
XX characterised by angiogenesis, neovascularisation or lymphangiogenesis.
XX The condition is diabetic retinopathy, psoriasis, arthropathy,
XX hemangioma, vascularised malignant or benign tumour, post-recovery
XX cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
XX trauma, substance-induced neovascularisation of the liver, excessive
XX hormone-related angiogenic dysfunction, diabetes induced neovascular
XX sequelae, hypertension induced neovascular sequelae, or chronic liver
XX infection. The peptides are also used to modulate vascular permeability
XX in a mammal (the mammal has a condition characterised by fluid
XX accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
XX or brain. The peptides are used to image blood vessels and lymphatic
XX vasculature. The monomeric and bicyclic peptides are used to interfere
XX with at least one biological activity induced by VEGF, VEGF-C or -D and
XX are also used in combination with an anti-inflammatory agent, to treat a
XX chronic inflammation, especially rheumatoid arthritis, psoriasis and
XX diabetic retinopathy

XX Sequence 11 AA;

Query Match 85.2%; Score 52; DB 4; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.049;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTSVPLTSVPC 11

DB 1 CTSPLTSVPC 11

RESULT 6

AAU04532

ID AAU04532 standard; peptide; 10 AA.

XX

AC AAU04532;

XX

DT 26-SEP-2001 (first entry)

XX

DE VEGF based monocyclic peptide 10.

XX

XX Human; VEGF; vascular endothelial growth factor; angiogenesis;

XX neovascularisation; lymphangiogenesis; psoriasis; tumour;

XX diabetes induced neovascular sequelae; rheumatoid arthritis;

XX diabetic retinopathy; chronic inflammation; cyclic.

XX

OS Synthetic.

XX

XX Key Location/Qualifiers

XX Disulfide-bond 1..10 /note= "This bond cyclises the peptide"

XX

XX WO200152875-A1.

XX

XX 26-JUL-2001.

XX

XX 18-JAN-2001; 2001WO-US001533.

XX

XX 18-JAN-2000; 2000US-0176293P.

XX

XX 16-MAY-2000; 2000US-0204590P.

XX

XX (LUDW-) LUDWIG INST CANCER RES.

XX

XX Achen MG, Hughes RA, Stackler S, Cendron A;

XX

XX WPI; 2001-442248/47.

XX

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
XX from an exposed loop of a growth factor protein by oxidizing the cysteine
XX residues.

XX

XX Claim 49; Page 32; 102pp; English.

XX

XX The sequence represents a monomeric monocyclic peptide of the invention,
XX whose 3-dimensional structure is modelled on the expose loop of human
XX VEGF (vascular endothelial growth factor). The invention relates to a
XX method of producing a monomeric monocyclic peptide by a measuring beta-
XX beta carbon separation distances on opposite antiparallel strands of a
XX peptide loop fragment from an exposed loop of a growth factor protein and
XX cyclising the peptide by oxidising the cysteine residues. The monocyclic
XX peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
XX peptides) and a cyclic peptide with at least one amino acid deleted prior
XX to cyclisation are used to interfere with angiogenesis,
XX neovascularisation or lymphangiogenesis in a mammal with a condition
XX characterised by angiogenesis, neovascularisation or lymphangiogenesis.
XX The condition is diabetic retinopathy, psoriasis, arthropathy,
XX hemangioma, vascularised malignant or benign tumour, post-recovery
XX cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
XX trauma, substance-induced neovascularisation of the liver, excessive
XX hormone-related angiogenic dysfunction, diabetes induced neovascular
XX sequelae, hypertension induced neovascular sequelae, or chronic liver
XX infection. The peptides are also used to modulate vascular permeability
XX in a mammal (the mammal has a condition characterised by fluid
XX accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
XX or brain. The peptides are used to image blood vessels and lymphatic
XX vasculature. The monomeric and bicyclic peptides are used to interfere
XX with at least one biological activity induced by VEGF, VEGF-C or -D and
XX are also used in combination with an anti-inflammatory agent, to treat a
XX chronic inflammation, especially rheumatoid arthritis, psoriasis and
XX diabetic retinopathy

XX

XX Sequence 10 AA;

XX

XX Query Match 74.6%; Score 45.5; DB 4; Length 10;

XX Best Local Similarity 90.9%; Pred. No. 0.52;

XX Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy

Sequence 9 AA;

Query Match 67.2%; Score 41; DB 4; Length 9;
Best Local Similarity 81.8%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 CTSVPLTSVPC 11
| | | | | | | | |
DB 1 CTSVPL--VPC 9

RESULT 8
AAU04529
ID AAU04529 standard; peptide; 9 AA.

AC AAU04529;

XX 26-SEP-2001 (first entry)

DE VEGF based monocyclic peptide 7.

Human; VEGF; vascular endothelial growth factor; angiogenesis;
neovascularisation; lymphangiogenesis; psoriasis; tumour;
diabetes induced neovascular sequelae; rheumatoid arthritis;
diabetic retinopathy; chronic inflammation; cyclic.

OS Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 1..9 /note= "This bond cyclises the peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

XX 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty stenosis, head, heat or cold

QY 1 CTSVPLTSVPC 11
| | | | | | | | |
DB 1 CTSVPL-SVPC 10

RESULT 7
AAU04533
ID AAU04533 standard; peptide; 9 AA.

AC AAU04533;

XX 26-SEP-2001 (first entry)

DE VEGF based monocyclic peptide 11.

Human; VEGF; vascular endothelial growth factor; angiogenesis;
neovascularisation; lymphangiogenesis; psoriasis; tumour;
diabetes induced neovascular sequelae; rheumatoid arthritis;
diabetic retinopathy; chronic inflammation; cyclic.

OS Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 1..9 /note= "This bond cyclises the peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

XX 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty stenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver sequelae. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain). The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and

CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy

XX Sequence 9 AA;
 SQ Query Match 52.5%; Score 32; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLTSV 9
 DB 2 SVPLTSV 8
 |||||
 |||||

RESULT 9
 AAR58418 standard; protein; 8 AA.
 ID AAR58418
 AC AAR58418;
 XX 25-MAR-2003 (revised)
 DT 13-APR-1995 (first entry)
 DE Partial peptide 7 from TSAR C46.9-2 binding domain.

XX TSAR; totally synthetic affinity reagent; synthetic; binding domain;
 KW effector domain; concatenated heterofunctional protein; linker; direct;
 KW rapid; detection; screening; treatment; monoclonal antibody; WAB; C46;
 KW anti-carcinoma antigen; anti-CEA.
 XX Synthetic.
 OS WO9418318-A1.
 XX 18-AUG-1994.
 XX 01-FEB-1994; 94WO-US000977.
 XX 01-FEB-1993; 93US-00013416.
 XX 30-DEC-1993; 93US-00176500.
 XX 31-JAN-1994; 94US-00189331.
 XX (UNCL) UNIV NORTH CAROLINA.
 XX Kay BK, Fowlkes DM;
 XX WPI; 1994-279739/34.
 XX Identifying proteins or peptide(s) which bind a ligand - by screening a
 XX recombinant vector library expressing fusion proteins comprising a
 XX binding domain and an effector domain.
 XX Example 7.5; Page 108; 255pp; English.

XX AAR58412-42 are overlapping 8-mer peptides of the binding domain of TSAR
 CC (Totally Synthetic Affinity Reagents) peptide TSAR C46.9-2 (AAR58411).
 CC These bind (partially) a monoclonal antibody, ie. anti-CEA C46 (anti
 CC carcinoembryonic antigen). TSAR peptides are generated using generic
 CC oligonucleotides (see AA070470-73 for examples). TSARs are concatenated
 CC heterofunctional proteins or peptides, comprising at least two functional
 CC regions - a binding domain with affinity for a ligand and a second
 CC effector peptide portion that is chemically or biologically active. They
 CC may further comprise a linker peptide between the 2 domains. The TSARs or

CC compens. comprising a TSAR binding domain can be used in vivo to deliver
 CC a chemically or biologically active moiety, eg. metal ion, radioisotope,
 CC peptide, toxin or enzyme, to the specific target or on the cell. They can
 CC also replace the function of macromolecules eg. monoclonal or polyclonal
 CC antibodies and therefore circumvent the need for complex methods of
 CC hybridoma formation or in vivo antibody production. The TSARs are easily
 CC characterised and have designed activity allowing direct and rapid
 CC detection in a screening process. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX Sequence 8 AA;
 SQ Query Match 49.2%; Score 30; DB 2; Length 8;
 Best Local Similarity 62.5%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTSVPLTS 8
 DB 1 CTSVPLTS 8
 |||||
 |||||

RESULT 10
 AAE34703
 ID AAE34703 standard; peptide; 9 AA.
 XX AAE34703;
 AC AAE34703;
 XX 14-MAY-2003 (first entry)
 DT CA125/MUC16 O-glycosylation site #1.
 DE CA125; antigen; cancer; gene therapy; vaccine; MUC16.
 XX Unidentified.
 OS WO200292836-A2.
 XX 21-NOV-2002.
 XX 09-MAY-2002; 2002WO-US014768.
 XX 11-MAY-2001; 2001US-0290480P.
 XX (SLOK) SLOAN KETTERING INST CANCER RES.
 XX Lloyd KO, Yin BWI;
 XX WPI; 2003-129305/12.
 XX New isolated nucleic acid molecule comprising sequences encoding the
 XX CA125 protein, useful for diagnosing, preventing and/or treating cancer,
 XX e.g. ovarian, pancreatic, breast, endometrial or lung carcinomas.
 XX Disclosure; Page 19; 70pp; English.

XX The invention relates to a nucleic acid molecule encoding an ovarian
 CC cancer antigen, CA125. Nucleic acid molecules, vaccine and methods are
 CC useful for diagnosing, preventing and treating cancer, e.g. pancreatic,
 CC lung, ovarian, breast or endometrial carcinoma. The invention is useful
 CC in gene therapy and as vaccines. The present sequence is CA125/MUC16 O-
 CC glycosylation site
 XX Sequence 9 AA;
 SQ Query Match 49.2%; Score 30; DB 6; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SVPLTSVP 10
 DB 2 SVPLTSVP 9
 |||||
 |||||

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RESULT 11
AAW12561
ID AAW12561 standard; peptide; 10 AA.
XX AC AAW12561;
XX DT 08-APR-1997 (first entry)
XX DE SH2 binding peptide core sequence #11.
XX KW Core peptide; src homology region 2 binding peptide; SH2; cell growth;
XX KW differentiation; regulation; receptor tyrosine kinase pathway; cancer;
XX KW signal transduction pathway; non-insulin dependent diabetes;
XX KW insulin-resistant diabetes.
XX OS Synthetic.
XX PH Key Location/Qualifiers
FT Modified-site 3
FT /label= OTHER
FT /note= "given in the patent as pI, no further details
FT given. May be intended to be phosphotyrosine"
XX WO9623813-A1.
XX PD 08-AUG-1996.
XX PF 31-JAN-1996; 96WO-US001544.
XX PR 01-FEB-1995; 95US-00382100.
XX PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX PI Patel DV, Gordeev MF, Gordon E, Grove JR, Hart CP, Kim MH;
XX PI Szardenings AK;
XX DR WPI; 1996-371373/37.
XX PT Peptide(s) which bind to SH2 domains - are used to treat diseases
XX PT associated with aberrant cell growth, differentiation or regulation
XX PT associated with defects in receptor tyrosine kinase pathways.
XX PS Claim 8; Page 116; 203pp; English.
XX CC The sequences given in AAW12551-70 represent core peptides of an src
XX CC homology region 2 (SH2) binding peptide which correspond to the formula:
XX CC Z7-X-Z8-X = any D- or L- amino acid; Z7 = phosphotyrosine or its
XX CC isostere; Z8 = asparagine or its isostere; the amino terminus is
XX CC acylated, and the peptide is less than 14 residues in length, with the
XX CC proviso that if Z7 is phosphotyrosine and Z8 is asparagine, then the
XX CC peptide is not GDGZ7XZ8XPLLL. SH2 binding peptides containing these core
XX CC peptides are used to treat of diagnose diseases associated with aberrant
XX CC cell growth, differentiation or regulation which is associated with
XX CC defects in receptor tyrosine kinase pathways, by partially blocking or
XX CC inhibiting a cellular signal transduction pathway. The disease may be
XX CC cancer, a developmental or differentiation disease or insulin-resistant
XX CC (or non-insulin dependent) diabetes
XX SQ Sequence 10 AA;
    Query Match 49.2%; Score 30; DB 2; Length 10;
    Best Local Similarity 71.4%; Pred. No. 1.9e+02;
    Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
    QY 1 C1SVPLT 7
    DB 2 C1NVPT 8
    RESULT 12
    AAW12615
    ID AAW12615 standard; peptide; 11 AA.
    XX

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AC AAW12615;
XX DT 08-APR-1997 (first entry)
XX DE SH2 binding peptide core sequence #21.
XX KW Core peptide; src homology region 2 binding peptide; SH2; cell growth;
XX KW differentiation; regulation; receptor tyrosine kinase pathway; cancer;
XX KW signal transduction pathway; non-insulin dependent diabetes;
XX KW insulin-resistant diabetes.
XX OS Synthetic.
XX PN WO9623813-A1.
XX PD 08-AUG-1996.
XX PF 31-JAN-1996; 96WO-US001544.
XX PR 01-FEB-1995; 95US-00382100.
XX PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX PI Patel DV, Gordeev MF, Gordon E, Grove JR, Hart CP, Kim MH;
XX PI Szardenings AK;
XX DR WPI; 1996-371373/37.
XX PT Peptide(s) which bind to SH2 domains - are used to treat diseases
XX PT associated with aberrant cell growth, differentiation or regulation
XX PT associated with defects in receptor tyrosine kinase pathways.
XX PS Claim 13; Page 117; 203pp; English.
XX CC This sequence represents a core peptide of an src homology region 2 (SH2)
XX CC binding peptide corresponding to the formula: Z7-X-Z8-X = any D- or L-
XX CC amino acid; Z7 = phosphotyrosine or its isostere; Z8 = asparagine or its
XX CC isostere; the amino terminus is acylated, and the peptide is less than 14
XX CC residues in length, with the proviso that if Z7 is phosphotyrosine and Z8
XX CC is asparagine, then the peptide is not GDGZ7XZ8XPLLL. SH2 binding
XX CC peptides containing this core peptide are used to treat of diagnose
XX CC diseases associated with aberrant cell growth, differentiation or
XX CC regulation which is associated with defects in receptor tyrosine kinase
XX CC pathways, by partially blocking or inhibiting a cellular signal
XX CC transduction pathway. The disease may be cancer, a developmental or
XX CC differentiation disease or insulin-resistant (or non-insulin dependent)
XX CC diabetes
XX SQ Sequence 11 AA;
    Query Match 49.2%; Score 30; DB 2; Length 11;
    Best Local Similarity 71.4%; Pred. No. 2.1e+02;
    Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
    QY 1 C1SVPLT 7
    DB 2 C1NVPT 8
    RESULT 13
    ABP47579
    ID ABP47579 standard; peptide; 11 AA.
    XX AC ABP47579;
    XX DT 19-AUG-2002 (first entry)
    XX DE N. meningitidis LOS peptidic mimotope related peptide SEQ ID NO:155.
    XX KW Neisseria meningitidis; meningococcus; meningococcal; vaccine; LOS;
    KW lipooligosaccharide; monoclonal antibody; antibacterial; infection;
    KW antiinflammatory; meningococcal disease.
    XX

```

XXI

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PS Example 4; Page 40; 56pp; English.
 XX CAIR-1 protein (AAR77365), responsible for CAI resistance in A2058 human
 CC melanoma cells, contains a unique proline-rich sequence which fulfills
 CC the consensus definition for Src homology 3 (SH3) binding proteins
 CC (AAR77366). 4 Unique versions (AAR77367-70) are present
 XX

SQ Sequence 10 AA;

Query Match 44.3%; Score 27; DB 2; Length 10;
 Best Local Similarity 62.5%; Pred. No. 6e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 VPLTSVPC 11
 ||||
 Db 1 VPPAPVPC 8

Search completed: March 8, 2004, 12:09:26
 Job time : 53 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model
Run on: March 8, 2004, 12:10:46 ; Search time 33 Seconds
(without alignments)
70.384 Million cell updates/sec

Title: US-09-761-636A-7
Perfect score: 61
Sequence: 1 CISVPLTSVPC 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues
Total number of hits satisfying chosen parameters: 129820

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA.*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	11	9 US-09-761-636A-7	Sequence 7, Appl
2	59	96.7	11	9 US-09-761-636A-23	Sequence 23, Appl
3	57	93.4	11	9 US-09-761-636A-26	Sequence 26, Appl
4	54	88.5	11	9 US-09-761-636A-24	Sequence 24, Appl
5	52	85.2	11	9 US-09-761-636A-25	Sequence 25, Appl
6	45.5	74.6	10	9 US-09-761-636A-13	Sequence 13, Appl
7	41	67.2	9	9 US-09-761-636A-14	Sequence 14, Appl
8	32	52.5	9	9 US-09-761-636A-10	Sequence 10, Appl
9	29	47.5	9	15 US-10-245-871-332	Sequence 332, App
10	29	47.5	11	14 US-10-126-845-89	Sequence 89, Appl
11	28	45.9	9	15 US-10-154-884B-11221	Sequence 11221, A
12	27	44.3	9	15 US-10-154-884B-11228	Sequence 11228, A
13	27	44.3	9	15 US-10-154-884B-11250	Sequence 11250, A
14	27	44.3	9	15 US-10-154-884B-11254	Sequence 11254, A
15	27	44.3	9	15 US-10-154-884B-11258	Sequence 11258, A

16	27	44.3	9	15	US-10-154-884B-11259	Sequence 11259, A
17	27	44.3	9	15	US-10-154-884B-11265	Sequence 11265, A
18	27	44.3	9	15	US-10-154-884B-11275	Sequence 11275, A
19	27	44.3	9	15	US-10-154-884B-11280	Sequence 11280, A
20	26	42.6	9	13	US-10-066-151-20	Sequence 20, Appl
21	26	42.6	9	15	US-10-358-052-20	Sequence 20, Appl
22	26	42.6	10	11	US-09-833-245-1011	Sequence 1011, Ap
23	25	41.0	9	13	US-10-066-151-19	Sequence 19, Appl
24	25	41.0	9	15	US-10-358-052-19	Sequence 19, Appl
25	25	41.0	9	15	US-10-428-335-52	Sequence 52, Appl
26	25	41.0	10	10	US-09-572-404B-2047	Sequence 2047, Ap
27	25	41.0	11	14	US-10-126-845-12	Sequence 12, Appl
28	25	41.0	11	14	US-10-126-845-70	Sequence 70, Appl
29	25	41.0	11	15	US-10-116-275-100	Sequence 100, App
30	24	39.3	5	9	US-09-866-135-5	Sequence 5, Appl
31	24	39.3	5	10	US-09-886-135-5	Sequence 5, Appl
32	24	39.3	7	9	US-09-761-636A-11	Sequence 11, Appl
33	24	39.3	7	14	US-10-220-033-28	Sequence 28, Appl
34	24	39.3	9	13	US-10-066-151-21	Sequence 21, Appl
35	24	39.3	9	14	US-10-277-292-249	Sequence 249, App
36	24	39.3	9	14	US-10-277-292-322	Sequence 322, App
37	24	39.3	9	14	US-10-277-292-349	Sequence 349, App
38	24	39.3	9	14	US-10-277-292-464	Sequence 464, App
39	24	39.3	9	15	US-10-280-340-249	Sequence 249, App
40	24	39.3	9	15	US-10-280-340-322	Sequence 322, App
41	24	39.3	9	15	US-10-280-340-349	Sequence 349, App
42	24	39.3	9	15	US-10-280-340-464	Sequence 464, App
43	24	39.3	9	15	US-10-358-052-21	Sequence 21, Appl
44	24	39.3	9	15	US-10-107-532-250	Sequence 250, App
45	24	39.3	9	15	US-10-107-532-256	Sequence 256, App

ALIGNMENTS

RESULT 1
US-09-761-636A-7
; Sequence 7, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761.636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-7

Query Match 100.0%; Score 61; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CISVPLTSVPC 11
Db 1 CISVPLTSVPC 11

RESULT 2
US-09-761-636A-23
; Sequence 23, Application US/09761636A
; Patent No. US20020065218A1

us-09-761-636a-7.closed.rapb

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; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761.636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-23

Query Match          96.7%; Score 59; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0049;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTSVPLTSVPC 11
Db 1 CTSVPLTSVPC 11

RESULT 3
US-09-761-636A-26
; Sequence 26, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761.636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-26

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Best Local Similarity 91.8%; Pred. No. 0.01;
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QY 1 CTSVPLTSVPC 11
Db 1 CTSVPLTSVPC 11

RESULT 4
US-09-761-636A-24
; Sequence 24, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761.636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-24

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Best Local Similarity 72.7%; Pred. No. 0.03;
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QY 1 CTSVPLTSVPC 11
Db 1 CTSVPLTSVPC 11

RESULT 5
US-09-761-636A-25
; Sequence 25, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761.636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-25

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Best Local Similarity 72.7%; Pred. No. 0.062;
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QY 1 CTSVPLTSVPC 11
Db 1 CTSVPLTSVPC 11

RESULT 6
US-09-761-636A-13
; Sequence 13, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761.636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-13
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;; PRIOR FILING DATE: 2000-01-18
;; PRIOR APPLICATION NUMBER: US 60/204,590
;; PRIOR FILING DATE: 2000-05-16
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 13
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-761-636A-13

Query Match 74.6%; Score 45.5; DB 9; Length 10;
Best Local Similarity 90.9%; Pred. No. 0.6;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 C1SVPLTVSVC 11
Db 1 C1SVPL--SVPC 10

RESULT 7
US-09-761-636A-14
; Sequence 14, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-14

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Best Local Similarity 81.8%; Pred. No. 7.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 C1SVPLTVSVC 11
Db 1 C1SVPL--VPC 9

RESULT 8
US-09-761-636A-10
; Sequence 10, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0

;; SEQ ID NO 10
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-761-636A-10

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Best Local Similarity 100.0%; Pred. No. 7.2e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLTSV 9
Db 2 SVPLTSV 8

RESULT 9
US-10-245-871-332
; Sequence 332, Application US/10245871
; Publication No. US20030235594A1
; GENERAL INFORMATION:
; APPLICANT: HUMFREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: II-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2013
; CURRENT APPLICATION NUMBER: US/10/245,871
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 332
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-245-871-332

Query Match 47.5%; Score 29; DB 15; Length 9;
Best Local Similarity 71.4%; Pred. No. 7.2e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPLTSVP 10
Db 2 VPITSTP 8

RESULT 10
US-10-126-845-89
; Sequence 89, Application US/10126845
; Publication No. US20030181367A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20058
; CURRENT APPLICATION NUMBER: US/10/126,845
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D form peptide
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(11)
; OTHER INFORMATION: D form retroinversion peptide
US-10-126-845-89

Mon Mar 8 13:11:03 2004

us-09-761-636a-7.closed.rapb

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Query Match      47.5%; Score 29; DB 14; Length 11;
Best Local Similarity 45.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Db 1 CLLVPLLVAC 11

RESULT 11
US-10-154-884B-11221
; Sequence 11221, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11221
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11228

Query Match      44.3%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUSVPL 6
   |:|:|:|
Db 4 CLSVFV 9

RESULT 13
US-10-154-884B-11250
; Sequence 11250, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11221
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11221

Query Match      45.9%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 7.2e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUSVPLT 7
   |:|:|:|
Db 2 CLSVFVS 8

RESULT 12
US-10-154-884B-11228
; Sequence 11228, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation

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; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11250
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11250

Query Match      44.3%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUSVPL 6
   |::|:
Db 4 CLSPVP 9

RESULT 14
; Sequence 11254, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11254
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11254

Query Match      44.3%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUSVPL 6
   |::|:
Db 4 CLSPVP 9

RESULT 15
; Sequence 11258, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11258
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11258

Query Match      44.3%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUSVPL 6
   |::|:
Db 4 CLSPVP 9

Search completed: March 8, 2004, 12:16:00
Job time : 33 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:53:09 ; Search time 22 Seconds
(without alignments)
30.506 Million cell updates/sec

Title: US-09-761-636A-5
Perfect score: 72
Sequence: 1 CASELKGKSTNTPC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 127817

Minimum DB seq length: 0
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	38.9	9	3 US-09-258-754-63	Sequence 63, Appl
2	28	38.9	9	3 US-09-042-107-63	Sequence 63, Appl
3	28	38.9	9	4 US-09-722-250D-63	Sequence 63, Appl
4	27	37.5	13	1 US-07-732-114A-2	Sequence 2, Appl
5	27	37.5	13	1 US-08-170-114A-2	Sequence 2, Appl
6	26	36.1	9	3 US-08-660-092-70	Sequence 70, Appl
7	26	36.1	9	3 US-09-160-513-70	Sequence 219, Appl
8	26	36.1	13	3 US-09-258-754-219	Sequence 219, Appl
9	26	36.1	13	3 US-09-042-107-219	Sequence 219, Appl
10	26	36.1	13	4 US-09-722-250D-219	Sequence 170, Appl
11	26	36.1	13	4 US-09-428-082B-170	Sequence 12, Appl
12	24.5	34.0	12	4 US-08-182-967-12	Sequence 3, Appl
13	24	33.3	9	6 US-08-645-193B-3	Patent No. 5217869
14	24	33.3	9	6 US-08-645-193B-3	Sequence 24, Appl
15	24	33.3	11	3 US-08-866-545-24	Sequence 116, Appl
16	24	33.3	11	4 US-09-428-082B-116	Sequence 24, Appl
17	24	33.3	11	4 US-09-627-775-24	Sequence 183, Appl
18	24	33.3	13	3 US-09-258-754-183	Sequence 183, Appl
19	24	33.3	13	3 US-09-042-107-183	Sequence 11, Appl
20	24	33.3	13	4 US-08-182-967-11	Sequence 183, Appl
21	24	33.3	13	4 US-09-722-250D-183	Sequence 6, Appl
22	23.5	32.6	11	1 US-07-732-114A-6	Sequence 6, Appl
23	23.5	32.6	11	1 US-08-170-114A-6	Sequence 7, Appl
24	23	31.9	7	2 US-08-645-193B-7	Sequence 59, Appl
25	23	31.9	7	2 US-08-645-193B-59	Sequence 150, Appl
26	23	31.9	9	3 US-08-660-092-150	Sequence 151, Appl
27	23	31.9	9	3 US-08-660-092-151	Sequence 151, Appl

Sequence 152, Appl
Sequence 150, Appl
Sequence 151, Appl
Sequence 152, Appl
Sequence 91, Appl
Sequence 344, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 35, Appl
Sequence 30, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 20, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 9, Appl
Sequence 1066, Appl
Sequence 1066, Appl

ALIGNMENTS

RESULT 1
US-09-258-754-63
; Sequence 63, Application US/09258754
; Patent No. 6174687

GENERAL INFORMATION:
APPLICANT: Ruoilahti, Erkki
APPLICANT: Rajotte, Daniel
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
TITLE OF INVENTION: Membrane Diptidase
FILE REFERENCE: P-LJ 3443
CURRENT APPLICATION NUMBER: US/09/258,754
CURRENT FILING DATE: 1999-02-26
EARLIER APPLICATION NUMBER: 09/042,107
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 452
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 63
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-258-754-63
Query Match 38.9%; Score 28; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 KSTNTPC 13
:|||||
Db 3 RSTNTPC 9

RESULT 2
US-09-042-107-63
; Sequence 63, Application US/09042107
; Patent No. 6232287

GENERAL INFORMATION:
APPLICANT: Ruoilahti, Erkki
APPLICANT: Rajotte, Renata
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
TITLE OF INVENTION: Tissues
FILE REFERENCE: P-LJ 2892
CURRENT APPLICATION NUMBER: US/09/042,107
CURRENT FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 436
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 63
LENGTH: 9

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;
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-63
    Query Match          38.9%; Score 28; DB 3; Length 9;
    Best Local Similarity 71.4%; Pred. No. 3e+05;
    Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 KSTNTPC 13
Db 3 RSTNTGC 9

RESULT 3
US-09-722-250D-63
; Sequence 63, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-63
    Query Match          38.9%; Score 28; DB 4; Length 9;
    Best Local Similarity 71.4%; Pred. No. 3e+05;
    Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 KSTNTPC 13
Db 3 RSTNTGC 9

RESULT 4
US-07-732-114A-2
; Sequence 2, Application US/07732114A
; Patent No. 5298396
; GENERAL INFORMATION:
; APPLICANT: KOTZIN, BRIAN L.
; APPLICANT: MARRACK, PHILIPPA
; APPLICANT: KAPPLER, JOHN
; APPLICANT: PALLIARD, XAVIER
; TITLE OF INVENTION: METHOD FOR IDENTIFYING T CELLS
; TITLE OF INVENTION: INVOLVED IN AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beaton & Swanson, P.C.
; STREET: 4582 South Ulster Street Parkway, #403
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80237
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 07/732,114
; FILING DATE: 18-JULY-1991
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/437,370
; FILING DATE: 15-NOVEMBER-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Julie L. Bernard
; REGISTRATION NUMBER: 36,450
; REFERENCE/DOCKET NUMBER: NJH217.3
```

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;
; APPLICATION NUMBER: US/07/732,114A
; FILING DATE: 18-JULY-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/488,353
; FILING DATE: 2-MARCH-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/437,370
; FILING DATE: 15-NOVEMBER-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 850-9900
; TELEFAX: (303) 850-9401
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-07-732-114A-2
    Query Match          37.5%; Score 27; DB 1; Length 13;
    Best Local Similarity 54.5%; Pred. No. 2.1e+02;
    Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELGSKSTNT 11
Db 1 CASSLYGTRNT 11

RESULT 5
US-08-170-114A-2
; Sequence 2, Application US/08170114A
; Patent No. 5776708
; GENERAL INFORMATION:
; APPLICANT: KOTZIN, BRIAN L.
; APPLICANT: MARRACK, PHILIPPA
; APPLICANT: KAPPLER, JOHN
; APPLICANT: PALLIARD, XAVIER
; TITLE OF INVENTION: METHOD FOR IDENTIFYING T CELLS
; TITLE OF INVENTION: INVOLVED IN AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0 (a) For Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,114A
; FILING DATE: 20-DECEMBER-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/732,114
; FILING DATE: 18-JULY-1991
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07,488,353
; FILING DATE: 2-MARCH-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07,437,370
; FILING DATE: 15-NOVEMBER-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Julie L. Bernard
; REGISTRATION NUMBER: 36,450
; REFERENCE/DOCKET NUMBER: NJH217.3
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-170-114A-2

Query Match 37.5%; Score 27; DB 1; Length 13;
Best Local Similarity 54.5%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0;

QY 1 CASELGKSTNT 11
||| : ||
Db 1 CASSLYGTRNT 11

RESULT 6

US-08-660-092-70
Sequence 70, Application US/08660092
Patent No. 6207160

GENERAL INFORMATION:
APPLICANT: Victoria, Edward J.

APPLICANT: Marquis, David M.

APPLICANT: Jones, David S.

APPLICANT: Yu, Lin

TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES

TITLE OF INVENTION: THEREOF AND METHODS OF TREATMENT FOR aPL ANTIBODY-MEDIATED

TITLE OF INVENTION: PATHOLOGIES

NUMBER OF SEQUENCES: 216

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/660,092

FILING DATE: 06-JUN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Park, Freddie K.

REGISTRATION NUMBER: 35,636

REFERENCE/DOCKET NUMBER: 25231-20061.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-660-092-70

Query Match 36.1%; Score 26; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0;

QY 1 CASELGK 7
||| : ||
Db 1 CAGVLGK 7

RESULT 7

US-09-160-513-70

Sequence 70, Application US/09160513

Patent No. 6410775

GENERAL INFORMATION:

APPLICANT: Victoria, Edward J.

APPLICANT: Marquis, David M.

APPLICANT: Jones, David S.

APPLICANT: Yu, Lin

TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND METHODS (

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/160,513

FILING DATE: 1998-DEC-24

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: CATHERINE M. POLIZZI

REGISTRATION NUMBER: 40,130

REFERENCE/DOCKET NUMBER: 25231-20061.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-160-513-70

Query Match 36.1%; Score 26; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0;

QY 1 CASELGK 7
||| : ||
Db 1 CAGVLGK 7

RESULT 8

US-09-258-754-219

Sequence 219, Application US/09258754

Patent No. 6174687

GENERAL INFORMATION:

APPLICANT: Ruoslahti, Erkki

APPLICANT: Pasqualini, Renata

APPLICANT: Rajotte, Daniel

TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using

TITLE OF INVENTION: Membrane Diptidase

FILE REFERENCE: P-LJ 3443

CURRENT APPLICATION NUMBER: US/09/258,754

CURRENT FILING DATE: 1999-02-26

EARLIER APPLICATION NUMBER: 09/042,107

EARLIER FILING DATE: 1998-03-13

NUMBER OF SEQ ID NOS: 452

SOFTWARE: Patent in ver. 2.0

SEQ ID NO 219

LENGTH: 13

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-219

Query Match          36.1%; Score 26; DB 3; Length 13;
Best Local Similarity 30.8%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
   |||:|
Db 1 CGSHCGQLCKSLC 13

RESULT 9
US-09-042-107-219
; Sequence 219, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 219
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-219

Query Match          36.1%; Score 26; DB 3; Length 13;
Best Local Similarity 30.8%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
   |||:|
Db 1 CGSHCGQLCKSLC 13

RESULT 10
US-09-722-250D-219
; Sequence 219, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 219
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-219

Query Match          36.1%; Score 26; DB 4; Length 13;
Best Local Similarity 30.8%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
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QY 1 CASELGKSTNTFC 13
   |||:|
Db 1 CGSHCGQLCKSLC 13

RESULT 11
US-09-428-082B-170
; Sequence 170, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: ROONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 170
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CALMODULIN ANTAGONIST PEPTIDE
US-09-428-082B-170

Query Match          36.1%; Score 26; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NTFC 13
   ||||
Db 8 NTFC 11

RESULT 12
US-08-182-967-12
; Sequence 12, Application US/08182967
; Patent No. 6413516
; GENERAL INFORMATION:
; APPLICANT: Chang, Jennie C.C.
; APPLICANT: Brostoff, Steven W.
; APPLICANT: Carlo, Dennis J.
; TITLE OF INVENTION: Peptides and Methods Against Psoriasis
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,967
; FILING DATE: 14-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/462,471
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,867
; FILING DATE: 14-DEC-1991
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/644,611
FILING DATE: 22-JAN-1991
PRIOR APPLICATION DATA: US 07/530,229
FILING DATE: 30-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/382,085
FILING DATE: 18-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/382,086
FILING DATE: 18-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/326,314
FILING DATE: 21-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IM 9830
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-182-967-12

Query Match 34.0%; Score 24.5; DB 4; Length 12;
Best Local Similarity 63.6%; Pred. No. 5e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 CASELCKSTNT 11
Db 1 CASSL-NSLNT 10

RESULT 13
US-08-645-193B-3
Sequence 3, Application US/08645193B
Patent No. 5962253
GENERAL INFORMATION:
APPLICANT: Kupke, Thomas
APPLICANT: Gotz, Friedrich
APPLICANT: Kempter, Christoph
APPLICANT: Jung, Gunther
TITLE OF INVENTION: Oxidative Decarboxylation of Peptides
TITLE OF INVENTION: Catalyzed by Flavoprotein EpiD
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,193B
FILING DATE: 13-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.1540000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-645-193B-3

Query Match 33.3%; Score 24; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 STNTPC 13
Db 1 SFNSFC 6

RESULT 14
5217869-110
Patent No. 5217869
APPLICANT: KAUVAR, LAWRENCE M.
TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
REAGENTS
NUMBER OF SEQUENCES: 121
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/255,906
FILING DATE: 11-OCT-1988
SEQ ID NO: 110:
LENGTH: 9
5217869-110

Query Match 33.3%; Score 24; DB 6; Length 9;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GKSTNTP 12
Db 1 GKGSNNF 7

RESULT 15
US-08-866-545-24
Sequence 24, Application US/08866545
Patent No. 6265535
GENERAL INFORMATION:
APPLICANT: Greene, Mark I.
APPLICANT: Murali, Ramachandran
APPLICANT: Takasaki, Wataru
TITLE OF INVENTION: PEPTIDES AND PEPTIDE
TITLE OF INVENTION: ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR
TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,545
FILING DATE: 30-MAY-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009113-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6265535e
US-08-866-545-24

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Query Match 33.3%; Score 24; DB 3; Length 11;
Best Local Similarity 57.1%; Pred. No. 5.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Oy 1 CASELQK 7
Db 2 CRRELQK 8

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Search completed: March 8, 2004, 11:56:31
Job time : 23 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:00:00 ; Search time 20 Seconds
(without alignments)
38.477 Million cell updates/sec

Title: US-09-761-636a-6

Perfect score: 46

Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 605

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	17	37.0	6	2 S29637	jacalin beta-II ch
2	17	37.0	6	2 I37263	Y protein - human
3	15	32.6	6	2 JU0355	lipopeptide WS1279
4	15	32.6	7	2 B39040	calsequestrin, fas
5	15	32.6	8	2 S59622	metallothionein is
6	15	32.6	8	2 S19288	acylase - Kluveria
7	15	32.6	8	2 S69165	ferredoxin a2 - Ja
8	14	30.4	6	2 B31263	dihydrofolate redu
9	14	30.4	6	2 S29881	Na+/K+-exchanging
10	14	30.4	7	1 XEYDGD	galactose oxidase
11	14	30.4	8	2 B47594	aspartate kinase (
12	13	28.3	5	2 A32014	tram protein - Esc
13	13	28.3	8	2 A37521	R-phycoerythrin ga
14	12	26.1	6	2 H48394	glycoprotein compo
15	12	26.1	7	2 B34818	vicilin 57K chain
16	12	26.1	7	2 A12016	formylglycinamide
17	12	26.1	8	2 PC1002	leucine-tRNA ligas
18	11	23.9	4	2 A41890	protein D - Escher
19	11	23.9	5	2 A26830	mitosis inhibiting
20	11	23.9	5	2 B22565	R-phycoerythrin al
21	11	23.9	5	2 A44692	fulicin - giant Af
22	11	23.9	6	2 A31263	dihydrofolate redu
23	11	23.9	7	2 A58512	venom heptapeptide
24	11	23.9	7	2 I46868	alpha-myosin heavy
25	11	23.9	8	2 C61512	variant surface gl
26	11	23.9	8	2 PT0454	T-cell receptor be
27	10	21.7	4	2 S55338	pallidipin - assas
28	10	21.7	5	2 A60803	neuropeptide - sea
29	10	21.7	5	2 PT0610	T-cell receptor be

hydrogensulfite re
tubulin beta-3 cha
glutathione transf
hypothetical prote
cadmium-binding he
T-cell receptor be
Na+-transporting A
globulin IV alpha
variant surface gl
gene Ctr protein
cytochrome P450 AL
tocopherol-binding
gene Tnslow prote
L-serine ammonia-1
R-phycoerythrin al
metallothionein-A

ALIGNMENTS

RESULT 1

S29637 jacalin beta-II chain - Artocarpus champeden (fragment)

C:Species: Artocarpus champeden

C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998

C:Accession: S29637

R:Ngoc, L.D.; Brillard, M.; Hosbeke, J.

Biochim. Biophys. Acta 1156, 219-222, 1993

A:Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-

A:Reference number: S29635; MUID:93152601; PMID:8427879

A:Accession: S29637

A:Molecule type: protein

A:Residues: 1-6 <NGO>

A:Experimental source: seed

A:Complex: heterotetramer; two alpha and two beta chains

C:Function:

A:Description: seed storage protein

A:Note: lectin for D-galactosyl-beta-1-3-N-acetylgalactosamine

C:Keywords: heterotetramer; lectin; seed; storage protein

Query Match 37.0%; Score 17; DB 2; Length 6;

Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NEES 5

Db 1 NEQS 4

RESULT 2

I37263

Y protein - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999

C:Accession: I37263

R:Waerber, G.; Habener, J.F.

Endocrinology 131, 2010-2015, 1992

A:Title: Novel testis germ cell-specific transcript of the CREB gene contains an alter

A:Reference number: I37263; MUID:93010691; PMID:1396344

A:Accession: I37263

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: RNA

A:Residues: 1-6 <RES>

A:Cross-references: EMBL:X68994; NID:G396171; PIDN:CAA48780.1; PID:G579816

C:Genetics:

A:Gene: CREB

Query Match 37.0%; Score 17; DB 2; Length 6;

Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 SLIC 8

Db 1 SLFC 4

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

Query 1 CN 2
Db 1 CN 2

RESULT 3

lipopeptide WS1279 [validated] - Streptomyces willmorei
C:Species: Streptomyces willmorei
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: J00355
R:Tsuda, Y.; Okada, Y.; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.
Chem. Pharm. Bull. 39, 607-611, 1991
A:Title: Structure and synthesis of an immunoreactive lipopeptide, WS1279, of microbial origin
A:Reference number: J00355; MUID:91300586; PMID:2070441
A:Accession: J00355
A:Molecule type: protein
A:Residues: 1-6 <TSU>
A>Note: the structure was confirmed by synthesis
C:Keywords: blocked amino end; lipoprotein
F1/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental
F1/Modified site: fatty acylated amino end (Cys) #status experimental

Query Match 32.6%; Score 15; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

Query 1 CN 2
Db 1 CN 2

RESULT 4

B39040
calsequestrin, fast skeletal muscle - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997
C:Accession: B39040
R:Gala, S.E.; Jones, L.R.
J. Biol. Chem. 266, 391-398, 1991
A:Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein
A:Reference number: A39040; MUID:91093153; PMID:1985907
A:Accession: B39040
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <CAL>
C:Keywords: phosphoprotein; skeletal muscle

Query Match 32.6%; Score 15; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;

Query 2 NEESL 6
Db 2 DEEDL 6

RESULT 5

S59622
metallothionein isoform a, cadmium-binding - Ariantha arbustorum (terrestrial snail) (fragment)
C:Species: Ariantha arbustorum
C>Date: 19-Mar-1997 #sequence_revision 24-Oct-1997 #text_change 07-May-1999
C:Accession: S59622
R:Berger, B.; Hunziker, P.E.; Hauer, C.R.; Birchler, N.; Dallinger, R.
Biochem. J. 311, 951-957, 1995
A:Title: Mass spectrometry and amino acid sequencing of two cadmium-binding metallothionein
A:Reference number: S59621; MUID:96067616; PMID:7487956
A:Accession: S59622
A:Molecule type: protein
A:Residues: 1-8 <BER>
C:Superfamily: metallothionein
C:Keywords: chelation; metal binding; metal-thiolate cluster

Query Match 32.6%; Score 15; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

Query 1 CN 2
Db 1 CN 2

RESULT 6

acylase - Kluyvera cryocrescens
C:Species: Kluyvera cryocrescens
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S19288
R:Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.
Biochem. J. 280, 659-662, 1991
A:Title: Chemical modification of serine at the active site of penicillin acylase from Kluyvera cryocrescens
A:Reference number: S19288; MUID:92109664; PMID:11764029
A:Accession: S19288
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <MAR>

Query Match 32.6%; Score 15; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

Query 1 CN 2
Db 1 CN 2

RESULT 7

S69165
ferredoxin a2 - Japanese radish (fragment)
C:Species: Kaiware daikon (Japanese radish)
C>Date: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 17-Apr-1998
C:Accession: S69165
R:Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.
Arch. Biochem. Biophys. 316, 797-802, 1995
A:Title: Four ferredoxins from Japanese radish leaves.
A:Reference number: S69164; MUID:95168867; PMID:7864635
A:Accession: S69165
A:Molecule type: protein
A:Residues: 1-8 <OBA>
C:Keywords: 2Fe-2S; electron transfer; iron-sulfur protein

Query Match 32.6%; Score 15; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05; Mismatches 2; Indels 0; Gaps 0;

Query 3 RESLI 7
Db 4 BEDIV 8

RESULT 8

B31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium falciparum
C:Species: Plasmodium falciparum
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: B31263
R:Peterson, D.S.; Walliker, D.; Wellem, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9119, 1988
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
A:Reference number: A94217; MUID:89057886; PMID:2904149
A:Accession: B31263
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <PEI>
C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match 30.4%; Score 14; DB 2; Length 6;

Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NEESL 6
| | | |
Db 2 NWESI 6

RESULT 9

S29881
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 19-Apr-2002
C:Accession: S29881
R:Walderhaug, M.O.; Post, R.L.; Saccomani, G.; Leonard, R.T.; Briskin, D.P.
J. Biol. Chem. 260, 3852-3859, 1985
A>Title: Structural relatedness of three ion-transport adenosine triphosphatases around
A:Reference number: S29881; MUID:85131201; PMID:3156136
A:Accession: S29881
A:Molecule type: protein
A:Residues: 1-6 <NAL>
A:Experimental source: kidney
C:Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;
F;4/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 30.4%; Score 14; DB 2; Length 6;
Best Local Similarity 20.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEES 5
| | | |
Db 2 CSDKT 6

RESULT 10

KEYDGD
galactose oxidase inhibitor - fungus (Cladobotryum dendroides)
C:Species: Cladobotryum dendroides
C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 31-Dec-1993
C:Accession: A01341
R:Avigad, G.; Markus, Z.
Fed. Proc. 31, 447, 1972
A:Reference number: A01341
A:Accession: A01341
A:Molecule type: protein
A:Residues: 1-7 <AVI>
C:Comment: The mycelia of this imperfect fungus produce the metalloenzyme galactose oxidase, an apoenzyme, may inactivate the enzyme by binding to its prosthetic copper group.
C:Superfamily: galactose oxidase inhibitor
C:Keywords: copper

Query Match 30.4%; Score 14; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 NEES 5
| | | |
Db 4 NTES 7

RESULT 11

B47594
aspartate kinase (EC 2.7.2.4) beta chain - Corynebacterium flavum (strain N13) (fragment)
C:Species: Corynebacterium flavum
C>Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 19-Dec-1997
C:Accession: B47594
R:Follettie, M.T.; Peoples, O.P.; Agoropoulou, C.; Sinskey, A.J.
J. Bacteriol. 175, 4096-4103, 1993
A>Title: Gene structure and expression of the Corynebacterium flavum N13 ask-aid operon.
A:Reference number: A47594; MUID:93308089; PMID:8100567
A:Accession: B47594
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA

A:Residues: 1-8 <POL>
C:Keywords: phosphotransferase

Query Match 30.4%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 BESLI 7
| | | |
Db 2 BEAVL 6

RESULT 12

A32014
tram protein - Escherichia coli plasmid R100 (fragment)
C:Species: Escherichia coli
C>Date: 22-Jun-1989 #sequence_revision 22-Jun-1989 #text_change 16-Feb-1997
C:Accession: A32014
R:Imamoto, S.; Yoshioka, Y.; Ohtsubo, E.
J. Bacteriol. 170, 2749-2757, 1988
A>Title: Identification and characterization of the products from the traJ and traY genes
A:Reference number: A32014; MUID:88227859; PMID:2836369
A:Accession: A32014
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-5 <INA>
C:Genetics:
A:Genome: plasmid
C:Keywords: DNA binding

Query Match 28.3%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NEE 4
| | |
Db 2 NDE 4

RESULT 13

A37521
R-phycoerythrin gamma-E chain - red alga (Gastrocloonium coulteri) (fragment)
C:Species: Gastrocloonium coulteri
C>Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: A37521; J22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A>Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601; PMID:3886644
A:Accession: A37521
A:Molecule type: protein
A:Residues: 1-8 <KLO>

Query Match 28.3%; Score 13; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SLIC 8
| | | |
Db 4 ALAC 7

RESULT 14

H48394
glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (J)
C:Species: Bos primigenius taurus (cattle)
C>Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C:Accession: H48394
R:Mathier, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A>Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig II-like sequences.
A:Reference number: A48394; MUID:93250576; PMID:8485470

A:Accession: H48394
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-6 <MAW>
 A:Experimental source: milk
 A>Note: sequence extracted from NCBI backbone (NCBIP:131518)
 C:Keywords: glycoprotein

Query Match 26.1%; Score 12; DB 2; Length 6;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ESLIC 8
 | | |
 Db 2 ELIGC 6

RESULT 15
 B34818
 vicilin 57K chain - pigeon pea (fragment)
 C:Species: Cajanus cajan (pigeon pea)
 C>Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 30-Sep-1993
 C:Accession: B34818
 R:Mawal, Y.R.; Mawal, M.R.; Ranjekar, P.K.
 Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990
 A>Title: Unusual denaturation properties of vicilin from Cajanus cajan.
 A:Reference number: A34818; MUID:90165956; PMID:2306256
 A:Accession: B34818
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <MAW>

Query Match 26.1%; Score 12; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNE 3
 | |
 Db 3 CME 5

Search completed: March 8, 2004, 12:03:35
 Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:56:34 ; Search time 11 Seconds
(without alignments)
37.869 Million cell updates/sec

Title: US-09-761-636A-6
Perfect score: 46
Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 158

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	30.4	7	1	IGAO_DACDE
2	13	28.3	5	1	TRM3_ECOLI
3	13	28.3	8	1	PLP_BRANA
4	12	26.1	7	1	UF03_MOUSE
5	12	26.1	8	1	UPA1_HUMAN
6	11	23.9	7	1	BRHP_CONTM
7	11	23.9	7	1	FAR1_ASCSU
8	11	23.9	8	1	CADI_ENTFA
9	10	21.7	8	1	ACT_CARMA
10	9	19.6	6	1	TMOF_SARBU
11	9	19.6	8	1	COM2_CONFU
12	9	19.6	8	1	GLUR_HUMAN
13	8	17.4	6	1	ACPH_RABIT
14	8	17.4	6	1	ASPT_LACSN
15	8	17.4	7	1	CCFI_ENTFA
16	8	17.4	7	1	FAR1_PROCL
17	8	17.4	7	1	GFRE_MOUSE
18	8	17.4	7	1	WWAI_ACHFU
19	8	17.4	7	1	WWA3_ACHFU
20	8	17.4	8	1	FAR4_HOMAM
21	8	17.4	8	1	FAR6_CALVO
22	7	15.2	7	1	FAR2_ASCSU
23	7	15.2	7	1	UH11_RAT
24	7	15.2	8	1	CLP_THICU
25	7	15.2	8	1	CPDI_ENTFA
26	7	15.2	8	1	PPK3_PERAM
27	7	15.2	8	1	UH09_RAT
28	7	15.2	4	1	WPI_PERAT
29	6	13.0	4	1	ROSI_HUMAN
30	6	13.0	4	1	FLRN_ATEL
31	6	13.0	5	1	TPIS_CANFA
32	6	13.0	5	1	UXA4_CHLFR
33	6	13.0	6	1	FARP_MONEX

34 6 13.0 6 1 UN06_CLOPA
35 6 13.0 6 1 VP19_HSVIK
36 6 13.0 7 1 ALL2_CARMA
37 6 13.0 7 1 ALL5_CARMA
38 6 13.0 7 1 CHOX_ALGSP
39 6 13.0 7 1 EI05_LITRU
40 6 13.0 7 1 FAR1_WACHS
41 6 13.0 7 1 FAR2_PROCL
42 6 13.0 7 1 FAR4_PANRE
43 6 13.0 7 1 FAR6_CALVO
44 6 13.0 7 1 LANC_CARUI
45 6 13.0 7 1 MNP1_LEPDE

P81351 clostridium
P23210 herpes simp
P81805 carcinus ma
P81808 carcinus ma
P16101 alcaligenes
P82101 litoria rub
P83274 macrobrachi
P38498 procamburus
P41875 pangreillus
P41866 calliphora
P36960 carnobacter
P42984 leptinotars

ALIGNMENTS

RESULT 1
IGAO_DACDE STANDARD; PRT; 7 AA.
AC P06294;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Galactose oxidase inhibitor.
OS Dactylium dendroides (Cladobotryum dendroides).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypomyces.
OX NCBI_TaxID=5132;
RN [1]
RP SEQUENCE.
RA Avigad G., Markus Z.;
RT "Identification of a peptide inhibitor of galactose oxidase from
RT Dactylium dendroides.";
RL Fed. Proc. 31:447-447 (1972).
CC -|- FUNCTION: Binds one copper ion per molecule but does not bind the
CC galactose oxidase apoenzyme. It may inactivate the enzyme by
CC binding to its prosthetic copper group.
DR PIR; A01341; XEYDGD.
KW Copper; Metalloenzyme inhibitor.
SQ SEQUENCE 7 AA; 706 MW; 75BB01A456D87DB0 CRC64;

Query Match 30.4%; Score 14; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NEES 5
Db 4 NTES 7

RESULT 2
TRM3_ECOLI STANDARD; PRT; 5 AA.
ID TRM3_ECOLI
AC P13973;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TraM protein (Fragment).
GN TRAM.
OS Escherichia coli.
OG Plasmid IncFII R100.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=88227859; PubMed=2836369;
RA Inamoto S., Yoshioka Y., Ohtsubo E.;
RT "Identification and characterization of the products from the tra
RT and tray genes of plasmid R100.";
RL J. Bacteriol. 170:2749-2757 (1988).
CC -|- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION

CC PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the tram family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC
CC -----
DR EMBL; M20941; -; NOT ANNOTATED_CDS.
DR PIR; A32014; A32014.
KW Conjugation; plasmid; DNA-binding.
FT NON TER 1
SQ SEQUENCE 5 AA; 634 MW; 5E1B1AA43500000 CRC64;

Query Match 28.3%; Score 13; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NEE 4
Db |:
2 NDE 4

RESULT 3
PLP_BRANA STANDARD; PRT; 8 AA.
AC P81707;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Plastidial lipid-associated protein (Fragment).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE.
RC STRAIN=CV. TOPAZ; TISSUE=Tapetum;
RX MEDLINE=99349136; PubMed=10420651;
RA Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
Murphy D.J.;
RT "Composition and role of tapetal lipid bodies in the biogenesis of the
RT pollen coat of Brassica napus."
RL Planta 208:588-598(1999).
CC -!- FUNCTION: May play a structural role in the elaioplast, a tapetum-
CC specific plastidial lipid organelle.
CC -!- TISSUE SPECIFICITY: Tapetum of anthers.
FT NON TER 8
SQ SEQUENCE 8 AA; 989 MW; 9D7B1AA452CAA042 CRC64;

Query Match 28.3%; Score 13; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NEE 4
Db |:
5 NDE 7

RESULT 4
UF03_MOUSE STANDARD; PRT; 7 AA.
AC P38641;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P36) (Fragment).
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast; PubMed=7523108;
RX MEDLINE=95009907; Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis."
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.1, its MW is: 36 kDa.
FT NON TER 7
SQ SEQUENCE 7 AA; 842 MW; 6AA72B1DD81B1180 CRC64;

Query Match 26.1%; Score 12; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NEE 5
Db |:
1 HEEA 4

RESULT 5
UPA1_HUMAN STANDARD; PRT; 8 AA.
AC P30087;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing."
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 4.9, its MW is: 65 kDa.
DR SWISS-2DPAGE; P30087; HUMAN.
FT NON TER 1
FT UNSURE 8
FT NON TER 8
SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;

Query Match 26.1%; Score 12; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NEE 5
Db |:
1 DOES 4

RESULT 6
BRHP_CONIM STANDARD; PRT; 7 AA.
AC P58803;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bromoheptapeptide Im.
OS Conus imperialis (Imperial cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=35631;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=97184108; PubMed=9030520;
 RA Craig A.G., Jimenez E.C., Dykert J., Nielsen D.B., Gulyas J.,
 RA Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M.,
 RA McIntosh J.M.;
 RT "A novel post-translational modification involving bromination of
 RT tryptophan. Identification of the residue, L-6-bromotryptophan, in
 RT peptides from *Conus imperialis* and *Conus radiatus* venom.";
 RL J. Biol. Chem. 272:4689-4698(1997).
 CC -|- FUNCTION: Does not elicit gross behavioral symptoms when injected
 CC centrally or peripherally in mice.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -|- MASS SPECTROMETRY: MW=853.19; METHOD=LSIMS.
 DR PIR; A58512; A58512.
 KW Bromination; Amidation; Pyrrolidone carboxylic acid.
 FT DISULFID 2 7
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 6 6 BROMINATION.
 FT MOD_RES 7 7 AMIDATION.
 SQ SEQUENCE 7 AA; 795 MW; 6EA37DC6D87EA6B0 CRC64;
 Query Match 23.9%; Score 11; DB 1; Length 7;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CNE 3
 Db 2 CGQ 4
 RESULT 7
 FARI ASCSU
 ID FARI ASCSU STANDARD; PRT; 7 AA.
 AC P31889;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRamide-like neuropeptide AF1.
 OS Ascaris suum (pig roundworm) (*Ascaris lumbricoides*).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
 OC Ascarididae; Ascaris.
 OX NCBI_TaxID=6253;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90180465; PubMed=2627377;
 RA Cowden C., Stretton A.O.W., Davis R.E.;
 RT "AF1, a sequenced bioactive neuropeptide isolated from the nematode
 RT *Ascaris suum*.";
 RL Neuron 2:1465-1473(1989).
 CC -|- FUNCTION: Potent modulator of inhibitory motoneurons. Reduces the
 CC input resistance and blocks slow oscillatory potentials in these
 CC cells.
 CC -|- TISSUE SPECIFICITY: Found in the nerve cords and a variety of
 CC ganglia particularly in the anterior regions.
 CC -|- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
 CC family.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7 7
 FT MOD_RES 7 7 AMIDATION.
 SQ SEQUENCE 7 AA; 953 MW; 69D40059CB144350 CRC64;
 Query Match 23.9%; Score 11; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NE 3
 Db 2 NE 3

RESULT 8
 CADI_ENTFA
 ID CADI_ENTFA STANDARD; PRT; 8 AA.
 AC P13268;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CADI.
 OS Enterococcus faecalis (*Streptococcus faecalis*).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85051889; PubMed=6437872;
 RA Mori M., Sagakami Y., Narita M., Fujino M., Kitada C.,
 RA Craig R.A., Clewell D.B., Suzuki A.;
 RT "Isolation and structure of the bacterial sex pheromone, CADI, that
 RT induces plasmid transfer in *Streptococcus faecalis*.";
 RL FEBS Lett. 178:97-100(1984).
 CC -|- FUNCTION: CADI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC HEMOLYSIN PLASMID PAD1.
 KW Pheromone.
 SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;
 Query Match 23.9%; Score 11; DB 1; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 5 SLI 7
 Db 3 SLV 5
 RESULT 9
 ACT_CARMA
 ID ACT_CARMA STANDARD; PRT; 8 AA.
 AC P80709;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Actin (Fragment).
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RX Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
 RA Baghdasarian D.;
 RT "A transaldolase. An enzyme implicated in crab steroidogenesis.";
 RL Endocrine 5:23-32(1996).
 CC -|- FUNCTION: Actins are highly conserved proteins that are involved
 CC in various types of cell motility and are ubiquitously expressed
 CC in all eukaryotic cells.
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
 CC 6.8, ITS MW IS: 46 kDa.
 CC -|- SIMILARITY: Belongs to the actin family.
 DR InterPro; IPR004001; Actin.
 DR InterPro; IPR004000; Actin_like.
 DR PROSITE; PS00406; ACTINS_1; PARTIAL.
 DR PROSITE; PS00432; ACTINS_2; PARTIAL.
 DR PROSITE; PS01132; ACTINS_ACT LIKE; PARTIAL.
 KW Structural protein.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 976 MW; 1424005AB2CAAB3 CRC64;
 Query Match 21.7%; Score 10; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CN 2
Db 2 CD 3

RESULT 10
TMOF SARB
ID TMOF SARB
AC P41495; STANDARD; PRT; 6 AA.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Trypsin-modulating oostatic factor (TMOF).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Ovary;
RX MEDLINE=94211930; PubMed=8159807;
RA Bytemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
de Loof A.;
RT "Sequencing and characterization of trypsin modulating oostatic
factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria
bullata."
RL Regul. Pept. 50:61-72 (1994).
CC -!- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis
in the midgut which indirectly reduces the vitellogenin
concentration in the hemolymph resulting in inhibition of oocyte
development.
CC -!- DEVELOPMENTAL STAGE: Synthesized and released from follicular
epithelium after a blood meal.
KW Hormone.
SQ SEQUENCE 6 AA; 695 MW; 61E7451B7642000 CRC64;

Query Match 19.6%; Score 9; DB 1; Length 6;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NEESL 6
Db 1 NPTNL 5

RESULT 11
COW2 CONFU
ID COW2 CONFU STANDARD; PRT; 8 AA.
AC P58785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu-contryphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=41690;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC STRAIN=Clipperton Island; TISSUE=Venom;
RX MEDLINE=9938839; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
dynamics in the contryphan family."
RL J. Pept. Res. 54:93-99 (1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.

CC -!- SIMILARITY: Belongs to the contryphan family.
KW Toxin; Hydroxylation; D-amino acid.

FT DISULFID 2 8
FT MOD RES 4 4 D-LEUCINE.
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 19.6%; Score 9; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 2 C 2

RESULT 12

GLUR_HUMAN
ID GLUR_HUMAN STANDARD; PRT; 8 AA.

AC P02729;
DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Urine glycopeptide.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=72062338; PubMed=5126885;

RA Lote C.J., Weiss J.B.;

RT "Identification in urine of a low-molecular-weight highly polar
glycopeptide containing cysteinyl-galactose."

RL Biochem. J. 123:25P-25P (1971).

CC -!- FUNCTION: The identity of the glycoprotein from which this peptide
is derived is unknown. No physiological function has been
attributed. An erythrocyte membrane glycopeptide having a
similar structure has also been found.

DR PIR; A03188; XGHUHU.

DR GO; GO:0005576; C:extracellular; NAS.

KW Glycoprotein.

FT CARBOHYD 1 1 S-LINKED (GAL. . .).

SQ SEQUENCE 8 AA; 855 MW; C2D87AALF5B1B1E CRC64;

Query Match 19.6%; Score 9; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 1 C 1

RESULT 13

ACPH_RABIT

ID ACPH_RABIT STANDARD; PRT; 6 AA.

AC P35154;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (AARE) (Acyl-peptide
hydrolase) (APH) (Acylaminoacyl-peptidase) (Fragment).

GN APEH.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

NCBI_TaxID=9986;

RN [1]

RP SEQUENCE.

RC TISSUE=Muscle;

RX MEDLINE=92222120; PubMed=1807161;

RA Krishna R.G., Chin C.C.Q., Wolf F.;

RT "N-terminal sequence analysis of N alpha-acetylated proteins after

RT unblocking with N-acylaminoacyl-peptide hydrolase."
RL Anal. Biochem. 199;45:50(1991).
CC -!- FUNCTION: This enzyme catalyzes the hydrolysis of the N-terminal
CC peptide bond of an N-acetylated peptide to generate an N-
CC acetylated amino acid and a peptide with a free N-terminus. It
CC preferentially cleaves off Ac-Ala, Ac-Met and Ac-Ser.
CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H₂O = acylamino acid
CC + peptide.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to peptidase family S9C.
DR PIR: A49792; A49792.
DR MEROPS: S09.004; --.
DR InterPro: IPR002471; Pept S9 AS.
DR PROSITE: PS00708; PRO_ENDOPEP_SER; PARTIAL.
KW Hydrolase; Acetylation.
FT MOD_RES 1 ACETYLATION.
FT NON_TER 1 6
SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

Query Match 17.4%; Score 8; DB 1; Length 6;
Best Local Similarity 20.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 ERSLI 7
| : :
Db 2 ERQVL 6

RESULT 14
ASP2_LACSN
ID ASP2_LACSN STANDARD; PRT; 6 AA.
AC P82655;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acid shock protein 2 (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE
RC STRAIN=CBI;
RX MEDLINE=21322712; PubMed=11429463;
RA De Angelis M., Bini L., Pallini V., Cocconcelli P.S., Gobbetti M.;
RT "The acid-stress response in Lactobacillus sanfranciscensis CBI."
RL Microbiology 147:1863-1873(2001).
CC -!- INDUCTION: Overexpressed in acid environments.
FT NON_TER 6
SQ SEQUENCE 6 AA; 778 MW; 6AA45B5B132A8000 CRC64;

Query Match 17.4%; Score 8; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NE 3
| :
Db 5 ND 6

RESULT 15
CCFL_ENTFA
ID CCFL_ENTFA STANDARD; PRT; 7 AA.
AC P20104;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone cCF10.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]

RP SEQUENCE.
RX MEDLINE=89008313; PubMed=2139658;
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
RA Adait J.C., Dunny G.M., Suzuki A.;
RT "Structure of cCF10, a peptide sex pheromone which induces
RT conjugative transfer of the Streptococcus faecalis tetracycline
RT resistance plasmid, pCF10."
RL J. Biol. Chem. 263:14574-14578(1988).
CC -!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC HEMOLYSIN PLASMID PCF10.
DR PIR: A30812; A30812.
KW Pheromone.
SQ SEQUENCE 7 AA; 730 MW; 72C9D2C731B2C740 CRC64;

Query Match 17.4%; Score 8; DB 1; Length 7;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLI 7
| : :
Db 3 TLV 5

Search completed: March 8, 2004, 12:02:10
Job time : 11 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:59:40 ; Search time 38 Seconds
(without alignments)
66.425 Million cell updates/sec

Title: US-09-761-636A-6
Perfect score: 46
Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 488

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25.*

```
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	39.1	8	10 Q9SAY7	Q9SAY7 dioscorea t
2	16	34.8	7	12 Q67113	Q67113 influenza vi
3	16	34.8	7	13 Q42564	Q42564 fugu rubrip
4	14	30.4	8	Q81V87	Q81V87 homo sapien
5	13	28.3	7	11 Q55184	Q55184 rattus norv
6	13	28.3	8	Q32560	Q32560 escherichia
7	12	26.1	8	Q9ZEZ9	Q9ZEZ9 buchnera ap
8	12	26.1	8	Q9BYV5	Q9BYV5 homo sapien
9	12	26.1	8	Q15895	Q15895 homo sapien
10	12	26.1	8	Q15890	Q15890 homo sapien
11	12	26.1	8	Q9BF82	Q9BF82 ursus arcto
12	12	26.1	8	Q9BFC2	Q9BFC2 macropus eu
13	12	26.1	8	Q9BF90	Q9BF90 tragelaphus
14	12	26.1	8	Q9BFB1	Q9BFB1 echinops te
15	12	26.1	8	Q9BF93	Q9BF93 megaptera n
16	12	26.1	8	Q9BFA1	Q9BFA1 ateles fusc

17	12	26.1	8	6 Q9BF87	Q9BF87 tapirus ind
18	12	26.1	8	6 Q9BF89	Q9BF89 euphratus
19	12	26.1	8	6 Q9BF88	Q9BF88 chaetophrac
20	12	26.1	8	6 Q9BFA0	Q9BFA0 macaca mula
21	12	26.1	8	6 Q9BFA8	Q9BFA8 loxodonta a
22	12	26.1	8	6 Q9BFA9	Q9BFA9 procavia ca
23	12	26.1	8	6 Q9BFB2	Q9BFB2 sorex arane
24	12	26.1	8	6 Q9BFB5	Q9BFB5 erinaceus c
25	12	26.1	8	6 Q9BFB6	Q9BFB6 myrmecophag
26	12	26.1	8	6 Q9BFB3	Q9BFB3 condylura c
27	12	26.1	8	6 Q9BF88	Q9BF88 equus cabal
28	12	26.1	8	6 Q9BF95	Q9BF95 roussetus l
29	12	26.1	8	6 Q9BF99	Q9BF99 hylobates c
30	12	26.1	8	6 Q9BF84	Q9BF84 panthera on
31	12	26.1	8	6 Q9BFC3	Q9BFC3 didelphis m
32	12	26.1	8	6 Q9BFA4	Q9BFA4 tupaiia mino
33	12	26.1	8	6 Q9BFA2	Q9BFA2 tarsius ban
34	12	26.1	8	6 Q9BF85	Q9BF85 leopardus p
35	12	26.1	8	6 Q9BFC1	Q9BFC1 choleopus h
36	12	26.1	8	6 Q9BF89	Q9BF89 okapia john
37	12	26.1	8	6 Q9BF96	Q9BF96 pteropus gi
38	12	26.1	8	6 Q9BF90	Q9BF90 trichechus
39	12	26.1	8	6 Q9BF86	Q9BF86 felis silve
40	12	26.1	8	6 Q9BF92	Q9BF92 tursiops tr
41	12	26.1	8	6 Q9BF87	Q9BF87 tamandua te
42	12	26.1	8	6 Q9BF91	Q9BF91 hippopotamu
43	12	26.1	8	6 Q9BF84	Q9BF84 taipa alta
44	12	26.1	8	6 Q9BFC0	Q9BFC0 choleopus d
45	12	26.1	8	6 Q9BF98	Q9BF98 callimico g

ALIGNMENTS

RESULT 1
Q9SAY7 PRELIMINARY; PRT; 8 AA.

AC Q9SAY7; (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Phosphoglucose isomerase (Fragment).
OS Dioscorea tokoro.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Dioscoreales; Dioscoreaceae;
OC Dioscorea.
OX NCBI_TaxID=64475;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DT17-1;
RX MEDLINE=20279211; PubMed=10821191;
RA Terauchi R., Kahl G.;
RT "Rapid isolation of promoter sequences by TAIL-PCR: the 5'-flanking
RT regions of Pal and pgi genes from yams (Dioscorea).";
RL Mol. Gen. Genet. 263:554-560 (2000).
DR EMBL; AB016716; BAA32235.1; -;
DR GO; GO:0016853; F:isomerase activity; IEA.
KW Isomerase.
FT NON TER
SQ SEQUENCE 8 AA; 839 MW; F7B05731B5A1ADD6 CRC64;

Query Match 39.1%; Score 18; DB 10; Length 8;
Best local Similarity 75.0%; Pred. No. 1e+06; 0; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 1;

QY 5 SLIC 8
DB 5 TLIC 8

RESULT 2
Q67113 PRELIMINARY; PRT; 7 AA.
ID Q67113

Q67113;
 AC 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE 01-NOV-1996 (TREMBlrel. 22, Last annotation update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Influenza virus type A (Udorn/72) hemagglutinin (Seg 4) cDNA, 3' end
 DE (Fragment).
 OS Influenzavirus A.
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses.
 OX NCBI_TaxID=197911;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81001892; PubMed=7407922;
 RA Dhar R., Chanock R.M., Lai C.-J.;
 RT "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza
 RT viral mRNA deduced from cloned complete genomic sequences.";
 RL Cell 21:495-500(1980).
 DR EMBL; M25045; AAA43202.1; -.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;
 Query Match 34.8%; Score 16; DB 12; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 QY 1 CNEESLIC 8
 DB ||||
 3 CN----IC 6
 RESULT 3
 ID 042564 PRELIMINARY; PRT; 7 AA.
 AC 042564;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
 GN SCN8A.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97442476; PubMed=9295353;
 RA Plummer N.W., McBurney M.W., Meisler M.H.;
 RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
 RT two-domain protein in fetal brain and non-neuronal cells.";
 RL J. Biol. Chem. 272:24008-24015(1997).
 DR EMBL; U97673; AAB80916.1; -.
 DR GO; GO:0005216; F:ion channel activity; IEA.
 KW Ionic channel.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;
 Query Match 34.8%; Score 16; DB 13; Length 7;
 Best Local Similarity 56.7%; Pred. No. 1e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 6 LIC 8
 DB ||||
 3 LVC 5
 RESULT 4
 ID Q8IV87 PRELIMINARY; PRT; 8 AA.
 AC Q8IV87;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Dui07712.2 (Serine palmitoyltransferase, long chain base subunit
 DE 2-like (Aminotransferase 2), variant 1) (Fragment).
 GN SPTLC2L.
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smith M.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL050320; CAD54807.1; -.
 DR GO; GO:0016740; F:transferase activity; IEA.
 KW Transferase.
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 908 MW; 8E533682CEBEB042 CRC64;
 Query Match 30.4%; Score 14; DB 4; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 6 LIC 8
 DB ||||
 1 VIC 3
 RESULT 5
 ID 055184 PRELIMINARY; PRT; 7 AA.
 AC 055184;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Orphan receptor TR4-NS (Fragment).
 GN TR4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Sprague-Dawley;
 EX MEDLINE=96198747; PubMed=8612486;
 RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
 RA Detera-Wadleigh S.D.;
 RT "Splice variants of rat TR4 orphan receptor: differential expression
 RT of novel sequences in the 5'-untranslated region and C-terminal
 RT domain.";
 RL Endocrinology 137:1562-1571(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Sprague-Dawley;
 RX MEDLINE=96299786; PubMed=86611150;
 RA Yoshikawa T., DuPont B.R., Leach R.J., Detera-Wadleigh S.D.;
 RT "New variants of the human and rat nuclear hormone receptor, TR4:
 RT expression and chromosomal localization of the human gene.";
 RL Genomics 35:361-366(1996).
 DR EMBL; U59454; AAB91433.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 663 MW; 6DDA8787EB05350 CRC64;
 Query Match 28.3%; Score 13; DB 11; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 IC 8
 DB ||||
 2 IC 3

RESULT 6

O32560
ID O32560 PRELIMINARY; PRT; 8 AA.
AC O32560;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Propionate kinase (Fragment).
GN TDCO.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W3110;
RX MEDLINE=99449059; PubMed=10520749;
RA Hesselinger C., Savers G.;
RT "The tdc gene in Escherichia coli W3110 is separated from the rest of
RT the tdc operon by insertion of IS5 elements.";
RL DNA Seq. 9:183-188 (1998).
DR EMBL; AJ001620; CAA04875.1; --
DR GO; GO:0016301; F:kinase activity; IEA.
KW Kinase.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 1000 MW; 3A505EB044140DC4 CRC64;

Query Match 28.3%; Score 13; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 IC 8
Db 5 IC 6

RESULT 7

O9ZEZ9
ID O9ZEZ9 PRELIMINARY; PRT; 8 AA.
AC O9ZEZ9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 2-isopropylmalate synthase (RC 4.1.3.12) (Fragment).
GN LEUA.
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=9;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99028904; PubMed=9812361;
RA Silva F.J., Van Ham R.C.H.J., Sabater B., Latorre A.;
RT "Structure and evolution of the leucine plasmids carried by the
RT endosymbiont (Buchnera aphidicola) from aphids of the family
RT Aphididae.";
RL FEMS Microbiol. Lett. 168:43-49 (1998).
DR EMBL; AJ006874; CAA07290.1; --
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0003852; F:2-isopropylmalate synthase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
KW Lyase; Plasmid.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 917 MW; FE205042D6C5B446 CRC64;

Query Match 26.1%; Score 12; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NEESLI 7
Db 2 NSQVII 7

RESULT 8

O9BYV5
ID O9BYV5 PRELIMINARY; PRT; 8 AA.
AC O9BYV5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618 (2001).
DR EMBL; AV011664; AAG47575.1; --
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0003677; F:DNA binding; NAS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 1006 MW; DF02C331EBAB572A CRC64;

Query Match 26.1%; Score 12; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 LIC 8
Db 2 LYC 4

RESULT 9

O15895
ID O15895 PRELIMINARY; PRT; 8 AA.
AC O15895;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP6A10A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay B.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0 (1995).
DR EMBL; L32075; AAA73885.1; --
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 921 MW; C6C735B33686C1AA CRC64;

Query Match 26.1%; Score 12; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ESLI 7
Db 5 KSLV 8

```

RESULT 10
Q15890 ID Q15890 PRELIMINARY; PRT; 8 AA.
AC Q15890;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP19G12A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.,
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; I32083; AAA73880.1; -.
FT NON TER 1 1
FT NON TER 8 8
SQ SEQUENCE 8 AA; 975 MW; 605BA6CSBEA5A2D3 CRC64;

Query Match 26.1%; Score 12; DB 4; Length 8;
Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNE 3
DB 4 CSQ 6

RESULT 11
Q9BF82 ID Q9BF82 PRELIMINARY; PRT; 8 AA.
AC Q9BF82;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE cAMP responsive element moderator (Fragment).
GN CREM.
OS Ursus arctos (Brown bear) (Grizzly bear).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=9644;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011683; AAG47591.1; -.
FT NON TER 1 1
FT NON TER 8 8
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EEAB572A CRC64;

Query Match 26.1%; Score 12; DB 6; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 LIC 8
DB 2 LVC 4

RESULT 12
Q9BFC2 ID Q9BFC2 PRELIMINARY; PRT; 8 AA.
AC Q9BFC2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)

RESULT 13
Q9BF90 ID Q9BF90 PRELIMINARY; PRT; 8 AA.
AC Q9BF90;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE cAMP responsive element moderator (Fragment).
GN CREM.
OS Tragelaphus eurycerus (Bongo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Tragelaphus.
OX NCBI_TaxID=69297;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011673; AAG47583.1; -.
FT NON TER 1 1
FT NON TER 8 8
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EEAB572A CRC64;

Query Match 26.1%; Score 12; DB 6; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 LIC 8
DB 2 LVC 4

RESULT 14
Q9BFB1 ID Q9BFB1 PRELIMINARY; PRT; 8 AA.
AC Q9BFB1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE cAMP responsive element moderator (Fragment).
GN CREM.
OS Echinops telfairi (Lesser hedgehog tenrec).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Insectivora; Tenrecidae; Tenrecinae; Echinops.
 OX NCBI_TaxID=9371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21082082; PubMed=11214319;
 RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
 RA O'Brien S.J.,
 RT "Molecular phylogenetics and the origins of placental mammals."
 RL Nature 409:614-618(2001).
 DR EMBL; AY011632; AAG47547.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 978 MW; DF1DD331EEAB572A CRC64;

Query Match 26.1%; Score 12; DB 6; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 LIC 8
 Db 2 LYC 4

RESULT 15

Q9BF93
 ID Q9BF93 PRELIMINARY; PRT; 8 AA.
 AC Q9BF93;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CAMP responsive element moderator (Fragment).
 GN CREM.
 OS Megaptera novaeangliae (Humpback whale).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
 OC Balaeopteridae; Megaptera.
 OX NCBI_TaxID=9773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21082082; PubMed=11214319;
 RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
 RA O'Brien S.J.,
 RT "Molecular phylogenetics and the origins of placental mammals."
 RL Nature 409:614-618(2001).
 DR EMBL; AY011669; AAG47580.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 1025 MW; DF02C3240EAB572A CRC64;

Query Match 26.1%; Score 12; DB 6; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 LIC 8
 Db 2 LYC 4

Search completed: March 8, 2004, 12:03:02
 Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:55:59 ; Search time 52 Seconds
(without alignments)
43.469 Million cell updates/sec

Title: US-09-761-636A-6

Perfect score: 46

Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 122046

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003s:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	100.0	8	AAU04525	VEGF base
2	43	93.5	8	AAU04539	VEGF base
3	42	91.3	8	AAU04541	VEGF base
4	41	89.1	8	AAU04538	VEGF base
5	39	84.8	8	AAU04540	VEGF base
6	30	65.2	8	AAU04540	Conformat
7	30	65.2	8	AAU04526	Human CD4
8	26	56.5	8	AAU04526	Human TSH
9	26	56.5	8	AAU04526	Human TSH
10	26	56.5	8	AAU04526	Human TSH
11	26	56.5	8	AAU04526	Feline im
12	25	54.3	8	AAU04526	Peptide A
13	25	54.3	8	AAU04526	Protein p
14	25	54.3	8	AAU04526	Human TSH
15	25	54.3	8	AAU04526	Human TSH
16	24	52.2	8	AAU04526	Endostati
17	23	50.0	7	AAU04526	Peptide C
18	23	50.0	7	AAU04526	Beta-2-m1
19	23	50.0	8	AAU04526	Human TSH
20	23	50.0	8	AAU04526	Human TSH
21	23	50.0	8	AAU04526	RGD-bind
22	23	50.0	8	AAU04526	Membrane
23	23	50.0	8	AAU04526	Membrane
24	23	50.0	8	AAU04526	Membrane
25	23	50.0	8	AAU04526	Claudin-2
				AAU17353	Integrin-

26	23	50.0	8	AAE08176	Peptide #
27	23	50.0	8	AAE08175	Peptide #
28	23	50.0	8	ABG34995	Human pro
29	23	50.0	8	ABG34987	Human pro
30	23	50.0	8	AAU081097	Integrin-
31	23	50.0	8	ABG72952	Integrin-
32	22	47.8	6	AAU093979	Partial p
33	22	47.8	6	AAU093979	Partial p
34	22	47.8	6	AAU093979	Partial p
35	22	47.8	6	AAU093979	Partial p
36	22	47.8	6	AAU093979	Partial p
37	22	47.8	6	AAU093979	Partial p
38	22	47.8	6	AAU093979	Partial p
39	22	47.8	6	AAU093979	Partial p
40	22	47.8	6	AAU093979	Partial p
41	22	47.8	6	AAU093979	Partial p
42	21	45.7	5	AAU093979	Partial p
43	21	45.7	5	AAU093979	Partial p
44	21	45.7	5	AAU093979	Partial p
45	21	45.7	5	AAU093979	Partial p

ALIGNMENTS

RESULT 1
AAU04525
ID AAU04525 standard; peptide; 8 AA.
XX
AC AAU04525;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 2.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..8
FT /note="This bond cyclises the peptide"
XX
PN WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR WPI; 2001-442248/47.
XX
PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
XX residues.
XX
PS Claim 49; Page 32; 102pp; English.
XX
CC The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the exposed loop of human
CC VEGF (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and
CC cyclizing the peptide by oxidising the cysteine residues. The monocyclic
CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC peptides) and a cyclic peptide with at least one amino acid deleted prior
CC to cyclisation are used to interfere with angiogenesis,
CC neovascularisation or lymphangiogenesis in a mammal with a condition
CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC The condition is diabetic retinopathy, psoriasis, arthropathy,
CC hemangioma, vascularised malignant or benign tumour, post-recovery
CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC trauma, substance-induced neovascularisation of the liver, excessive
CC hormone-related angiogenic dysfunction, diabetes induced neovascular
CC sequelae, hypertension induced neovascular sequelae, or chronic liver
CC infection. The peptides are also used to modulate vascular permeability
CC in a mammal (the mammal has a condition characterised by fluid
CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC or brain. The peptides are used to image blood vessels and lymphatic
CC vasculature. The monomeric and bicyclic peptides are used to interfere
CC with at least one biological activity induced by VEGF, VEGF-C or -D and
CC are also used in combination with an anti-inflammatory agent, to treat a
CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC diabetic retinopathy
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 46; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db |||||
1 CNEESLIC 8

RESULT 2
AAU04539
ID AAU04539 standard; peptide; 8 AA.
XX
AC AAU04539;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 17.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1.8 /note= "This bond cyclises the peptide"
XX
FN W0200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stacker S, Cendron A;
XX
XX WPI; 2001-442248/47.
DR
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine

PT residues.
XX Example 25; Page 47; 102pp; English.
PS
XX The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the exposed loop of human
CC VEGFD (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a
CC peptide loop fragment from an exposed loop of a growth factor protein and
CC cyclizing the peptide by oxidising the cysteine residues. The monocyclic
CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC peptides) and a cyclic peptide with at least one amino acid deleted prior
CC to cyclisation are used to interfere with angiogenesis,
CC neovascularisation or lymphangiogenesis in a mammal with a condition
CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC The condition is diabetic retinopathy, psoriasis, arthropathy,
CC hemangioma, vascularised malignant or benign tumour, post-recovery
CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC trauma, substance-induced neovascularisation of the liver, excessive
CC hormone-related angiogenic dysfunction, diabetes induced neovascular
CC sequelae, hypertension induced neovascular sequelae, or chronic liver
CC infection. The peptides are also used to modulate vascular permeability
CC in a mammal (the mammal has a condition characterised by fluid
CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC or brain. The peptides are used to image blood vessels and lymphatic
CC vasculature. The monomeric and bicyclic peptides are used to interfere
CC with at least one biological activity induced by VEGF, VEGF-C or -D and
CC are also used in combination with an anti-inflammatory agent, to treat a
CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC diabetic retinopathy
XX
SQ Sequence 8 AA;

Query Match 93.5%; Score 43; DB 4; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.4e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db |||||
1 CNEESLIC 8

RESULT 3
AAU04541
ID AAU04541 standard; peptide; 8 AA.
XX
AC AAU04541;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 19.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1.8 /note= "This bond cyclises the peptide"
XX
FN W0200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX

PA (LUDW-) LUDWIG INST CANCER RES.
 XX Achen MG, Hughes RA, Stacker S, Cendron A;
 XX WPI; 2001-442248/47.
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX Example 25; Page 47; 102pp; English.
 PS The sequence represents a monomeric monocyclic peptide of the invention,
 XX whose 3-dimensional structure is modelled on the exposed loop of human
 CC VEGF (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphopathy.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 8 AA;
 Query Match 91.3%; Score 42; DB 4; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CNEESLIC 8
 |||||:
 Db 1 CNEESVVC 8
 RESULT 4
 AAU04538
 ID AAU04538 standard; peptide; 8 AA.
 XX
 AC AAU04538;
 XX
 XX 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 16.
 XX
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 1. 8
 FT /note= "This bond cyclises the peptide"
 FT
 XX

PN W0200152875-AL.
 XX 26-JUL-2001.
 XX 18-JAN-2001; 2001WO-US001533.
 XX 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA Achen MG, Hughes RA, Stacker S, Cendron A;
 XX WPI; 2001-442248/47.
 DR Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX Example 25; Page 47; 102pp; English.
 PS The sequence represents a monomeric monocyclic peptide of the invention,
 XX whose 3-dimensional structure is modelled on the exposed loop of human
 CC VEGF (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 8 AA;
 Query Match 89.1%; Score 41; DB 4; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CNEESLIC 8
 |||||:
 Db 1 CNEESLIC 8
 RESULT 5
 AAU04540
 ID AAU04540 standard; peptide; 8 AA.
 XX
 AC AAU04540;
 XX
 XX 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 18.
 XX
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;

KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 XX diabetic retinopathy; chronic inflammation; cyclic.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..8
 FT /note= "this bond cyclises the peptide"
 XX WO200152875-A1.
 PN 26-JUL-2001.
 PD 18-JAN-2001; 2001WO-US001533.
 XX 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA Achen MG, Hughes RA, Stackler S, Cendron A;
 XX WPI; 2001-442248/47.
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX Example 25; Page 47; 102pp; English.
 PS The sequence represents a monomeric monocyclic peptide of the invention,
 XX whose 3-dimensional structure is modelled on the exposed loop of human
 CC VEGF (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty stenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 8 AA;
 Query Match 84.8%; Score 39; DB 4; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CNEESLIC 8
 |||:|
 Db 1 CNEESLIC 8
 RESULT 6
 AAR24954
 ID AAR24954 standard; protein; 8 AA.

XX AAR24954;
 AC 25-MAR-2003 (revised)
 DT 04-DEC-1992 (first entry)
 XX Conformationally constrained HIV inhibitory peptide.
 DE Human immunodeficiency virus; AIDS; envelope glycoproteins; CD4;
 XX cell surface protein; infection.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH Disulfide-bond 1..8
 FT Region 1..2
 FT /note= "conformationally constraining gp."
 FT Peptide 3..6
 FT /note= "beta-turn or beta-turn mimic tetrapeptide"
 FT Region 7..8
 FT /note= "conformationally constraining gp."
 XX WO9209625-A1.
 PN 11-JUN-1992.
 XX 27-NOV-1991; 91WO-US008873.
 PF 29-NOV-1990; 90US-00619782.
 PR (SMIK) SMITHKLINE BEECHAM CORP.
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 PA Bhatnagar PK, Jarlais RLD, Dixon JS, Hendrickson WA, Kopple KD;
 XX Kwong P, Peltshoff CE, Ryu SE, Truneh A, Sweet RW;
 XX WPI; 1992-217018/26.
 XX Conformationally constrained peptides used for inhibiting HIV - by
 PT mimicking the stereochemical regions of the CD4 receptor protein.
 XX Example; Page 24; 37pp; English.
 PS The peptide is conformationally constrained by groups attached to each
 XX side. The peptide mimics a beta turn and can bind to at least one HIV
 CC envelope protein, thus inhibiting infection. It inhibits the interaction
 CC between HIV envelope glycoproteins and human cell-surface protein CD4 by
 CC mimicking structures of CD4. See also AAR24950-R24959 and AAR25122.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 8 AA;
 Query Match 65.2%; Score 30; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 CNEESLIC 8
 |||:|
 Db 1 CNEESLIC 8
 RESULT 7
 AAY54526
 ID AAY54526 standard; peptide; 8 AA.
 XX AC AAY54526;
 XX 25-APR-2000 (first entry)
 DT Human CD4 protein target antigenic peptide p1615.
 DE Human; CD4 protein; antigenic peptide; CDR2-like domain; apoptosis;
 XX syncytia formation; human immune deficiency virus; HIV binding;
 KW

KW CD4-Class II interaction; immunisation; CD4 surface complex;
 KW immune response; transplant rejection; autoimmune disease; cyclic;
 KW rheumatoid arthritis; systemic lupus erythematosus; psoriasis.
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 1..8
 FT /note= "this peptide is conformationally restricted by
 FT cyclisation"
 XX
 XX WO967294-A1.
 XX
 XX 29-DEC-1999.
 XX
 XX 21-JUN-1999; 99WO-US014030.
 XX
 XX 20-JUN-1998; 98US-00100409.
 XX
 XX (UNBI-) UNITED BIOMEDICAL INC.
 XX
 XX Wang CY;
 XX
 XX WPI; 2000-160579/14.
 XX
 XX New antigenic peptide from the CDR2 domain of CD4, for immunization
 PT against e.g. human immune deficiency virus.
 XX
 XX Disclosure; Page 63; 106pp; English.
 XX
 CC The present sequence represents a target antigenic peptide derived from
 CC the CDR2-like domain of the human CD4 protein. The peptide is cyclised by
 CC the addition of cysteine residues at either end. The specification
 CC describes antigenic peptides derived from the CDR2-like domain of CD4
 CC (amino acids 27-66 of AAV54500). These antigenic peptides present
 CC neutralising receptor/co-receptor effector sites of the CDR2-like domain.
 CC The peptides evoke effective antibody responses by having optimised site-
 CC specificity. The induced antibodies block human immune deficiency virus
 CC (HIV) binding and syncytia formation. They may also block CD4-Class II
 CC interactions with other cells, deliver signals to T cells (inhibiting
 CC normal CD4+-mediated immunoregulatory functions) or induce apoptosis of
 CC CD4 cells by simultaneous engagement of T cell receptors. Conjugates and
 CC peptides containing the antigenic peptides are used for active
 CC immunisation to generate antibodies against CD4 surface complexes,
 CC especially to prevent binding of HIV to CD4 and thus HIV infection, but
 CC also to treat undesirable immune responses such as transplant rejection,
 CC or autoimmune diseases (rheumatoid arthritis, systemic lupus
 CC erythematosus or psoriasis). These conjugates produce high-titre
 CC antibodies which are broadly neutralising against primary isolates from
 CC all classes of HIV-1 and of HIV-2. The peptides may include a promiscuous
 CC T helper epitope that is active in genetically diverse subjects
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 55.2%; Score 30; DB 3; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CNEESLIC 8
 DB 1 CNOQSFLC 8
 RESULT 8
 AAR73351
 ID AAR73351 standard; peptide; 8 AA.
 AC AAR73351;
 XX
 XX 12-DEC-1995 (first entry)
 DT Human TSH receptor (residues 301-308).
 DE

XX thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;
 KW affinity; detection.
 XX
 XX Synthetic.
 OS
 OS JP07089991-A.
 PN
 XX 04-APR-1995.
 PD
 XX 28-SEP-1993; 93JP-00240853.
 PF
 XX 28-SEP-1993; 93JP-00240853.
 PR
 XX (MTP) MITSUBISHI PETROCHEMICAL CO LTD.
 XX
 XX WPI; 1995-167251/22.
 DR
 XX Novel polypeptide(s) having affinity for the human TSH receptor antibody
 PT - used in detection of the TSH antibody.
 PT
 XX Example 1; Page 25; 54pp; Japanese.
 PS
 XX Peptides with affinity to human TSH (thyroid stimulating hormone)
 CC receptor antibody are used for detection of the antibody. (See also
 CC AAR73201-592)
 CC
 XX Sequence 8 AA;
 SQ
 Query Match 56.5%; Score 26; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CNEESL 6
 DB 1 CNESSM 6
 RESULT 9
 AAR73350
 ID AAR73350 standard; peptide; 8 AA.
 XX
 XX AAR73350;
 AC
 XX 12-DEC-1995 (first entry)
 DT Human TSH receptor (residues 291-298).
 DE
 XX thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;
 KW affinity; detection.
 KW
 XX Synthetic.
 OS
 OS JP07089991-A.
 PN
 XX 04-APR-1995.
 PD
 XX 28-SEP-1993; 93JP-00240853.
 PF
 XX 28-SEP-1993; 93JP-00240853.
 PR
 XX (MTP) MITSUBISHI PETROCHEMICAL CO LTD.
 XX
 XX WPI; 1995-167251/22.
 DR
 XX Novel polypeptide(s) having affinity for the human TSH receptor antibody
 PT - used in detection of the TSH antibody.
 PT
 XX Example 1; Page 25; 54pp; Japanese.
 PS
 XX Peptides with affinity to human TSH (thyroid stimulating hormone)
 CC receptor antibody are used for detection of the antibody. (See also
 CC AAR73201-592)
 CC

XX
SQ Sequence 8 AA;

Query Match 56.5%; Score 26; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CNEESL 6
|||:
Db 3 CNESSM 8

RESULT 10

AAV57040
ID AAV57040 standard; peptide; 8 AA.

XX
AC AAV57040;

XX
DT 21-FEB-2000 (first entry)

XX Feline immunodeficiency virus immunogenic fragment.

XX Feline immunodeficiency virus; FIV; infection; diagnosis; gp130; p55;
XX immunogenic fragment; antibody; env precursor; gag precursor; cat;
XX antibody binding composition.

XX Feline immunodeficiency virus.

XX
PN BP962774-A1.

XX
PD 08-DEC-1999.

XX
PF 14-MAY-1999; 99BP-00303760.

XX
PR 15-MAY-1998; 98US-0085615P.

XX
PR 03-JUN-1998; 98US-00089878.

XX (IDEX-) IDEX LAB INC.

XX Groat RG, Mermer B, O'Connor TP;

XX
WPI; 2000-025671/03.

XX Diagnosing Feline Immunodeficiency Virus infection.

XX Disclosure, Page 4; 15pp; English.

XX This sequence is an immunogenic fragment of feline immunodeficiency virus
(FIV) glycoprotein 130. Peptides AAV57038-757039 (also fragments of
gp130) are used in the invention as capture polypeptides when diagnosing
FIV infection. The invention relates to an antibody binding composition
which consists of an enhanced capture polypeptide, which contains an
immunogenic fragment of FIV gag precursor p55, and a second fragment
which is part of the env precursor gp130, and an antibody-binding
detection composition. The invention also includes a device for
performing an assay which determines whether a feline is infected with
FIV. The novel method is used for the diagnosis of Feline
Immunodeficiency Virus infection

XX Sequence 8 AA;

Query Match 56.5%; Score 26; DB 3; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 CNEESLIC 8
|||:
Db 1 CNQNPFC 8

RESULT 11

AAU08451
ID AAU08451 standard; peptide; 8 AA.

XX
AC AAU08451;

XX
DT 21-NOV-2001 (first entry)

XX Peptide A6 encoded by human VEGF-A forward primer A6-F.

XX Human; vascular endothelial growth factor; VEGF-A; vasculogenesis;
XX angiogenesis; blood vessel; cancer; proliferative retinopathy; psoriasis;
XX age-related macular degeneration; rheumatoid arthritis; cardiovascular;
XX primer; mutant; mutein.

XX Homo sapiens.

XX Synthetic.

XX
PN WO200162942-A2.

XX
PD 30-AUG-2001.

XX
PF 26-FEB-2001; 2001WO-US006113.

XX
PR 25-FEB-2000; 2000US-0185205P.

XX
PR 18-MAY-2000; 2000US-0205331P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (LICN) LICENTIA OY.

XX Alitalo K, Jeltsch MM;

XX
WPI; 2001-536640/59.

XX
N-PSDB; AAS12807.

XX Polypeptides that bind cellular receptors for vascular endothelial growth
factors, polynucleotides encoding them.

XX Claim 9; Fig 7C; 261pp; English.

XX The present invention relates to polypeptides that bind cellular
receptors for vascular endothelial growth factors (VEGFs), the
polynucleotides encoding them, and their use for identifying agents that
modulate interactions between VEGFs and their receptors. VEGFs and their
receptors play an important role in vasculogenesis, the development of
the embryonic vasculature from early differentiating endothelial cells
and angiogenesis, the process of forming new blood vessels from pre-
existing ones. Modulators of interactions between VEGF and its receptors
may be used to treat dysfunction of the endothelial cell regulatory
system. Such disorders include cancers, abnormal angiogenesis, rheumatoid
proliferative retinopathies, age-related macular degeneration, rheumatoid
arthritis and psoriasis. The polypeptides of the invention exhibit unique
receptor binding profiles compared to known naturally occurring VEGFs.
XX AAU08446-AAU08454 represent the peptides A1-A9 which are encoded by human
CC VEGF-A forward primers used in the methods of the present invention

XX Sequence 8 AA;

Query Match 56.5%; Score 26; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CNEESL 6
|||:
Db 3 CNEESL 8

RESULT 12

AAAR0365
ID AAAR0365 standard; peptide; 8 AA.

XX
AC AAAR0365;

XX
DT 19-APR-1996 (first entry)

XX Protein polymeric adhesion substrate glutamine donor peptide #15.

XX KW Pendent group; repeating unit; enzyme recognition site; sealant; fibrin;
 KW enzymatic cross-linking; biocompatible material; structural integrity;
 KW medical adhesive; wound closure; tissue repair; transglutaminase;
 KW protein polymer adhesive substrate.
 XX OS Synthetic.
 XX PN WO9523611-A1.
 XX PD 08-SEP-1995.
 XX PF 03-MAR-1995; 95WO-US002728.
 XX PR 03-MAR-1994; 94US-00205518.
 XX PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 XX PI Cappello J;
 XX DR WPI; 1995-320413/41.
 XX PT Protein polymers comprising repeating units and sequences - capable of
 PT enzyme-catalysed covalent bond formation useful as a biocompatible
 PT material for wound closure and tissue repair.
 XX PS Example 9; Page 75; 138pp; English.
 XX CC The peptides AAR0351-70 are examples of glutamine donor peptides which
 CC can be used to generate protein polymeric adhesion substrate (PPAS)
 CC contg. repeats of non-fibrin cross-linking donor peptide sequences (see
 CC AAR0345-50 for examples of PPAS proteins). The PPAS proteins can be used
 CC as substrates in enzymatic cross-linking reactions catalysed by a
 CC transglutaminase enzyme e.g. Factor VIII or XIII. The polymers can be
 CC used in biological systems where in situ formation of a biocompatible
 CC material with structural integrity is required e.g. as medical adhesives
 CC and sealants or for wound closure or tissue repair.
 XX SQ Sequence 8 AA;
 Query Match 54.3%; Score 25; DB 2; Length 8;
 Best Local Similarity 37.5%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CNEESLIC 8
 Db | : : ||
 1 CGQSKVIC 8
 RESULT 13
 AAW49750
 ID AAW49750 standard; peptide; 8 AA.
 XX AC AAW49750;
 XX XX 25-MAR-2003 (revised)
 DT 12-OCT-1998 (first entry)
 XX DE Glutamine donor peptide.
 XX KW Protein polymer; adhesive sealant; wound healing; cross-linking.
 XX OS Synthetic.
 XX PN US5773577-A.
 XX PD 30-JUN-1998.
 XX PF 02-MAR-1995; 95US-00397633.
 XX PR 03-MAR-1994; 94US-00205518.
 XX PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

XX PI Cappello J;
 XX DR WPI; 1998-387091/33.
 XX PT New recombinant protein polymers - containing naturally occurring
 PT repetitive units for crosslinking by enzymes, useful as medical adhesives
 PT and sealants, depots and matrices.
 XX PS Example 9; Col 49; 70pp; English.
 XX CC This is an example of a glutamine donor peptide that can be utilised in
 CC novel recombinant protein polymers of the invention. Such polymers (see
 CC AAW49710-28) typically comprise a repetitive amino acid backbone of
 CC repetitive units having a collagen, fibroin, elastin or keratin motif and
 CC at least 2 enzyme recognition sequences comprising a glutamine and/or
 CC lysine capable of enzyme catalysed isopeptide formation. The polymers are
 CC capable of covalent crosslinking by enzymatic reaction to form products
 CC which set quickly and have good adhesive properties and high strength.
 CC They can be used as medical adhesives and sealants, in the closure of
 CC wounds and repair of damaged tissues, prosthesis coatings, drug depots,
 CC and matrices for the transplantation of cells. (Updated on 25-MAR-2003 to
 CC correct PF field.)
 XX SQ Sequence 8 AA;
 Query Match 54.3%; Score 25; DB 2; Length 8;
 Best Local Similarity 37.5%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CNEESLIC 8
 Db | : : ||
 1 CGQSKVIC 8
 RESULT 14
 AAW48644
 ID AAW48644 standard; peptide; 8 AA.
 XX AC AAW48644;
 XX XX 20-MAR-2003 (revised)
 DT 10-DEC-1999 (first entry)
 XX DE Membrane dipeptidase-binding lung homing peptide #15.
 XX KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
 KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
 KW membrane dipeptidase.
 XX OS Synthetic.
 OS Homo sapiens.
 XX PN WO9946284-A2.
 XX PD 16-SEP-1999.
 XX PF 10-MAR-1999; 99WO-US005284.
 XX PR 13-MAR-1998; 98US-00042107.
 XX PR 26-FEB-1999; 99US-00258754.
 XX PA (BURN-) BURNHAM INST.
 XX PI Rajotte D, Pasqualini R, Ruoslahti EI;
 XX DR WPI; 1999-571717/48.
 XX PT New peptides which selectively home to organs or tissues, used for, e.g.
 PT identifying target ligands and for therapy of pathological conditions.
 XX PS Example 6; Page 144; 193pp; English.
 XX XX

CC The present invention describes peptides that selectively home to a
 CC tissue or organ. The peptides can be used for identifying an organ or
 CC tissue, for identifying a target molecule expressed by an organ or tissue
 CC or for treating an organ or tissue pathology, where the organ or tissue
 CC is selected from prostate, lung, skin, retina, pancreas, gut, ovary,
 CC adrenal gland, liver, and lymph node. The peptide bind to the membrane
 CC dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are
 CC used in the exemplification of the present invention. (Updated on 20-MAR-
 CC 2003 to correct PR field.)
 XX
 SQ Sequence 8 AA;

Query Match 54.3%; Score 25; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
 | | | |
 Db 1 CGNETLRC 8

RESULT 15
 ABG35021
 ID ABG35021 standard; peptide; 8 AA.

AC ABG35021;

XX 15-JUL-2002 (first entry)
 DT Endostatin targeting peptide #20.

XX Targeting peptide; cancer; Hodgkin's disease; cytostatic;
 KW immunosuppressive; anti-inflammatory; antiarthritic; antiviral;
 KW antiatherosclerotic; antidiabetic; antibacterial; diabetes mellitus;
 KW inflammatory disease; arthritis; atherosclerosis; cancer;
 KW autoimmune disease; bacterial infection; viral infection.

XX Unidentified.

XX WO200220722-A2.

XX 14-MAR-2002.

XX 07-SEP-2001; 2001WO-US027702.

XX 08-SEP-2000; 2000US-0231266P.

XX 17-JAN-2001; 2001US-00765101.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Arap W, Pasqualini R;

XX WPI; 2002-383050/41.

XX Identifying targeting peptides useful for treating e.g. diabetes
 PT mellitus, inflammatory diseases, cancer, or autoimmune diseases,
 PT comprises exposing a sample to a phage display library and recovering
 PT phage bound to the sample.

XX Claim 56; Page 242; 298pp; English.

XX This invention relates to a novel method for identifying disease
 CC targeting peptides. The method comprises exposing a sample from an organ,
 CC tissue or cell type of interest, to a phage display library and
 CC recovering phage bound to the sample (the phage expresses targeting
 CC peptides). The peptides identified by the method of the invention may
 CC have cytostatic, immunosuppressive, anti-inflammatory, antiarthritic,
 CC antiatherosclerotic, antidiabetic, antibacterial and antiviral
 CC activities. The methods and composition are useful for identifying
 CC targeting peptides and one or more receptors for a targeting peptide. The
 CC targeting peptides are used for selective delivery of therapeutic agents,
 CC including gene therapy vectors and fusion proteins, to specific organs,
 CC tissues, or cell types in subject. The targeting peptide may also be used

CC for treating diseases such as diabetes mellitus, inflammatory diseases,
 CC arthritis, atherosclerosis, cancer, autoimmune diseases, bacterial and
 CC viral infections and Hodgkin's disease. The present sequence represents a
 CC targeting peptide of the invention
 XX
 SQ Sequence 8 AA;

Query Match 54.3%; Score 25; DB 5; Length 8;
 Best Local Similarity 37.5%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
 | | | |
 Db 1 CSRSSFLC 8

Search completed: March 8, 2004, 12:01:47
 Job time : 53 secs

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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:03:05 ; Search time 33 Seconds
(without alignments)
51.189 Million cell updates/sec

Title: US-09-761-636A-6

Perfect score: 46

Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 52204

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	100.0	8	9 US-09-761-636A-6	Sequence 6, Appl
2	43	93.5	8	9 US-09-761-636A-20	Sequence 20, Appl
3	42	91.3	8	9 US-09-761-636A-22	Sequence 22, Appl
4	41	89.1	8	9 US-09-761-636A-19	Sequence 19, Appl
5	39	84.8	8	9 US-09-761-636A-21	Sequence 21, Appl
6	26	56.5	8	9 US-09-795-006A-133	Sequence 133, App
7	24	52.2	8	9 US-09-795-006A-142	Sequence 142, App
8	23	50.0	7	10 US-09-827-345-14	Sequence 14, Appl
9	23	50.0	8	9 US-09-840-277-25	Sequence 25, Appl
10	23	50.0	8	9 US-09-185-908-115	Sequence 115, App
11	22	47.8	6	14 US-10-006-869-3664	Sequence 3664, Ap
12	22	47.8	6	15 US-10-395-032-3665	Sequence 3665, Ap
13	22	47.8	7	14 US-10-006-869-983	Sequence 983, Appl
14	22	47.8	7	14 US-10-190-082-92	Sequence 92, Appl
15	22	47.8	7	15 US-10-395-032-3665	Sequence 3665, Ap

16	22	47.8	8	14 US-10-006-869-1071	Sequence 1071, Ap
17	22	47.8	8	14 US-10-006-869-3624	Sequence 3624, Ap
18	22	47.8	8	15 US-10-395-032-1071	Sequence 1071, Ap
19	22	47.8	8	15 US-10-395-032-3624	Sequence 3624, Ap
20	21	45.7	5	14 US-10-006-869-3663	Sequence 3663, Ap
21	21	45.7	5	15 US-10-395-032-3663	Sequence 3663, Ap
22	21	45.7	6	14 US-10-006-869-985	Sequence 985, App
23	21	45.7	6	14 US-10-006-869-2242	Sequence 2242, Ap
24	21	45.7	6	15 US-10-395-032-985	Sequence 985, App
25	21	45.7	6	15 US-10-395-032-2242	Sequence 2242, Ap
26	21	45.7	7	14 US-10-006-869-989	Sequence 989, App
27	21	45.7	7	14 US-10-006-869-2246	Sequence 2246, Ap
28	21	45.7	7	15 US-10-395-032-989	Sequence 989, App
29	21	45.7	7	15 US-10-395-032-2246	Sequence 2246, Ap
30	21	45.7	8	9 US-09-185-908-221	Sequence 221, App
31	21	45.7	8	13 US-10-012-756-36	Sequence 36, Appl
32	21	45.7	8	14 US-10-094-401-175	Sequence 175, App
33	21	45.7	8	14 US-10-140-164-9	Sequence 9, Appl
34	21	45.7	8	14 US-10-140-164-39	Sequence 39, Appl
35	21	45.7	8	14 US-10-006-869-2160	Sequence 2160, Ap
36	21	45.7	8	14 US-10-006-869-3609	Sequence 3609, Ap
37	21	45.7	8	14 US-10-073-333A-9	Sequence 9, Appl
38	21	45.7	8	14 US-10-022-066-438	Sequence 438, App
39	21	45.7	8	15 US-10-395-032-2160	Sequence 2160, Ap
40	21	45.7	8	15 US-10-395-032-3609	Sequence 3609, Ap
41	21	45.7	8	15 US-10-369-226-13	Sequence 13, Appl
42	21	45.7	8	15 US-10-369-226-24	Sequence 24, Appl
43	21	45.7	8	15 US-10-462-262-143	Sequence 143, App
44	20	43.5	5	14 US-10-006-869-983	Sequence 983, App
45	20	43.5	5	14 US-10-006-869-2240	Sequence 2240, Ap

ALIGNMENTS

RESULT 1

US-09-761-636A-6
; Sequence 6, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761.636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-6

Query Match 100.0%; Score 46; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.2e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 1 CNEESLIC 8

RESULT 2

US-09-761-636A-20
; Sequence 20, Application US/09761636A
; Patent No. US20020065218A1

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; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
; US-09-761-636A-20

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Query Match          93.5%; Score 43; DB 9; Length 8;
Best Local Similarity 87.5%; Pred. No. 7.2e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 CNEESLIC 8
Db 1 CNEETLIC 8

```

```

RESULT 3
US-09-761-636A-22
; Sequence 22, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
; US-09-761-636A-22

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```

Query Match          91.3%; Score 42; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 7.2e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

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QY 1 CNEESLIC 8
Db 1 CNEESVVC 8

```

```

RESULT 4
US-09-761-636A-19
; Sequence 19, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela

```

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; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
; US-09-761-636A-19

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```

Query Match          89.1%; Score 41; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 7.2e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 CNEESLIC 8
Db 1 CNEESLIC 8

```

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RESULT 5
US-09-761-636A-21
; Sequence 21, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
; US-09-761-636A-21

```

```

Query Match          84.8%; Score 39; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 7.2e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CNEESLIC 8
Db 1 CNEESFIC 8

```

```

RESULT 6
US-09-795-006A-133
; Sequence 133, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205

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; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 133
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-795-006A-133

Query Match          56.5%; Score 26; DB 9; Length 8;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CNEESL 6
DB      3 CNDGL 8

RESULT 7
US-09-795-006A-142
; Sequence 142, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Allitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 142
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-795-006A-142

Query Match          52.2%; Score 24; DB 9; Length 8;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CNEESL 6
DB      3 CNDGL 8

RESULT 8
US-09-827-345-14
; Sequence 14, Application US/09827345
; Publication No. US20030021800A1
; GENERAL INFORMATION:
; APPLICANT: CHERMANN, JEAN-CLAUDE
; APPLICANT: LE CORTEL, CAROLE
; APPLICANT: GALEA, PASCALE
; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING AN
; TITLE OF INVENTION: INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND
; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF
; TITLE OF INVENTION: DIAGNOSIS
; FILE REFERENCE: 065691-0216
; CURRENT APPLICATION NUMBER: US/09/827,345
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/599,549
; PRIOR FILING DATE: 2000-06-23
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; PRIOR APPLICATION NUMBER: PCT/FR96/01006
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 08/973,551
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: FR 95/07914
; PRIOR FILING DATE: 1995-06-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-827-345-14

Query Match          50.0%; Score 23; DB 10; Length 7;
Best Local Similarity 80.0%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CNEESL 5
DB      2 CNPES 6

RESULT 9
US-09-840-277-25
; Sequence 25, Application US/09840277
; Patent No. US20020168363A1
; GENERAL INFORMATION:
; APPLICANT: FEIGS, ULRICH
; APPLICANT: KOHNO, TADAHIKO
; APPLICANT: LACEY, DAVID LEE
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
; FILE REFERENCE: A-688A
; CURRENT APPLICATION NUMBER: US/09/840,277
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/198,919
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 60/201,394
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Integrin antagonist peptide
US-09-840-277-25

Query Match          50.0%; Score 23; DB 9; Length 8;
Best Local Similarity 37.5%; Pred. No. 7.2e+05;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 CNEESLIC 8
DB      1 CWDGLMC 8

RESULT 10
US-09-185-908-115
; Sequence 115, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; TITLE OF INVENTION: FUNCTIONS
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
```

; CURRENT FILING DATE: 1998-11-03
 ; NUMBER OF SEQ ID NOS: 269
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 115
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Product of
 ; OTHER INFORMATION: synthesis based on mouse claudin-2 sequence
 ; FEATURE:
 ; OTHER INFORMATION: Cyclic Peptide
 ;
 US-09-185-908-115

Query Match 50.0%; Score 23; DB 9; Length 8;
 Best Local Similarity 37.5%; Pred. No. 7.2e+05;
 Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CNEESLIC 8
 Db 1 CRTSSVC 8

RESULT 11

US-10-006-869-3664
 ; Sequence 3664, Application US/10006869
 ; Publication No. US20030082166A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Blaschuk, Orest W.
 ; APPLICANT: Symonds, James Matthew
 ; APPLICANT: Gour, Barbara J.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 ; FILE REFERENCE: 100086.407C7
 ; CURRENT FILING DATE: 2001-12-03
 ; NUMBER OF SEQ ID NOS: 4052
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3664
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Representative cyclic modulating agent based on
 ; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
 ; OTHER INFORMATION: recognition sequence
 ;
 US-10-006-869-3664

Query Match 47.8%; Score 22; DB 14; Length 6;
 Best Local Similarity 60.0%; Pred. No. 7.2e+05;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNEES 5
 Db 1 CNEKT 5

RESULT 12

US-10-395-032-3664
 ; Sequence 3664, Application US/10395032
 ; Publication No. US20030229199A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Blaschuk, Orest W.
 ; APPLICANT: Symonds, James Matthew
 ; APPLICANT: Gour, Barbara J.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 ; FILE REFERENCE: 100086.407C9
 ; CURRENT FILING DATE: 2003-03-21
 ; NUMBER OF SEQ ID NOS: 4052
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3664

; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Representative cyclic modulating agent based on
 ; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
 ; OTHER INFORMATION: recognition sequence
 ;
 US-10-395-032-3664

Query Match 47.8%; Score 22; DB 15; Length 6;
 Best Local Similarity 60.0%; Pred. No. 7.2e+05;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNEES 5
 Db 1 CNEKT 5

RESULT 13

US-10-006-869-3665
 ; Sequence 3665, Application US/10006869
 ; Publication No. US20030082166A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Blaschuk, Orest W.
 ; APPLICANT: Symonds, James Matthew
 ; APPLICANT: Gour, Barbara J.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 ; FILE REFERENCE: 100086.407C7
 ; CURRENT FILING DATE: 2001-12-03
 ; NUMBER OF SEQ ID NOS: 4052
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3665
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Representative cyclic modulating agent based on
 ; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
 ; OTHER INFORMATION: recognition sequence
 ;
 US-10-006-869-3665

Query Match 47.8%; Score 22; DB 14; Length 7;
 Best Local Similarity 60.0%; Pred. No. 7.2e+05;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNEES 5
 Db 1 CNEKT 5

RESULT 14

US-10-190-082-92
 ; Sequence 92, Application US/10190082
 ; Publication No. US20030148264A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lasky, Lawrence A.
 ; APPLICANT: Sidhu, Sachdev S.
 ; APPLICANT: Held, Heike A.
 ; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS
 ; FILE REFERENCE: P1905R1
 ; CURRENT FILING DATE: 2002-07-03
 ; PRIOR APPLICATION NUMBER: US 60/303,634
 ; PRIOR FILING DATE: 2001-07-06
 ; NUMBER OF SEQ ID NOS: 683
 ; SEQ ID NO 92
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic

US-10-190-082-92

Query Match 47.8%; Score 22; DB 14; Length 7;
 Best Local Similarity 57.1%; Pred. No. 7.2e+05;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CNEESLI 7
 ||||:
 DB 1 CNIESWV 7

RESULT 15

US-10-395-032-3665
 ; Sequence 3665, Application US/10395032
 ; Publication No. US20030229199A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Blaschuk, Orest W.
 ; APPLICANT: Symonds, James Matthew
 ; APPLICANT: Gour, Barbara J.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 ; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
 ; FILE REFERENCE: 100086.407C9
 ; CURRENT APPLICATION NUMBER: US/10/395,032
 ; CURRENT FILING DATE: 2003-03-21
 ; NUMBER OF SEQ ID NOS: 4052
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3665
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Representative cyclic modulating agent based on
 ; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
 ; OTHER INFORMATION: recognition sequence
 US-10-395-032-3665

Query Match 47.8%; Score 22; DB 15; Length 7;
 Best Local Similarity 60.0%; Pred. No. 7.2e+05;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEES 5
 ||||:
 DB 1 CNEKT 5

Search completed: March 8, 2004, 12:08:20
 Job time : 33 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:16:07 ; Search time 15.5 Seconds
(without alignments)
29.976 Million cell updates/sec

Title: US-09-761-636A-14
Perfect score: 52
Sequence: 1 C1SVPLVPC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 89883

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/prodata/2/iaa/5A_COMB.pcp.*
- 2: /cgn2_6/prodata/2/iaa/5B_COMB.pcp.*
- 3: /cgn2_6/prodata/2/iaa/6A_COMB.pcp.*
- 4: /cgn2_6/prodata/2/iaa/6B_COMB.pcp.*
- 5: /cgn2_6/prodata/2/iaa/PCTUS_COMB.pcp.*
- 6: /cgn2_6/prodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	51.9	9	4	US-09-535-852-1681
2	26	50.0	9	4	US-09-187-859-2726
3	26	50.0	9	4	US-09-839-542B-2726
4	24	46.2	7	1	US-08-261-206A-18
5	23	44.2	8	1	US-08-189-331-147
6	23	44.2	8	1	US-08-189-331-148
7	23	44.2	8	1	US-08-189-331-149
8	23	44.2	8	1	US-08-189-331-150
9	23	44.2	8	1	US-08-633-760-9
10	23	44.2	8	2	US-08-471-068-147
11	23	44.2	8	2	US-08-471-068-148
12	23	44.2	8	2	US-08-471-068-149
13	23	44.2	8	2	US-08-471-068-150
14	23	44.2	9	3	US-08-891-271-4
15	23	44.2	9	3	US-09-258-754-373
16	23	44.2	9	3	US-09-042-107-373
17	23	44.2	9	4	US-09-987-579-19
18	23	44.2	9	4	US-09-722-250D-373
19	22	42.3	4	3	US-09-357-952-69
20	22	42.3	4	4	US-09-521-650-69
21	22	42.3	4	4	US-09-168-888-69
22	22	42.3	5	3	US-09-357-952-68
23	22	42.3	5	3	US-09-357-952-116
24	22	42.3	5	4	US-09-521-650-68
25	22	42.3	5	4	US-09-521-650-116
26	22	42.3	5	4	US-09-168-888-68
27	22	42.3	5	4	US-09-168-888-116

28 22 42.3 6 3 US-09-357-952-67 Sequence 67, Appl
29 22 42.3 6 3 US-09-357-952-115 Sequence 115, App
30 22 42.3 6 4 US-09-521-650-67 Sequence 67, Appl
31 22 42.3 6 4 US-09-521-650-115 Sequence 115, App
32 22 42.3 6 4 US-09-168-888-67 Sequence 67, Appl
33 22 42.3 6 4 US-09-168-888-115 Sequence 115, App
34 22 42.3 7 1 US-08-261-206A-22 Sequence 22, Appl
35 22 42.3 7 3 US-09-357-952-114 Sequence 114, App
36 22 42.3 7 4 US-09-521-650-114 Sequence 114, App
37 22 42.3 7 4 US-09-168-888-114 Sequence 114, App
38 22 42.3 7 4 US-09-428-082B-302 Sequence 302, App
39 22 42.3 8 3 US-09-357-952-113 Sequence 113, App
40 22 42.3 8 4 US-09-521-650-113 Sequence 113, App
41 22 42.3 8 4 US-09-168-888-113 Sequence 113, App
42 22 42.3 9 2 US-08-456-670B-26 Sequence 26, Appl
43 22 42.3 9 3 US-09-258-754-249 Sequence 249, App
44 22 42.3 9 3 US-08-660-092-123 Sequence 123, App
45 22 42.3 9 3 US-08-660-092-126 Sequence 126, App

ALIGNMENTS

RESULT 1
US-09-535-852-1681
; Sequence 1681, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1681
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmocollin-2 cell adhesion recognition sequence
US-09-535-852-1681

Query Match 51.9%; Score 27; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 C1SVPLVPC 9
||: ||
Db 1 C1AFATTPC 9

RESULT 2
US-09-187-859-2726
; Sequence 2726, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 2726
; LENGTH: 9
; TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-09-187-859-2726

Query Match          50.0%; Score 26; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTSVPLVPC 9
   | : | | |
Db 1 CFALDLVTC 9

RESULT 3
US-09-839-542B-2726
; Sequence 2726, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2726
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-09-839-542B-2726

Query Match          50.0%; Score 26; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTSVPLVPC 9
   | : | | |
Db 1 CFALDLVTC 9

RESULT 4
US-08-261-206A-18
; Sequence 18, Application US/08261206A
; Patent No. 5574007
; GENERAL INFORMATION:
; APPLICANT: Zushi, Mitichitaka
; APPLICANT: Gomi, Komakazu
; APPLICANT: Yamamoto, Shuji
; APPLICANT: Suzuki, Koji
; APPLICANT: Matsuda, Akio
; TITLE OF INVENTION: A Polypeptide Capable of Interacting
; TITLE OF INVENTION: with Thrombin
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,206A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/740,492
; FILING DATE: 03-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 216-275P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-261-206A-18

Query Match          46.2%; Score 24; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLVPC 9
   | : | |
Db 2 PVAPC 6

RESULT 5
US-08-189-331-147
; Sequence 147, Application US/08189331
; Patent No. 5747334
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; APPLICANT: Fomkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,331
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 147:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-189-331-147
```

Query Match 44.2%; Score 23; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CUSVP 5
|:|
Db 4 CVSAP 8

RESULT 6
US-08-189-331-148
; Sequence 148, Application US/08189331
; Patent No. 5747334
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,331
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-155
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-189-331-148

Query Match 44.2%; Score 23; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CUSVP 5
|:|
Db 3 CVSAP 7

RESULT 7
US-08-189-331-149
; Sequence 149, Application US/08189331
; Patent No. 5747334
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,331
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-155
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 149:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-189-331-149

Query Match 44.2%; Score 23; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CUSVP 5
|:|
Db 2 CVSAP 6

RESULT 8
US-08-189-331-150
; Sequence 150, Application US/08189331
; Patent No. 5747334
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,331
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-155
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-189-331-150

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-189-331-150

Query Match 44.2%; Score 23; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CUSVP 5
|:|
Db 1 CVSAP 5

RESULT 9

US-08-633-760-9
; Sequence 9, Application US/08633760
; Patent No. 5804429

GENERAL INFORMATION:

APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: FUJIMURA, TAKAO
APPLICANT: ISHII, YOSHINORI
APPLICANT: NOGUCHI, YUJI
TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,760
FILING DATE: 01-MAY-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-929-0 PCT
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-633-760-9

Query Match 44.2%; Score 23; DB 1; Length 8;
Best Local Similarity 42.9%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CUSVPLV 7
|:|:|:|
Db 2 CAAVPLV 8

RESULT 10

US-08-471-068-147
; Sequence 147, Application US/08471068
; Patent No. 5948635
; GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,068
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/189,331
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-155
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 147:

SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-068-147

Query Match 44.2%; Score 23; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CUSVP 5
|:|
Db 4 CVSAP 8

RESULT 11

US-08-471-068-148
; Sequence 148, Application US/08471068
; Patent No. 5948635
; GENERAL INFORMATION:

APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/471,068
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION NUMBER: 08/189,331
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mistrock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-155
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212 790-9090
;; TELEFAX: 212 869-8864/9741
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 148:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-08-471-068-148

Query Match 44.2%; Score 23; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 3e+05; 1; Indels 0;
Matches 3; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 CISVP 5
|:|
Db 3 CVSAP 7

RESULT 12
US-08-471-068-149
; Sequence 149, Application US/08471068
; Patent No. 5948635
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,068
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 08/189,331
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 149:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids

;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-08-471-068-149

Query Match 44.2%; Score 23; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 3e+05; 1; Indels 0;
Matches 3; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 CISVP 5
|:|
Db 2 CVSAP 6

RESULT 13
US-08-471-068-150
; Sequence 150, Application US/08471068
; Patent No. 5948635
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,068
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 08/189,331
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-068-150

Query Match 44.2%; Score 23; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 3e+05; 1; Indels 0;
Matches 3; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 CISVP 5
|:|
Db 1 CVSAP 5

RESULT 14
US-08-891-271-4
; Sequence 4, Application US/08891271
; Patent No. 6165476

GENERAL INFORMATION:
APPLICANT: Strom, Terry B.
APPLICANT: Sytkowski, Arthur J.
APPLICANT: Zheng, Xin Xiao
TITLE OF INVENTION: Fusion Proteins with an Immunoglobulin
TITLE OF INVENTION: Hing Region Linker
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,271
FILING DATE: 10-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hogle, Doreen M.
REGISTRATION NUMBER: 36,361
REFERENCE/DOCKET NUMBER: BIH97-07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-891-271-4

Query Match 44.2%; Score 23; DB 3; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 C1SVPLVPC 9
| : | | |
Db 2 CVECP--PC 8

RESULT 15
US-09-258-754-373
Sequence 373, Application US/09258754
Patent No. 6174687
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Pasqualini, Renata
APPLICANT: Rajotte, Daniel
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
FILE REFERENCE: P-LJ 3443
CURRENT APPLICATION NUMBER: US/09/258,754
CURRENT FILING DATE: 1999-02-26
EARLIER APPLICATION NUMBER: 09/042,107
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 452
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 373
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-373

Query Match 44.2%; Score 23; DB 3; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLVPC 9
| : | | |
Db 4 PLVAC 8

Search completed: March 8, 2004, 12:21:09
Job time : 16.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:52:24 ; Search time 20 seconds
(without alignments)
62.524 Million cell updates/sec

Title: US-09-761-636A-5

Perfect score: 72

Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1827

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33.5	46.5	12	2	PT0216
2	30	41.7	12	2	S47394
3	29.5	41.0	13	2	S47357
4	29	40.3	12	2	S26549
5	28	38.9	12	2	PH1463
6	28	38.9	12	2	PH1466
7	28	38.9	13	2	S47400
8	27	37.5	11	2	PT0217
9	27	37.5	12	2	S47391
10	27	37.5	13	2	S47383
11	26	36.1	11	2	S57575
12	26	36.1	12	2	S47395
13	26	36.1	13	2	S47381
14	25.5	35.4	13	2	S47382
15	25	34.7	10	2	S23371
16	25	34.7	11	2	PH0947
17	25	34.7	12	2	PH1469
18	25	34.7	12	2	PH0931
19	24.5	34.0	12	2	PH1457
20	24	33.3	11	2	PH1583
21	24	33.3	12	2	S26552
22	24	33.3	12	2	S26559
23	24	33.3	12	2	S26554
24	24	33.3	12	2	S47363
25	24	33.3	12	2	PH1467
26	24	33.3	12	2	PH1468
27	24	33.3	13	2	S47390
28	23.5	32.6	12	2	PH1459
29	23.5	32.6	13	2	S47377

30 23 31.9 12 2 S26557 T-cell receptor be
31 23 31.9 12 2 S26556 T-cell receptor be
32 23 31.9 12 2 S26553 T-cell receptor be
33 23 31.9 12 2 PH1452 T-cell receptor be
34 23 31.9 12 2 PH1470 T-cell receptor be
35 23 31.9 12 2 PH1464 T-cell receptor be
36 23 31.9 13 2 A23695 myosin heavy chain
37 22.5 31.2 12 2 S26541 T-cell receptor be
38 22.5 31.2 12 2 PH1458 T-cell receptor be
39 22.5 31.2 13 2 S47356 T-cell antigen rec
40 22.5 31.2 13 2 S47378 T-cell antigen rec
41 22.5 31.2 13 2 S47385 T-cell antigen rec
42 22 30.6 10 2 PH0927 T-cell receptor be
43 22 30.6 12 2 S26546 T-cell receptor be
44 22 30.6 12 2 S26547 T-cell receptor be
45 22 30.6 12 2 S26555 T-cell receptor be

ALIGNMENTS

RESULT 1

PT0216

T-cell receptor beta chain V-J region (4-1-G.4) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C:Accession: PT0216

R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restr

A:Reference number: PT0209; MUID:91217621; PMID:1902501

A:Accession: PT0216

A:Molecule type: mRNA

A:Residues: 1-12 <NAK>

C:Keywords: T-cell receptor

Query Match 46.5%; Score 33.5; DB 2; Length 12;

Best Local Similarity 72.7%; Pred. No. 12;

Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 CASELGKSTNT 11

Db 1 CASSLG-TTNT 10

RESULT 2

S47394

T-cell antigen receptor VJ junction beta chain - human

C:Species: Homo sapiens (man)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C:Accession: S47394; S47369

R:Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T

A:Reference number: S47355

A:Accession: S47394

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-12 <LEH>

A:Cross-references: EMBL:Z35714; NID:g527523; PIDN:CAA84783.1; PID:g527524; EMBL:Z3569

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 41.7%; Score 30; DB 2; Length 12;

Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CASELGKSTNT 12

Db 1 CASSIGNGYTF 12

RESULT 3

S47357

```
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47357
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47357
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35681; NID:G527451; PIDN:CAA84750.1; PID:G527452
C:Keywords: T-cell receptor

Query Match 41.0%; Score 29.5; DB 2; Length 13;
Best Local Similarity 63.6%; Pred. No. 68;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 CASELGKSTNT 11
   ||| |||
Db 1 CASS-GRSTDT 10

RESULT 4
S26549
T-cell receptor beta chain (clone Cw3/A8, Cw3/Cas1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C:Accession: S26549; S26550
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: S26549
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Cross-references: EMBL:X67999
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/A8
A:Accession: S26550
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Cross-references: EMBL:X68000
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 40.3%; Score 29; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 77;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELGKS 8
   ||| |||
Db 1 CASSLGKT 8

RESULT 5
PH1463
T-cell receptor beta chain (clone A24/10.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C:Accession: PH1463
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; MUID:93171821; PMID:8436911
A:Accession: PH1463
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Superfamily: immunoglobulin homology
C:Keywords: receptor; T-cell

Query Match 38.9%; Score 28; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELGKS 8
   ||| |||
Db 1 CASSLGKT 8

RESULT 6
PH1466
T-cell receptor beta chain (clone A3/74.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C:Accession: PH1466
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.;
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompat
A:Reference number: PH1430; MUID:93171821; PMID:8436911
A:Accession: PH1466
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Superfamily: immunoglobulin homology
C:Keywords: receptor; T-cell

Query Match 38.9%; Score 28; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELGK 7
   ||| |||
Db 1 CASSLGQ 7

RESULT 7
S47400
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47400
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47400
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35678; NID:G527535; PIDN:CAA84747.1; PID:G527536
C:Keywords: T-cell receptor

Query Match 38.9%; Score 28; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASELGKSTNTF 12
   ||| |||
Db 1 CASSVALATEAF 12

RESULT 8
PT0217
T-cell receptor beta chain V-J region (4-1-E.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C:Accession: PT0217
R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restr
A:Reference number: PT0209; MUID:91217621; PMID:1902501
A:Accession: PT0217
A:Molecule type: mRNA
```

A;Residues: 1-11 <NAK>
C;Keywords: T-cell receptor

Query Match 37.5%; Score 27; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELGL 6
Db 1 CASRLGL 6

RESULT 9

S47391
T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47391; S47386
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A;Reference number: S47355
A;Accession: S47391
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12 <LEH>
A;Cross-references: EMBL:Z35712; NID:G527519; PIDN:CAA84781.1; PID:G527520; EMBL:Z35701;
C;Keywords: T-cell receptor

Query Match 37.5%; Score 27; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CASELGLKSTNTF 12
Db 1 CASSTGSGYGVTF 12

RESULT 10

S47383
T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47383
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A;Reference number: S47355
A;Accession: S47383
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
A;Cross-references: EMBL:Z35709; NID:G527513; PIDN:CAA84778.1; PID:G527514
C;Keywords: T-cell receptor

Query Match 37.5%; Score 27; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELGLKS 8
Db 1 CASNMGGS 8

RESULT 11

S57575
T cell receptor V-J junctional alpha chain region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C;Accession: S57575
R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Arguet, V.F.
submitted to the EMBL Data Library, June 1995
A;Description: T cell receptor repertoire for a viral epitope in humans is diversified B

A;Reference number: S57494
A;Accession: S57575
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-11 <BUR>
A;Cross-references: EMBL:Z49953; NID:G887510; PIDN:CAA90224.1; PID:G887511
C;Keywords: T-cell receptor

Query Match 36.1%; Score 26; DB 2; Length 11;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELGLK 7
Db 1 CASQGGK 7

RESULT 12

S47395
T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47395
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A;Reference number: S47355
A;Accession: S47395
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12 <LEH>
A;Cross-references: EMBL:Z35715; NID:G527525; PIDN:CAA84784.1; PID:G527526
C;Keywords: T-cell receptor

Query Match 36.1%; Score 26; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CASELGLKSTNTF 12
Db 1 CASQSGSYGVTF 12

RESULT 13

S47381
T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47381
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A;Reference number: S47355
A;Accession: S47381
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
A;Cross-references: EMBL:Z35698; NID:G527487; PIDN:CAA84767.1; PID:G527488
C;Keywords: T-cell receptor

Query Match 36.1%; Score 26; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CASELGLKSTNTF 12
Db 1 CASSTRGNTFAF 12

RESULT 14

S47382
T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47382; S47370
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HUA-A0201 restricted recognition of influenza A is dominated by T
A;Reference number: S47355
A;Accession: S47382
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
A;Cross-references: EMBL:Z35687; NID:G527463; PIDN:CAA84756.1; PID:G527464; EMBL:Z35695;
C;Keywords: T-cell receptor

Query Match 35.4%; Score 25.5; DB 2; Length 13;
Best Local Similarity 54.5%; Pred. No. 3.6e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
Qy 1 CASELGKSTNT 11
||| : ||| :
Db 1 CASSM-RSTD 10

RESULT 15

S23371
T-cell receptor alpha chain J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S23371
E;Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichman
Bur. J. Immunol. 21, 2749-2754, 1991
A;Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rheu
A;Reference number: S23364; MUID:92037820; PMID:1657615
A;Accession: S23371
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-10 <PIU>
A;Cross-references: EMBL:X58166
C;Keywords: T-cell receptor

Query Match 34.7%; Score 25; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 2 ASELGKST 9
: |||||
Db 2 SGEAGKST 9

Search completed: March 8, 2004, 11:55:55
Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:48:53 ; Search time 11 Seconds
(without alignments)

61.537 Million cell updates/sec

Title: US-09-761-636A-5

Perfect score: 72

Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 597

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	31.9	12	1 PSP3_PHYPA	P80662 physcomitre
2	20	27.8	12	1 V23K_WSSV	P82005 white spot
3	20	27.8	13	1 LIGA_TRAVE	F20011 trametes ve
4	20	27.8	13	1 PSP_PINPS	P81668 pinus pinas
5	19	26.4	10	1 COXM_RAT	P80431 rattus norv
6	18	25.0	12	1 UR2B_CATCO	P04559 catostomus
7	18	25.0	13	1 FARB_ASCSU	P43173 ascaris suu
8	17	23.6	12	1 UR2B_CYPCA	P04561 cyprinus ca
9	16	22.2	9	1 XYIA_STRSQ	P19149 streptomyc
10	16	22.2	11	1 TKC2_CALVO	P41518 calliphora
11	16	22.2	12	1 CX13_CONMR	P58809 conus marmo
12	16	22.2	12	1 TA10_TREME	P01371 tremella me
13	16	22.2	13	1 CXAA_CONST	P28878 conus stria
14	16	22.2	13	1 HPR9_FANES	P32416 rana escul
15	15	20.8	9	1 CNAP_CARMA	P38556 carcinus ma
16	15	20.8	9	1 FAR5_ASCSU	P43170 ascaris suu
17	15	20.8	9	1 SAMP_MUSCA	P19095 musculus ca
18	15	20.8	9	1 SAP_STOVA	P24047 stomopneute
19	15	20.8	10	1 COXQ_RABIT	P80336 oryctolagus
20	15	20.8	11	1 ODP2_BOVIN	P11180 bos taurus
21	15	20.8	11	1 CX5A_CONAL	P58848 conus aulic
22	15	20.8	11	1 CX5B_CONAL	P58849 conus aulic
23	15	20.8	11	1 FAR9_CALVO	P41864 calliphora
24	15	20.8	11	1 TIN1_HOFTI	P82651 hoplobatr
25	15	20.8	12	1 CXA1_CONIM	P50983 conus imper
26	15	20.8	12	1 NO40_LORJA	O22426 lotus japon
27	15	20.8	12	1 SO15_BACSU	P80863 bacillus su
28	15	20.8	13	1 CREL_VESTR	P17231 vespa tropi
29	15	20.8	13	1 CXA2_CONGE	P01520 conus geogr
30	15	20.8	13	1 GER1_HORVU	P28525 hordeum vul
31	15	20.8	13	1 GER2_HORVU	P28526 hordeum vul
32	14	19.4	7	1 IGAO_DACDE	P06294 dactylum d
33	14	19.4	7	1 UC24_WAIZE	P80630 zea mays (m

34	14	19.4	9	1 FAR8_MACRS	P83281 macrobrachi
35	14	19.4	10	1 LPK2_LOCFI	P41488 locusta mig
36	13	18.1	10	1 SYK_CAMUP	O46464 campylobact
37	13	18.1	10	1 TKL4_LOCFI	P30250 locusta mig
38	13	18.1	10	1 TKNB_CHICK	P19851 gallus gall
39	13	18.1	10	1 TKNB_ONCMY	P28500 oncorhynch
40	13	18.1	10	1 TKNC_RANCA	P22590 rana catesb
41	13	18.1	10	1 URA6_HUMAN	P32080 homo sapien
42	13	18.1	10	1 VEG6_BACSU	P80699 bacillus su
43	13	18.1	12	1 UR2_FOLSP	P81022 polyodon sp
44	13	18.1	13	1 CREL_VESMA	P17232 vespa manda
45	13	18.1	13	1 ITB5_BOVIN	P80747 bos taurus

ALIGNMENTS

RESULT 1
PSP3_PHYPA
ID PSP3_PHYPA STANDARD; PRT; 12 AA.
AC P80662;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Oxygen-evolving enhancer protein 2 (OE2) (24 kDa subunit of oxygen
evolving system of photosystem II) (fragment).
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;
RN [1]
RP SEQUENCE.
RC TISSUE=Protonema;
RX MEDLINE=97275459; PubMed=9129336;
RA Kasten B., Buck F., Nuske J., Reski R.;
RT "Cytokinin affects nuclear- and plastome-encoded energy-converting
plastid enzymes.";

RL Planta 201:261-272(1997).
CC -!- FUNCTION: May be involved in the regulation of photosystem II.
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
CC with the photosystem II complex.
CC -!- INDUCTION: By light.
CC -!- SIMILARITY: Belongs to the psbP family.
KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane;
KW Multigene family.
FT NON TER 12
SQ SEQUENCE 12 AA; 1182 MW; 8D2B0D54D7C44DC5 CRC64;

Query Match 31.9%; Score 23; DB 1; Length 12;

Best Local Similarity 57.1%; Pred. No. 3.2e+02;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 GKSTNTF 12

|:|:|

3 GESANVF 9

RESULT 2

V23K_WSSV
ID V23K_WSSV STANDARD; PRT; 12 AA.
AC P82005;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 23 kDa structural polypeptide (Fragment).
OS White spot syndrome virus (WSSV).
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.

OX NCBI_TaxID=92652;

RN [1]

RP SEQUENCE.

RC STRAIN=South Carolina;

RX MEDLINE=20214217; PubMed=10752552;

RA Wang Q., Poulos B.T., Lightner D.V.;

RT "Protein analysis of geographic isolates of shrimp white spot syndrome virus."
 RL Arch. Virol. 145:263-274(2000).
 CC -1- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1323 MW; 0C0F41E91DS1A724 CRC64;

Query Match 27.8%; Score 20; DB 1; Length 12;
 Best Local Similarity 57.1%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 ELGKSTN 10
 Db 2 EFGNLTN 8

RESULT 3

LIGA_TRAVE STANDARD; PRT; 13 AA.
 AC P20011;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ligninase A (EC 1.11.1.14) (Diarylpropane peroxidase) (Lignin peroxidase) (Fragment).
 DE Trametes versicolor (White-rot fungus).
 OS Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Trametes.
 OX NCBI_TaxID=5325;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=89211432; PubMed=2707445;
 RA Joensson L., Karlsson O., Lundquist K., Nyman P.O.;
 RT "Trametes versicolor ligninase: isozyme sequence homology and substrate specificity."
 RL FEBS Lett. 247:143-146(1989).
 CC -1- FUNCTION: Depolymerization of lignin. Catalyzes the C(alpha)-C(beta) cleavage of the propyl side chains of lignin.
 CC -1- CATALYTIC ACTIVITY: 1,2-bis(3,4-dimethoxyphenyl)propane-1,3-diol + H2O(2) = veratraldehyde + 1-(3,4-dimethylphenyl)ethane-1,2-diol + 4 H(2)O.
 CC -1- PATHWAY: Lignin degradation; first step.
 CC -1- SIMILARITY: Belongs to the peroxidase family. Ligninase subfamily.
 DR InterPro; IPR002016; Peroxidase.
 DR PROSITE; PS00435; PEROXIDASE 1; PARTIAL.
 DR PROSITE; PS00436; PEROXIDASE 2; PARTIAL.
 KW Oxidoreductase; Peroxidase; Iron; Heme; Glycoprotein;
 KW Multigene family; Lignin degradation.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1298 MW; 22C50ED5872A4338 CRC64;

Query Match 27.8%; Score 20; DB 1; Length 13;
 Best Local Similarity 66.7%; Pred. No. 1.2e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GKSTNT 11
 Db 6 GKNVAT 11

RESULT 4

PSP_PINPS STANDARD; PRT; 13 AA.
 AC P81668;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Oxygen-evolving enhancer protein 2 (OEE2) (23 kDa subunit of oxygen evolving system of photosystem II) (Fragment).
 GN PSPP.
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine proteins."
 RL Electrophoresis 20:1098-1108(1999).
 CC -1- FUNCTION: May be involved in the regulation of photosystem II.
 CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated with the photosystem II complex (By similarity).
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this protein (spot N179) is: 5.9, its MW is: 22 kDa.
 CC -1- SIMILARITY: Belongs to the psbP family.
 KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1294 MW; C6772B0D54D7C44D CRC64;

Query Match 27.8%; Score 20; DB 1; Length 13;
 Best Local Similarity 42.9%; Pred. No. 1.2e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GKSTNTF 12
 Db 3 GBAANVF 9

RESULT 5

COXM_RAT STANDARD; PRT; 10 AA.
 AC P80431;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIIb, mitochondrial (EC 1.9.3.1) (Fragment).
 DE GN COX7B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Wistar; TISSUE=Liver;
 RX MEDLINE=95324529; PubMed=7601105;
 RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
 RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the adult liver isoform."
 RT Eur. J. Biochem. 230:235-241(1995).
 CC -1- FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport.
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.
 CC PIR; S65387; S65387.
 KW Oxidoreductase; Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1210 MW; CFC70EB771A33326 CRC64;

Query Match 26.4%; Score 19; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 KSTNTF 12
 Db 4 KKTPTF 9

RESULT 6

```

UR2B CATCO
ID UR2B CATCO STANDARD; PRT; 12 AA.
AC P04559;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Urotensin IIB (U-IIB) (UIIB).
OC Catostomus commersoni (White sucker).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Catostomidae; Catostomus.
OX NCBI_TaxID=7971;
RN [1]
RP SEQUENCE.
RX MEDLINE=84041959; PubMed=6138758;
RA McMaster D., Lederis K.;
RT "Isolation and amino acid sequence of two urotensin II peptides from
RT Catostomus commersoni urophyses.";
RL Peptides 4:367-373(1983).
CC -1- FUNCTION: Urotensin is found in the teleost caudal neurosecretory
CC system. It has a suggested role in osmoregulation and as a
CC corticotropin-releasing factor.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the urotensin 2 family.
DR PIR; JS0424; JS0424.
DR InterPro; IPR001483; Urotensin II.
DR Pfam; PF02083; Urotensin II; 1.
DR PROSITE; PS00984; UROTENSIN_II; 1.
KW Hormone.
FT DISULFID 6 11
SQ SEQUENCE 12 AA; 1437 MW; 73961BDB8879CEBB CRC64;

Query Match 25.0%; Score 18; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TWTFC 13
: |||
Db 2 SNTFC 6

RESULT 7
FARB_ASCSU
ID FARB_ASCSU STANDARD; PRT; 13 AA.
AC P43173;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFamide-like neuropeptide AF11.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
KW Neuropeptide; Amidation.
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1495 MW; 9CABC650D6886B05 CRC64;

Query Match 25.0%; Score 18; DB 1; Length 13;
Best Local Similarity 40.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 SELGKSTNTF 12
: |||
Db 1 SDIGISEPNF 10

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RESULT 8
UR2B_CYPCA
ID UR2B_CYPCA STANDARD; PRT; 12 AA.
AC P04561;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Urotensin II-beta (UII-beta) (U-II-beta).
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE.
RX Muneke E., Ohtaki T., Ichikawa T., McMaster D., Lederis K.;
RL (In) Rich D.H., Gross E. (eds.);
RL Proceedings of the 7th American peptide symposium, pp.69-72,
RL Pierce Chemical Co., Rockford IL. (1981).
CC -1- FUNCTION: Urotensin is found in the teleost caudal neurosecretory
CC system. It has a suggested role in osmoregulation and as a
CC corticotropin-releasing factor.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the urotensin 2 family.
DR InterPro; IPR001483; Urotensin II.
DR Pfam; PF02083; Urotensin II; 1.
DR PROSITE; PS00984; UROTENSIN_II; 1.
KW Hormone.
FT DISULFID 6 11
SQ SEQUENCE 12 AA; 1407 MW; 73960A9FB879CEBB CRC64;

Query Match 23.6%; Score 17; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 NTFC 13
: |||
Db 3 NTEC 6

RESULT 9
XYLA_STRSQ
ID XYLA_STRSQ STANDARD; PRT; 9 AA.
AC P19149;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Xylose isomerase (EC 5.3.1.5) (Fragment).
GN XYLA.
OS Streptomyces sp. (strain NCL 82-5-1).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=19311;
RN [1]
RP SEQUENCE.
RX MEDLINE=88326335; PubMed=3415697;
RA Pawar H.S., Kannan K., Srinivasan M.C., Vartak H.G.;
RT "Purification and characterisation of glucose (xylose) isomerase from
RT Chainia sp. (NCL 82-5-1).";
RL Biochem. Biophys. Res. Commun. 155:411-417(1988).
CC -1- FUNCTION: Involved in D-xylose catabolism.
CC -1- CATALYTIC ACTIVITY: D-xylose = D-xylulose.
CC -1- COFACTOR: Binds 2 magnesium ions per subunit (Potential).
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the xylose isomerase family.
DR PIR; A31576; A31576.
DR HAMAP; MF 00455; -; 1.
DR InterPro; IPR001998; Xylose isom.
DR PROSITE; PS00172; XYLOSE_ISOMERASE_1; PARTIAL.

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DR PROSITE; P500173; XYLOSE ISOMERASE 2; PARTIAL.
KW Isomerase; Pentose shunt; Xylose metabolism; Metal-binding; Magnesium.
FT NON TER 9
SQ SEQUENCE 9 AA; 983 MW; F64BA1EDC5B87DD1 CRC64;
Query Match 22.2%; Score 16; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 8 STNTP 12
DB 5 SAHFP 9
RESULT 10
TKC2 CALVO STANDARD; PRT; 11 AA.
ID TKC2 CALVO STANDARD; PRT; 11 AA.
AC P41518;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Callitachykinin II.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE AND SYNTHESIS.
RX MEDLINE=95075727; PubMed=7984492;
RA Lundquist C.T.; Clottens F.L.; Holman G.M.; Nichols R., Nachman R.J.,
RA Naessel D.R.;
RT "Callitachykinin I and II, two novel myotropic peptides isolated from
the blowfly, Calliphora vomitoria, that have resemblances to
tachykinins."
RL Peptides 15:761-768 (1994).
CC -1- FUNCTION: Myoactive peptide.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD RES 11 11
SQ SEQUENCE 11 AA; 1103 MW; 15D7E3F9C9CDD444 CRC64;
Query Match 22.2%; Score 16; DB 1; Length 11;
Best Local Similarity 42.9%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 6 GKSTNTP 12
DB 1 GLGNNAF 7
RESULT 11
CX13 CONNR STANDARD; PRT; 12 AA.
ID CX13 CONNR STANDARD; PRT; 12 AA.
AC P58809;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lambda-conotoxin CMX.
OS Conus marmoreus (Marble cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=42752;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=20564325; PubMed=10989292;
RA Balaji R.A.; Ohtake A.; Sato K.; Gopalakrishnakone P.; Kini R.M.,
RA Seow K.T.; Bay B.-H.;
RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide
pattern and protein folding. Isolation and characterization from the

RT venom of Conus marmoreus.";
RL J. Biol. Chem. 275:39516-39522 (2000).
CC -1- FUNCTION: Inhibits the neuronal noradrenergic transporter.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=1262.77; MW_ERR=0.07; METHOD=Electrospray.
CC -1- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
KW Neurotoxin; Toxin; Hydroxylation.
FT DISULFID 3 12
FT DISULFID 4 9
FT MOD RES 11 11
SQ SEQUENCE 12 AA; 1251 MW; 277AAE422D5A2C8 CRC64;
Query Match 22.2%; Score 16; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 6.2e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 11 TFC 13
DB 7 SFC 9
RESULT 12
TA10 TREME STANDARD; PRT; 12 AA.
ID TA10 TREME STANDARD; PRT; 12 AA.
AC P01371;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tremorgen A-10.
OS Tremella mesenterica (Jelly fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Tremella.
OX NCBI_TaxID=5217;
RN [1]
RP SEQUENCE.
RA Sakagami Y., Yoshida M., Isogai A., Suzuki A.;
RT "Peptide sex hormones inducing conjugation tube formation in
compatible mating-type cells of Tremella mesenterica.";
RL Science 212:1525-1527 (1981).
CC -1- FUNCTION: Tremorgen A-10 is produced by the mating-type cells
and induces formation of conjugation tubes in a mating-type cells.
CC PIR; A01642; JTG0.
DR Lipoprotein; Prenylation; Methylation; Pheromone.
KW Lipid 12 12
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1246 MW; 84EF574959676DC5 CRC64;
Query Match 22.2%; Score 16; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 6.2e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 10 NTFC 13
DB 9 NGVC 12
RESULT 13
CXAA CONST STANDARD; PRT; 13 AA.
ID CXAA CONST STANDARD; PRT; 13 AA.
AC P28878;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin SIA (SIA).
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6493;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;

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EX MEDLINE-9136955; PubMed-1892838;
RA Myers R.A., Kafarella G.C., Gray W.R., Abbot J., Cruz L.J.,
RT Olivera B.M.;
RA "Alpha-conotoxins, small peptide probes of nicotinic acetylcholine
RL receptors.";
RL Biochemistry 30:9370-9377(1991).
CC -i- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
CC inhibit them.
CC -i- SUBCELLULAR LOCATION: Secreted.
CC -i- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -i- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
CC family.
DR PIR; A40312; NTKNAS.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation.
FT DISULFID 2 7
FT DISULFID 3 13
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1461 MW; DEF1931982457EBD CRC64;

Query Match 22.2%; Score 16; DB 1; Length 13;
Best Local Similarity 37.5%; Pred. No. 6.7e+03;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELGKS 8
DB 3 CHPACGKN 10

RESULT 14
HPB9 RANES STANDARD; PRT; 13 AA.
AC P32416;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hemolytic protein B9 (Fragment).
OS Rana esculenta (Edible frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8401;
RN [1]
RP SEQUENCE
RC TISSUE=Skin secretion;
RX MEDLINE-9019965; PubMed-2317508;
RA Simmaco M., de Biase D., Severini C., Aita M., Erspamer G.F.,
RA Barra D., Bossa F.;
RT "Purification and characterization of bioactive peptides from skin
RT extracts of Rana esculenta.";
RL Biochim. Biophys. Acta 1033:318-323(1990).
CC -i- FUNCTION: Shows hemolytic activity.
CC -i- SUBCELLULAR LOCATION: Secreted.
CC -i- TISSUE SPECIFICITY: Skin.
DR PIR; S09019; S09019.
KW Amphibian defense peptide; Amidation; Hemolysis.
FT MOD RES 13 13
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1402 MW; C6B41A765DF9287D CRC64;

Query Match 22.2%; Score 16; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 6.7e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASELGK 7
DB 6 AGELGK 11

RESULT 15
CCAP_CARMA STANDARD; PRT; 9 AA.
ID CCAP_CARMA
AC P38556;

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DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cardioactive peptide (CCAP).
OS Carcinus maenas (Common shore crab) (Green crab),
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
OS Tenebrio molitor (Yellow mealworm), and
OS Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunodea; Portunidae; Carcinus.
OX NCBI_TaxID=6759, 7130, 7067, 37547;
RN [1]
RP SEQUENCE.
RC SPECIES=C.maenas; TISSUE=Pericardial organs;
RA Stangier J., Hilbich C., Beyreuther K., Keller R.;
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
RT shore crab Carcinus maenas.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=M.sexta;
RX MEDLINE-93050243; PubMed-1426284;
RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
RT "Primary structure of a cardioactive neuropeptide from the tobacco
RT hawkmoth, Manduca sexta.";
RL FEBS Lett. 313:165-168(1992).
RN [3]
RP SEQUENCE.
RC SPECIES=T.molitor, and S.eridania; TISSUE=Head;
RX MEDLINE-94176032; PubMed-8129851;
RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RA Schooley D.A.;
RT "Isolation and identification of a cardioactive peptide from Tenebrio
RT molitor and Spodoptera eridania.";
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
CC -i- FUNCTION: The effect of CCAP is both ino- and chronotropic.
CC -i- SUBCELLULAR LOCATION: Secreted.
CC -i- TISSUE SPECIFICITY: Stored in pericardial organs and released
CC into the hemolymph.
DR PIR; A26363; A26363.
DR PIR; S27233; S27233.
KW Neuropeptide; Amidation.
FT DISULFID 3 9
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

Query Match 20.8%; Score 15; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 FC 13
DB 2 FC 3

Search completed: March 8, 2004, 11:54:31
Job time : 11 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:51:58 ; Search time 39 Seconds
(without alignments)
105.173 Million cell updates/sec

Title: US-09-761-636A-5
Perfect score: 72
Sequence: 1 CASLKGSTNTFC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 3001

Minimum DB seq length: 0
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL 25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phase:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_virus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	ID	Description
1	27	37.5	13	13	Q8GZ5	Q8GZ5 fugu rubrip
2	26	36.1	13	12	Q918T4	Q918T4 human papil
3	26	36.1	13	12	Q918T6	Q918T6 human papil
4	23	31.9	12	13	Q9PS67	Q9PS67 gallus gall
5	21	29.2	12	12	Q85666	Q85666 reovirus (t
6	21	29.2	13	6	Q8GJU2	Q8GJU2 ovis aries
7	21	29.2	13	13	P82821	P82821 rana catesb
8	21	29.2	13	13	P82822	P82822 rana catesb
9	20	27.8	11	10	Q9TOL9	Q9TOL9 brassica ol
10	20	27.8	12	3	Q9UR22	Q9UR22 cryptococcu
11	20	27.8	12	13	P82820	P82820 rana catesb
12	20	27.8	13	11	Q80WZ0	Q80WZ0 rana catesb
13	20	27.8	13	13	P82823	P82823 rana catesb
14	19	26.4	12	11	Q61331	Q61331 mus musculu
15	19	26.4	13	11	O54809	O54809 mus musculu
16	18	25.0	8	7	Q95213	Q95213 cryotcolagus

17	18	25.0	11	9	Q37925	Q37925 bacterioph
18	18	25.0	11	13	Q9PS71	Q9PS71 agkistrodon
19	18	25.0	12	6	Q7YS46	Q7YS46 ovis aries
20	18	25.0	12	8	Q7YKE9	Q7YKE9 ribes divar
21	18	25.0	13	4	Q9UDC6	Q9UDC6 homo sapien
22	18	25.0	13	13	P82881	P82881 rana ciamit
23	17	23.6	11	2	Q9SUZ3	Q9SUZ3 escherichia
24	17	23.6	11	4	Q9HCN5	Q9HCN5 homo sapien
25	17	23.6	12	5	Q8TOY6	Q8TOY6 apis mellif
26	17	23.6	12	8	Q9BFV4	Q9BFV4 myrmecophag
27	17	23.6	12	8	Q7YKC9	Q7YKC9 ribes speci
28	17	23.6	13	4	Q13377	Q13377 homo sapien
29	17	23.6	13	11	Q35758	Q35758 rattus norv
30	16	22.2	8	2	Q7X139	Q7X139 staphylococ
31	16	22.2	9	2	Q30790	Q30790 erwinia amy
32	16	22.2	9	4	Q15999	Q15999 homo sapien
33	16	22.2	9	12	Q88612	Q88612 middelburg
34	16	22.2	10	4	Q8NEY9	Q8NEY9 homo sapien
35	16	22.2	10	6	Q9TRU6	Q9TRU6 bos taurus
36	16	22.2	11	11	P97330	P97330 mus musculu
37	16	22.2	11	11	Q9RLN6	Q9RLN6 mus musculu
38	16	22.2	12	2	Q9S550	Q9S550 streptococc
39	16	22.2	12	5	Q17140	Q17140 crassostrea
40	16	22.2	12	5	Q26429	Q26429 drosophila
41	16	22.2	12	11	Q84242	Q84242 rattus sp.
42	16	22.2	13	4	Q9UMK9	Q9UMK9 homo sapien
43	16	22.2	13	4	Q9GQ66	Q9GQ66 homo sapien
44	16	22.2	13	5	Q818F2	Q818F2 drosophila
45	16	22.2	13	5	Q818F1	Q818F1 drosophila

ALIGNMENTS

RESULT 1

Q8GZ5	PRELIMINARY;	PRT;	13 AA.
AC	Q8GZ5		
DT	01-JUN-2002 (TRENBLrel. 21, Created)		
DT	01-JUN-2002 (TRENBLrel. 21, Last sequence update)		
DT	01-JUN-2003 (TRENBLrel. 24, Last annotation update)		
DE	Guanine nucleotide binding protein (Fragment).		
GN	GNAO.		
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;		
OC	Tetraodontidae; Tetraodontidae; Takifugu.		
OX	NCBI_TaxID:31033;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE:97129408; PubMed:8973916;		
RA	Sarwal M.M., Sontag J.M., Hoang L., Brenner S., Wilkie T.M.;		
RT	"G protein alpha subunit multigene family in the Japanese puffer fish		
RT	Fugu rubripes: PCR from a compact vertebrate genome.";		
RL	Genome Res. 6:1207-1215 (1996).		
DR	EMSL; L79891; AAU77640.1; -		
DR	GO; GO:0004871; F-signal transducer activity; IEA.		
DR	GO; GO:0007186; P-G-protein coupled receptor protein signalin. .; IEA.		
DR	InterPro: IPR001019; Gprotein_alpha.		
DR	Pfam: PF00503; G-alpha; 1.		
FT	NON_TER		
FT	NON_TER		
FT	NON_TER		
SQ	SEQUENCE 13 AA; 1336 MW; 465B59640B4B5B3 CRC64;		

Query Match 37.5%; Score 27; DB 13; Length 13;

Best Local Similarity 75.0%; Pred. No. 3.6e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASELCKST 9

Db 1 AGESGKST 8

RESULT 2

Q91874 ID Q91874 PRELIMINARY; PRT; 13 AA.
 AC Q91874; DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE E1 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HPV16E2CCT;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human Papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF407220; AAL01406.1; --
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 13 AA; 1413 MW; 8AED73A03A52D865 CRC64;

Query Match 36.1%; Score 26; DB 12; Length 13;
 Best Local Similarity 54.5%; Pred. NO. 5.6e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 CASELGKSTNT 11
 DB 4 CVS--GQNTNT 12

RESULT 3

Q91876 ID Q91876 PRELIMINARY; PRT; 13 AA.
 AC Q91876; DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE E1 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HPV16E2CC6;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human Papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF407219; AAL01403.1; --
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 13 AA; 1413 MW; 8AED73A03A52D865 CRC64;

Query Match 36.1%; Score 26; DB 12; Length 13;
 Best Local Similarity 54.5%; Pred. NO. 5.6e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 CASELGKSTNT 11
 DB 4 CVS--GQNTNT 12

RESULT 4

Q9PS67 ID Q9PS67 PRELIMINARY; PRT; 12 AA.
 AC Q9PS67; DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE Myosin (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=92031443; PubMed=1931944;
 RA Garabedian T.E., Yount R.G.;
 RT "Direct photoaffinity labeling of gizzard myosin with vanadate-trapped
 RT adenosine diphosphate."
 RL Biochemistry 30:10126-10132(1991).
 DR PIR; A23695; A23695.
 FT NON TER 1
 FT NON TER 1
 FT NON TER 12
 FT NON TER 12
 SQ SEQUENCE 12 AA; 1178 MW; C1FC2E0D9AA3387D CRC64;

Query Match 31.9%; Score 23; DB 13; Length 12;
 Best Local Similarity 55.6%; Pred. NO. 1.9e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 SELGKSTNT 11
 DB 3 SGAGKNTNT 11

RESULT 5

Q85666 ID Q85666 PRELIMINARY; PRT; 12 AA.
 AC Q85666; DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Reovirus serotype 3 M3 (Fragment).
 OS Reovirus (type 3 / strain Dearing).
 OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
 OX NCBI_TaxID=10886;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=83017876; PubMed=6927854;
 RA Antczak J.B., Chmelo R., Pickup D.J., Joklik W.K.;
 RT "Sequences at both termini of the 10 genes of reovirus serotype 3
 RT (strain Dearing)."
 RL Virology 121:307-319(1982).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=83017877; PubMed=7123853;
 RA Gaillard R.K., Li J.K., Keene J.D., Joklik W.K.;
 RT "The sequences at the termini of four genes of the three reovirus
 RT serotypes."
 RL Virology 121:320-326(1982).
 DR EMBL; J02323; AAA47259.1; --
 FT NON TER 12
 FT NON TER 12
 SQ SEQUENCE 12 AA; 1275 MW; 4B292B17FCB9C873 CRC64;

Query Match 29.2%; Score 21; DB 12; Length 12;
 Best Local Similarity 60.0%; Pred. NO. 4.6e+03;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ASELGKSTNT 11
 DB 2 ASFKGSANT 11

RESULT 6

Q9GU2 ID Q9GU2 PRELIMINARY; PRT; 13 AA.
 AC Q9GU2; DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)

```

DE Calpastatin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chordata; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Nonneman D., Geesink G.H., Koohmariaie M.;
RT "Differential splicing and protein isoforms of ovine calpastatin.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF192536; AAC31688.1; -
DR EMBL; AF192535; AAC31687.1; -
RT NON_TER 1
SQ SEQUENCE 13 AA; 1335 MW; 479542C69BADD3 CRC64;

Query Match 29.2%; Score 21; DB 6; Length 13;
Best Local Similarity 80.0%; Pred. No. 5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 GKSTN 10
DB 9 GKSTS 13

RESULT 7
P82821 ID P82821 PRELIMINARY; PRT; 13 AA.
AC P82821;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE RANATUERIN 6.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN;
RX MEDLINE=98422096; PubMed=9751476;
RA Goraya J., Knoop F.C., Conlon J.M.;
RT "Ranaturins: antimicrobial peptides isolated from the skin of the
RT American bullfrog, Rana catesbeiana.";
RL Biochem. Biophys. Res. Commun. 250:589-592(1998).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE AGAINST GRAM-NEGATIVE BACTERIUM
CC S.AUREUS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
DR GO; GO:0006805; P: xenobiotic metabolism; IEA.
KW Antibiotic.
SQ SEQUENCE 13 AA; 1398 MW; C85480BDC0CF885BD CRC64;

Query Match 29.2%; Score 21; DB 13; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGK 7
DB 6 ASMLGK 11

RESULT 8
P82822 ID P82822 PRELIMINARY; PRT; 13 AA.
AC P82822;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE RANATUERIN 7.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;

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RN [1]
RP SEQUENCE.
RC TISSUE=SKIN;
RX MEDLINE=98422096; PubMed=9751476;
RA Goraya J., Knoop F.C., Conlon J.M.;
RT "Ranaturins: antimicrobial peptides isolated from the skin of the
RT American bullfrog, Rana catesbeiana.";
RL Biochem. Biophys. Res. Commun. 250:589-592(1998).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE AGAINST GRAM-NEGATIVE BACTERIUM
CC S.AUREUS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
DR GO; GO:0006805; P: xenobiotic metabolism; IEA.
KW Antibiotic.
SQ SEQUENCE 13 AA; 1398 MW; C85480B95DF885BD CRC64;

Query Match 29.2%; Score 21; DB 13; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGK 7
DB 6 ASMLGK 11

RESULT 9
Q970L9 ID Q970L9 PRELIMINARY; PRT; 11 AA.
AC Q970L9;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE SLG5 protein (Fragment).
GN SLG5.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99264316; PubMed=10330480;
RA Cabrilla D., Delorme V., Garin J., Ruffio-Chable V., Giranton J.L.,
RA Dumas C., Gaude T., Cock J.M.;
RT "The S15 self-incompatibility haplotype in Brassica includes three S
RT gene family members which are expressed in stigmas.";
RL Plant Cell 11:971-986(1999).
DR EMBL; Y18256; CAB41875.1; -
FT NON_TER 1
SQ SEQUENCE 11 AA; 1035 MW; CD3806DDA8772AAD CRC64;

Query Match 27.8%; Score 20; DB 10; Length 11;
Best Local Similarity 50.0%; Pred. No. 6.5e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASELGK 9
DB 3 AADLGTCT 10

RESULT 10
Q9UR22 ID Q9UR22 PRELIMINARY; PRT; 12 AA.
AC Q9UR22;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE STB12 alpha (Fragment).
GN STB12ALPHA.
OS Cryptococcus neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=40410;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=CBS884, BAL 3, and CBS6989;
RX MEDLINE=99380307; PubMed=10449476;
RA Halliday C.L., Bui T., Krockenberger M., Malik R., Ellis D.H.,
RT Carter D.A.;
RT "Presence of alpha and a mating types in environmental and clinical
RT collections of Cryptococcus neoformans var. gattii strains from
RT Australia.";
RL J. Clin. Microbiol. 37:2920-2926(1999).
DR EMBL; AF155349; AAF20374.1; -
DR EMBL; AF155347; AAF20372.1; -
DR EMBL; AF155348; AAF20373.1; -
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1307 MW; 5AF9B485DA735B7 CRC64;

Query Match 27.8%; Score 20; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TFC 13
DB 8 TFC 10

RESULT 11
P82820 PRELIMINARY; PRT; 12 AA.
AC P82820;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE RANATUERIN 5.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN;
RX MEDLINE=98422096; PubMed=9751476;
RA Goraya J., Knoop F.C., Conlon J.M.;
RT "Ranaturins: antimicrobial peptides isolated from the skin of the
RT American bullfrog, Rana catesbeiana.";
RL Biochem. Biophys. Res. Commun. 250:589-592(1998).
CC -|- SUBCELLULAR LOCATION: SECRETED.
SQ SEQUENCE 12 AA; 1335 MW; C8531D12A92735BD CRC64;

Query Match 27.8%; Score 20; DB 13; Length 12;
Best Local Similarity 83.3%; Pred. No. 7.1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASLKG 7
DB 5 ASLKG 10

RESULT 12
Q80WZ0 PRELIMINARY; PRT; 13 AA.
AC Q80WZ0;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE GTP-binding protein Golf alpha subunit (Fragment).
GN G-ALPHA-OLF.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96115117; PubMed=7494450;

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RA Herve D., Rogard M., Levi-Strauss M.;
RT "Molecular analysis of the multiple Golf alpha subunit mRNAs in the
RT rat brain.";
RL Brain Res. Mol. Brain Res. 32:125-134(1995).
DR EMBL; S80330; AAP32222.1; -
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1312 MW; 0B6E3319671CA5B4 CRC64;

Query Match 27.8%; Score 20; DB 11; Length 13;
Best Local Similarity 57.1%; Pred. No. 7.7e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 LKSTNT 11
DB 4 LGNSKT 10

RESULT 13
P82823 PRELIMINARY; PRT; 13 AA.
AC P82823;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE RANATUERIN 8.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN;
RX MEDLINE=98422096; PubMed=9751476;
RA Goraya J., Knoop F.C., Conlon J.M.;
RT "Ranaturins: antimicrobial peptides isolated from the skin of the
RT American bullfrog, Rana catesbeiana.";
RL Biochem. Biophys. Res. Commun. 250:589-592(1998).
CC -|- FUNCTION: ANTIBACTERIAL PEPTIDE AGAINST GRAM-NEGATIVE BACTERIUM
CC S-AUREUS.
CC -|- SUBCELLULAR LOCATION: SECRETED.
CC GO; GO:0006805; P: xenobiotic metabolism; IEA.
KW Antibiotic.
SQ SEQUENCE 13 AA; 1414 MW; C85480BD0CF7D5BD CRC64;

Query Match 27.8%; Score 20; DB 13; Length 13;
Best Local Similarity 83.3%; Pred. No. 7.7e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASLKG 7
DB 6 ASLKG 11

RESULT 14
Q61331 PRELIMINARY; PRT; 12 AA.
AC Q61331;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE N-acetylglucosamine (Beta1-4) galactosyl transferase (EC 2.4.1.90)
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89033997; PubMed=3141392;
RA Nakazawa K., Ando T., Kimura T., Narimatsu H.;
RT "Cloning and sequencing of a full-length cDNA of mouse N-
RT acetylglucosamine (beta1-4) galactosyltransferase.";
RL J. Biochem. 104:165-168(1988).

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DR EMBL; D00315; BAA00217.1; -.
 DR GO; GO:0003945; P:N-acetylglucosamine synthase activity; IEA.
 DR GO; GO:0016757; P:transferase activity, transferring glycosyl. . .; IEA.
 KW Glycosyltransferase; Transferase.
 FT NON TER 1
 FT NON TER 12
 SQ SEQUENCE 12 AA; 1283 MW; 304EA40668387728 CRC64;

Query Match 26.4%; Score 19; DB 11; Length 12;
 Best Local Similarity 57.1%; Pred. No. 1.1e+04;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKS 8
 Db 3 SSGGKGT 9

RESULT 15

OS4809
 ID 054809 PRELIMINARY; PRT; 13 AA.
 AC 054809;
 DT 01-JUN-1998 (TRENBLrel. 06, Created)
 DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Prolactin (fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Harigaya T., Imai H.;
 RT "Partial nucleotide sequence of mouse prolactin gene, intron2."
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB011669; BAA25091.1; -.
 FT NON TER 1
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1441 MW; 0B043B50DD1545B4 CRC64;

Query Match 26.4%; Score 19; DB 11; Length 13;
 Best Local Similarity 50.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 STNFC 13
 Db 7 SINGMC 12

Search completed: March 8, 2004, 11:55:23
 Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:48:18 ; Search time 53 Seconds
(without alignments)
69.304 Million cell updates/sec

Title: US-09-761-636A-5
Perfect score: 72
Sequence: 1 CASELKGKSTWTC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 383904

Minimum DB seq length: 0
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04 : *
1: Geneseq1980s : *
2: Geneseq1990s : *
3: Geneseq2000s : *
4: Geneseq2001s : *
5: Geneseq2002s : *
6: Geneseq2003as : *
7: Geneseq2003bs : *
8: Geneseq2004s : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	13	4	AAU04524
2	69	95.8	13	4	AAU04534
3	65	90.3	13	4	AAU04535
4	65	90.3	13	4	AAU04537
5	61	84.7	13	4	AAU04536
6	32	44.4	12	3	AAU04536
7	32	44.4	13	5	ABJ04094
8	30	41.7	13	3	ABJ04094
9	29	40.3	10	4	ABJ04094
10	29	40.3	13	3	ABJ04094
11	29	40.3	13	5	ABJ04094
12	28	38.9	9	2	AAU04536
13	28	38.9	9	3	AAU04536
14	28	38.9	9	5	AAU04536
15	28	38.9	10	3	AAU04536
16	28	38.9	13	5	AAU04536
17	28	38.9	13	5	AAU04536
18	27	37.5	9	5	AAU04536
19	27	37.5	10	4	AAU04536
20	27	37.5	10	4	AAU04536
21	27	37.5	12	2	AAU04536
22	27	37.5	12	2	AAU04536
23	27	37.5	12	4	AAU04536
24	27	37.5	12	4	AAU04536
25	27	37.5	12	5	ABG67372

26	27	37.5	12	6	ADA23476
27	27	37.5	13	3	AAU04534
28	27	37.5	13	4	AAU04534
29	27	37.5	13	5	ABJ00485
30	27	37.5	13	5	ABJ00490
31	27	37.5	13	5	ABJ00492
32	27	37.5	13	5	ABJ00493
33	26	36.1	8	4	AAU04534
34	26	36.1	9	2	AAU04534
35	26	36.1	9	2	AAU04534
36	26	36.1	9	2	AAU04534
37	26	36.1	9	3	AAU04534
38	26	36.1	9	6	ABP74688
39	26	36.1	9	7	ABP74688
40	26	36.1	10	4	AAU04534
41	26	36.1	10	4	AAU04534
42	26	36.1	10	4	AAU04534
43	26	36.1	10	4	AAU04534
44	26	36.1	10	5	ABP74688
45	26	36.1	10	7	ADC09548

ALIGNMENTS

RESULT 1	
AAU04524	
ID AAU04524 standard; peptide; 13 AA.	
XX AC AAU04524;	
DT 26-SEP-2001 (first entry)	
XX DE VEGF based monocyclic peptide 1.	
XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;	
XX KW neovascularisation; lymphangiogenesis; psoriasis; tumour;	
XX KW diabetes induced neovascular sequelae; rheumatoid arthritis;	
XX KW diabetic retinopathy; chronic inflammation; cyclic.	
OS Synthetic.	
XX FH Key Location/Qualifiers	
FT Disulfide-bond 1..13	
FT /note= "This bond cyclises the peptide"	
XX PN WO200152875-A1.	
XX PD 26-JUL-2001.	
XX PF 18-JAN-2001; 2001WO-US001533.	
XX PR 18-JAN-2000; 2000US-0176293P.	
XX PR 16-MAY-2000; 2000US-0204590P.	
XX PA (LUDW-) LUDWIG INST CANCER RES.	
XX PI Achen MG, Hughes RA, Stacker S, Cendron A;	
XX WP 2001-442248/47.	
XX PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,	
XX PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment	
XX PT from an exposed loop of a growth factor protein by oxidizing the cysteine	
XX PT residues.	
XX PS Claim 49; Page 32; 102pp; English.	
XX CC The sequence represents a monomeric monocyclic peptide of the invention,	
XX CC whose 3-dimensional structure is modelled on the exposed loop of human	
XX CC VEGF (vascular endothelial growth factor). The invention relates to a	
XX CC method of producing a monomeric monocyclic peptide by a measuring beta-	
XX CC beta carbon separation distances on opposite antiparallel strands of a	

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 13 AA;

Query Match 100.0%; Score 72; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CASELGKSTNTFC 13
 ||:|||||||
 Db 1 CASELGKSTNTFC 13

RESULT 2
 AAU04534
 ID AAU04534 standard; peptide; 13 AA.
 AC AAU04534;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 12.
 XX
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..13 /note= "This bond cyclises the peptide"
 XX
 PN W0200152875-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Achen MG, Hughes RA, Stacker S, Cendron A;
 XX
 DR WPI; 2001-442248/47.
 XX
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT

PT residues.
 XX
 PS Example 25; Page 47; 102pp; English.
 XX
 CC The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the exposed loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 13 AA;

Query Match 95.8%; Score 69; DB 4; Length 13;
 Best Local Similarity 92.3%; Pred. No. 6.8e-05;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CASELGKSTNTFC 13
 ||:|||||||
 Db 1 CASELGKSTNTFC 13

RESULT 3
 AAU04535
 ID AAU04535 standard; peptide; 13 AA.
 AC AAU04535;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 13.
 XX
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..13 /note= "This bond cyclises the peptide"
 XX
 PN W0200152875-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX

PA (LUDW-) LUDWIG INST CANCER RES.
 XX Achen MG, Hughes RA, Stacker S, Cendron A;
 XX WPI; 2001-442248/47.
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 XX from an exposed loop of a growth factor protein by oxidizing the cysteine
 XX residues.
 XX Example 25; Page 47; 102pp; English.
 XX The sequence represents a monomeric monocyclic peptide of the invention,
 XX whose 3-dimensional structure is modelled on the expose loop of human
 XX VEGF (vascular endothelial growth factor). The invention relates to a
 XX method of producing a monomeric monocyclic peptide by a measuring beta-
 XX metha carbon separation distances on opposite antiparallel strands of a
 XX peptide loop fragment from an exposed loop of a growth factor protein and
 XX cyclising the peptide by oxidising the cysteine residues. The monocyclic
 XX peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 XX peptides) and a cyclic peptide with at least one amino acid deleted prior
 XX to cyclisation are used to interfere with angiogenesis,
 XX neovascularisation or lymphangiogenesis in a mammal with a condition
 XX characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 XX The condition is diabetic retinopathy, psoriasis, arthropathy,
 XX hemangioma, vascularised malignant or benign tumour, post-recovery
 XX cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 XX trauma, substance-induced neovascularisation of the liver, excessive
 XX hormone-related angiogenic dysfunction, diabetes induced neovascular
 XX sequelae, hypertension induced neovascular sequelae, or chronic liver
 XX infection. The peptides are also used to modulate vascular permeability
 XX in a mammal (the mammal has a condition characterised by fluid
 XX accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 XX or brain. The peptides are used to image blood vessels and lymphatic
 XX vasculature. The monomeric and bicyclic peptides are used to interfere
 XX with at least one biological activity induced by VEGF, VEGF-C or -D and
 XX are also used in combination with an anti-inflammatory agent, to treat a
 XX chronic inflammation, especially rheumatoid arthritis, psoriasis and
 XX diabetic retinopathy

XX Sequence 13 AA;
 XX
 XX Query Match 90.3%; Score 65; DB 4; Length 13;
 XX Best Local Similarity 84.6%; Pred. No. 0.00033;
 XX Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 CASELGKSTNTFC 13
 XX |||||:|||||
 XX Db 1 CASELGKSTNTFC 13

RESULT 4
 AAU04537
 ID AAU04537 standard; peptide; 13 AA.
 XX AC AAU04537;
 XX DT 26-SEP-2001 (first entry)
 XX DE VEGF based monocyclic peptide 15.
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 XX neovascularisation; lymphangiogenesis; psoriasis; tumour;
 XX diabetes induced neovascular sequelae; rheumatoid arthritis;
 XX diabetic retinopathy; chronic inflammation; cyclic.
 XX OS Synthetic.
 XX Key Location/Qualifiers
 XX Disulfide-bond 1..13
 XX /note= "This bond cyclises the peptide"

PN WO200152875-A1.
 XX PD 26-JUL-2001.
 XX PF 18-JAN-2001; 2001WO-US001533.
 XX PR 18-JAN-2000; 2000US-0176293P.
 XX PT 16-MAY-2000; 2000US-0204590P.
 XX PA (LUDW-) LUDWIG INST CANCER RES.
 XX PI Achen MG, Hughes RA, Stacker S, Cendron A;
 XX WPI; 2001-442248/47.
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 XX from an exposed loop of a growth factor protein by oxidizing the cysteine
 XX residues.
 XX Example 25; Page 47; 102pp; English.
 XX The sequence represents a monomeric monocyclic peptide of the invention,
 XX whose 3-dimensional structure is modelled on the expose loop of human
 XX VEGF (vascular endothelial growth factor). The invention relates to a
 XX method of producing a monomeric monocyclic peptide by a measuring beta-
 XX metha carbon separation distances on opposite antiparallel strands of a
 XX peptide loop fragment from an exposed loop of a growth factor protein and
 XX cyclising the peptide by oxidising the cysteine residues. The monocyclic
 XX peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 XX peptides) and a cyclic peptide with at least one amino acid deleted prior
 XX to cyclisation are used to interfere with angiogenesis,
 XX neovascularisation or lymphangiogenesis in a mammal with a condition
 XX characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 XX The condition is diabetic retinopathy, psoriasis, arthropathy,
 XX hemangioma, vascularised malignant or benign tumour, post-recovery
 XX cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 XX trauma, substance-induced neovascularisation of the liver, excessive
 XX hormone-related angiogenic dysfunction, diabetes induced neovascular
 XX sequelae, hypertension induced neovascular sequelae, or chronic liver
 XX infection. The peptides are also used to modulate vascular permeability
 XX in a mammal (the mammal has a condition characterised by fluid
 XX accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 XX or brain. The peptides are used to image blood vessels and lymphatic
 XX vasculature. The monomeric and bicyclic peptides are used to interfere
 XX with at least one biological activity induced by VEGF, VEGF-C or -D and
 XX are also used in combination with an anti-inflammatory agent, to treat a
 XX chronic inflammation, especially rheumatoid arthritis, psoriasis and
 XX diabetic retinopathy

XX Sequence 13 AA;
 XX
 XX Query Match 90.3%; Score 65; DB 4; Length 13;
 XX Best Local Similarity 84.6%; Pred. No. 0.00033;
 XX Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 CASELGKSTNTFC 13
 XX |||||:|||||
 XX Db 1 CASELGKSTNTFC 13

RESULT 5
 AAU04536
 ID AAU04536 standard; peptide; 13 AA.
 XX AC AAU04536;
 XX DT 26-SEP-2001 (first entry)
 XX DE VEGF based monocyclic peptide 14.
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 XX neovascularisation; lymphangiogenesis; psoriasis; tumour;

KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.

OS Synthetic.

XX Key Location/Qualifiers
 FH Disulfide-bond 1..13
 FT /note= "This bond cyclises the peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

XX 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.

XX Example 25; Page 47; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGF (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides), and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy

XX Sequence 13 AA;

Query Match 84.7%; Score 61; DB 4; Length 13;
 Best Local Similarity 76.9%; Pred. No. 0.0016; Indels 0; Gaps 0;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
 |||:|||||:
 Db 1 CASDVGKSTNTWC 13

RESULT 6

AA57039

ID AAY57039 standard; peptide; 12 AA.

XX AAY57039;
 AC 21-FEB-2000 (first entry)
 XX Feline immunodeficiency virus env precursor peptide #2.
 DE Feline immunodeficiency virus; FIV; infection; diagnosis; gp130; p55;
 KW immunogenic fragment; antibody; env precursor; gag precursor; cat;
 KW antibody binding composition.
 XX Feline immunodeficiency virus.
 OS EP962774-A1.
 XX 08-DEC-1999.
 XX 14-MAY-1999; 99EP-00303760.
 XX 15-MAY-1998; 98US-0085615P.
 PR 03-JUN-1998; 98US-00089878.
 XX (IDEX-) IDEXX LAB INC.
 XX Groat RG, Mermer B, O'Connor TP;
 XX WPI; 2000-025671/03.
 XX Diagnosing Feline Immunodeficiency Virus infection.
 XX Claim 6; Page 9; 15pp; English.
 CC This sequence is a fragment of feline immunodeficiency virus (FIV)
 CC glycoprotein 130. Peptides AAY57038-Y57039 are used in the invention as
 CC capture polypeptides when diagnosing FIV infection. The invention relates
 CC to an antibody binding composition which consists of an enhanced capture
 CC polypeptide, which contains an immunogenic fragment of FIV gag precursor
 CC p55, and a second fragment which is part of the env precursor gp130, and
 CC an antibody-binding detection composition. The invention also includes a
 CC device for performing an assay which determines whether a feline is
 CC infected with FIV. The novel method is used for the diagnosis of Feline
 CC Immunodeficiency Virus infection
 XX Sequence 12 AA;
 Query Match 44.4%; Score 32; DB 3; Length 12;
 Best Local Similarity 60.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 4 ELGKSTNTFC 13
 |||:|:
 Db 2 ELGQNQFC 11
 RESULT 7
 ID AAY57039 standard; peptide; 13 AA.
 XX AAY57039;
 AC 01-OCT-2002 (first entry)
 XX Immunoglobulin binding peptide #14.
 DE Immunoglobulin binding peptide #14.
 KW Immunoglobulin binding peptide; autoimmune disease; rheumatoid arthritis;
 KW multiple sclerosis; myasthenia gravis; immunosuppressive; antirheumatic;
 KW neuroprotective.
 XX Synthetic.
 XX WO200238592-A2.
 XX 16-MAY-2002.

XX 08-NOV-2001; 2001WO-EP012933.
 XX 08-NOV-2000; 2000EP-00124418.
 XX (AFI-) AFFINA IMMUNTECHNIK GMBH.
 XX Egner R, Winkler D, Roenspeck W, Kunze R;
 XX WPI; 2002-557447/59.
 XX
 XX New immunoglobulin-binding peptides, useful for removing autoantibodies
 PT from serum, e.g. for treating rheumatism, also related solid phases.
 XX
 XX Claim 3; Page 40; 54pp; German.
 XX
 XX The present invention relates to immunoglobulin binding peptides. These
 CC can be used to remove autoantibodies from solutions, particularly
 CC autoantibodies associated with autoimmune diseases such as rheumatism,
 CC multiple sclerosis and myasthenia gravis, from body fluids. The present
 CC sequence is a peptide of the invention
 XX
 XX Sequence 13 AA;
 SQ
 Query Match 44.4%; Score 32; DB 5; Length 13;
 Best Local Similarity 85.7%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CASELCK 7
 DB |||||
 2 CASHLCK 8
 RESULT 8
 AAY66781
 ID AAY66781 standard; peptide; 13 AA.
 XX
 AC AAY66781;
 XX
 DT 11-APR-2000 (first entry)
 XX
 DE T cell antigen receptor Vbeta 5 chain peptide.
 XX
 KW Rheumatoid arthritis; arthrosis deformans; T-cell antigen receptor;
 KW Vbeta chain; autoantigen; immunological tolerance.
 XX
 OS Homo sapiens.
 XX
 PN WO9963084-A1.
 XX
 PD 09-DEC-1999.
 XX
 PF 28-MAY-1999; 99WO-JP002814.
 XX
 PR 29-MAY-1998; 98JP-00149855.
 PR 14-OCT-1998; 98JP-00328761.
 XX
 PA (TORI) TORII PHARM CO LTD.
 XX
 PI Nishioka K, Yoshino S;
 XX
 DR WPI; 2000-086978/07.
 DR N-PSDB; AA296511.
 XX
 PT T-cell antigen receptor V-beta chain CDR3 region sequences accumulated in
 PT synovial membranes of rheumatoid arthritis patients.
 XX
 PS Example 3; Page 25; 136pp; Japanese.
 XX
 CC The invention relates to peptide sequences present in the synovial fluid
 CC and membranes of rheumatoid arthritis patients, arising from the CDR
 CC region of oligoclonal pathogenic T-cell antigen receptor Vbeta chains.
 CC Compositions which contain autoantigenic peptides binding specifically to

CC T-cells expressing receptors containing the peptide sequences, which
 CC include antigen-specific immunological tolerance to rheumatoid arthritis
 CC can be used for the treatment and prevention of rheumatoid arthritis. The
 CC invention can be used for the diagnosis, treatment and prevention of
 CC rheumatoid arthritis. Sequences AAY66771-958 represent peptides from the
 CC various Vbeta chains of T cell antigen receptor
 XX
 XX Sequence 13 AA;
 SQ
 Query Match 41.7%; Score 30; DB 3; Length 13;
 Best Local Similarity 41.7%; Pred. No. 3.1e+02;
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CASELCKSTNTP 12
 DB |||||
 2 CASSIGTNNEQF 13
 RESULT 9
 AAB75626
 ID AAB75626 standard; peptide; 10 AA.
 XX
 AC AAB75626;
 XX
 DT 10-APR-2001 (first entry)
 XX
 DE HLA class I binding motif in HOM-TES-84 SEQ ID NO:29.
 XX
 KW Human; cancer associated antigen precursor; cancer associated antigen;
 KW seminoma; HLA; human leukocyte antigen; cytostatic; gene therapy;
 XX
 KW vaccine; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200100874-A2.
 XX
 PD 04-JAN-2001.
 XX
 PF 23-JUN-2000; 2000WO-US017207.
 XX
 PR 30-JUN-1999; 99US-00346498.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Sahin U, Tureci O, Pfrendschuh M;
 XX
 DR WPI; 2001-112465/12.
 XX
 PT Diagnosing a disorder characterized by expression of a human cancer
 PT associated antigen precursor, comprises detecting interaction of an agent
 PT with a nucleic acid molecule encoding the antigen precursor.
 XX
 PS Example 10; Page 62; 126pp; English.
 XX
 CC The present invention describes a method for diagnosing a disorder
 CC characterised by expression of a human cancer associated antigen (CAA)
 CC precursor (I) coded by a NA Group 1 nucleic acid molecule (N1) comprising
 CC contacting the biological sample with an agent (A) that specifically
 CC binds to N1, (I) or its fragment, complexed with an human leukocyte
 CC antigen (HLA) molecule and determining the interaction between the agent
 CC and N1 or (I). (I) has cytostatic activity and can be used in gene
 CC therapy and vaccine production. The method can be used for treating a
 CC subject with a condition characterised by expression of (I) in cells of a
 CC subject. AAB75607 and AAB75608 represent proteins from human cancer
 CC associated antigen precursors, and AAB75609 to AAB75802 represent HLA
 CC class I binding motifs in human cancer associated antigen precursors
 CC given in the exemplification of the present invention
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 40.3%; Score 29; DB 4; Length 10;
 Best Local Similarity 60.0%; Pred. No. 3.4e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 ELGKSTNTFC 13
: || || ||
Db 1 KLGPSEFNTNC 10

RESULT 10

AAV66787
ID AAV66787 standard; peptide; 13 AA.

XX AC AAV66787;

XX DT 11-APR-2000 (first entry)

XX DE T cell antigen receptor Vbeta 10 chain peptide.

XX KW Rheumatoid arthritis; arthrosis deformans; T-cell antigen receptor;
Vbeta chain; autoantigen; immunological tolerance.

XX OS Homo sapiens.

XX PN WO963084-A1.

XX PD 09-DEC-1999.

XX PF 28-MAY-1999; 99WO-JP002814.

XX PR 29-MAY-1998; 98JP-00149855.

XX FR 14-OCT-1998; 98JP-00328761.

XX PA (TORI) TORII PHARM CO LTD.

XX PI Nishioka K, Yoshino S;

XX DR WPI; 2000-086978/07.

XX DR N-PSDB; AAZ96517.

XX PT T-cell antigen receptor V-beta chain CDR3 region sequences accumulated in
synovial membranes of rheumatoid arthritis patients.

XX PS Example 3; Page 29; 136pp; Japanese.

XX CC The invention relates to peptide sequences present in the synovial fluid
and membranes of rheumatoid arthritis patients, arising from the CDR
region of oligoclonal pathogenic T-cell antigen receptor Vbeta chains.
XX CC Compositions which contain autoantigenic peptides binding specifically to
T-cells expressing receptors containing the peptide sequences, which
include antigen-specific immunological tolerance to rheumatoid arthritis
can be used for the treatment and prevention of rheumatoid arthritis. The
invention can be used for the diagnosis, treatment and prevention of
rheumatoid arthritis. Sequences AAV66771-958 represent peptides from the
various Vbeta chains of T cell antigen receptor

XX SQ Sequence 13 AA;

Query Match 40.3%; Score 29; DB 3; Length 13;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CASELGKST 9

Db 2 CASSKGTST 10

RESULT 11

ABJ04095
ID ABJ04095 standard; peptide; 13 AA.

XX AC ABJ04095;

XX DT 01-OCT-2002 (first entry)

XX DE Immunoglobulin binding peptide #15.

XX KW Immunoglobulin binding peptide; autoimmune disease; rheumatoid arthritis;
multiple sclerosis; myasthenia gravis; immunosuppressive; antirheumatic;
neuroprotective.

XX OS Synthetic.

XX PN WO200238592-A2.

XX PD 16-MAY-2002.

XX PF 08-NOV-2001; 2001WO-EP012933.

XX PR 08-NOV-2000; 2000EP-00124418.

XX PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.

XX PI Egner R, Winkler D, Roenspeck W, Kunze R;

XX DR WPI; 2002-557447/59.

XX CC New immunoglobulin-binding peptides, useful for removing autoantibodies
from serum, e.g. for treating rheumatism, also related solid phases.

XX PS Claim 3; Page 40; 54pp; German.

XX CC The present invention relates to immunoglobulin binding peptides. These
can be used to remove autoantibodies from solutions, particularly
autoantibodies associated with autoimmune diseases such as rheumatism,
multiple sclerosis and myasthenia gravis, from body fluids. The present
sequence is a peptide of the invention

XX SQ Sequence 13 AA;

Query Match 40.3%; Score 29; DB 5; Length 13;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELGK 7

Db 2 CATHLGK 8

RESULT 12

AAV48678

ID AAV48678 standard; peptide; 9 AA.

XX AC AAV48678;

XX DT 20-MAR-2003 (revised)

XX DT 10-DEC-1999 (first entry)

XX DE Membrane dipeptidase-binding lung homing peptide #49.
XX KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
membrane dipeptidase.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9946284-A2.

XX PD 16-SEP-1999.

XX PF 10-MAR-1999; 99WO-US005284.

XX PR 13-MAR-1998; 98US-00042107.

XX PR 26-FEB-1999; 99US-00258754.

XX PA (BURN-) BURNHAM INST.

XX PI Rajotte D, Pasqualini R, Ruoslahti EI;

XX WPI; 1999-571717/48.
 XX New peptides which selectively home to organs or tissues, used for, e.g.
 PT identifying target ligands and for therapy of pathological conditions.
 XX
 XX Example 6; Page 144; 193pp; English.
 XX
 CC The present invention describes peptides that selectively home to a
 CC tissue or organ. The peptides can be used for identifying an organ or
 CC tissue, for identifying a target molecule expressed by an organ or tissue
 CC or for treating an organ or tissue pathology, where the organ or tissue
 CC is selected from prostate, lung, skin, retina, pancreas, gut, ovary,
 CC adrenal gland, liver, and lymph node. The peptide bind to the membrane
 CC dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are
 CC used in the exemplification of the present invention. (Updated on 20-MAR-
 CC 2003 to correct PR field.)
 XX
 SQ Sequence 9 AA;
 Query Match 38.9%; Score 28; DB 2; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 7 KSTNTFC 13
 Db :|||||
 3 RSTNTGC 9
 RESULT 13
 AAB10896
 ID AAB10896 standard; protein; 9 AA.
 XX
 AC AAB10896;
 XX
 DT 26-JAN-2001 (first entry)
 XX
 DE Human 9D7 protein immunogenic fragment SEQ ID NO: 55.
 XX
 XX Tumor-associated antigen; 9D7; human; cytostatic; immunogenic;
 KW immunotherapy; cancer; cellular anticancer vaccine; diagnostic; kidney;
 KW lung; colon; breast; carcinoma; Hodgkin's lymphoma.
 XX
 OS Homo sapiens.
 XX
 XX DE19909503-A1.
 XX
 XX 07-SEP-2000.
 XX
 PF 04-MAR-1999; 99DE-01009503.
 XX
 PR 04-MAR-1999; 99DE-01009503.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX
 PI Klade C, Adolf G, Sommergruber W, Heider K;
 XX
 XX WPI; 2000-588357/56.
 XX
 XX New tumor-associated antigen 9D7, useful e.g. for immunotherapy of cancer
 PT and for producing diagnostic or therapeutic antibodies.
 PT
 PS Claim 6; Page 45; 50pp; German.
 XX
 CC This invention describes a novel tumor-associated antigen, designated 9D7
 CC which has cytostatic activity. The invention also describes a method for
 CC isolating (a) a polypeptide (i) that includes (SI) as part of its
 CC sequence; (b) an immunogenic protein fragment or peptide (II) derived
 CC from 9D7; (c) a pharmaceutical composition containing at least 1 of 9D7,
 CC (I) or (II) as active ingredients; (d) an isolated DNA (III) encoding a
 CC protein (IV) with the immunogenic properties of 9D7 or its fragments; (e)
 CC a recombinant DNA (IIIA) that includes (III); and (f) antibodies (Ab)
 CC directed against 9D7, (I) or (II). 9D7, or its derived immunogenic

CC peptides, are used to induce a humoral and/or cellular response for use
 CC in vivo or ex vivo immunotherapy of cancer. DNA (III) that encodes 9D7
 CC can be used similarly and cells that express 9D7 are useful in cellular
 CC anticancer vaccines. Antibodies (Ab) specific for 9D7 are useful for
 CC imaging, diagnosing and monitoring cancers, also, when conjugated to
 CC cytotoxic or radionuclide, as therapeutic agents. Peptides derived from
 CC 9D7 may also be used diagnostically to test for an immune response. 9D7-
 CC associated cancers are particularly kidney, lung, colon and breast
 CC carcinoma and Hodgkin's lymphoma. AAB10874-B10899 represent immunogenic
 CC fragments of the human tumor-associated antigen 9D7 which is described in
 CC the method of the invention
 XX
 SQ Sequence 9 AA;
 Query Match 38.9%; Score 28; DB 3; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 CASELGGK 7
 Db :|||||
 3 CGSLRGK 9
 RESULT 14
 AAE26783
 ID AAE26783 standard; peptide; 9 AA.
 XX
 AC AAE26783;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Fibrin binding peptide #36.
 XX
 XX Fibrin binding peptide; thrombosis; pulmonary embolism; atherosclerosis;
 KW myocardial infarct; ischemia; imaging; rheumatoid arthritis; vasotropic;
 KW anaemia; hypoxia; tumour; diabetic retinopathy; autoimmune disorder;
 XX inflammatory disorder; angiogenesis; stroke; cerebroprotective.
 OS Unidentified.
 XX
 XX WO200255544-A2.
 XX
 PD 18-JUL-2002.
 XX
 PF 21-DEC-2001; 2001WO-US049534.
 XX
 PR 23-DEC-2000; 2000US-00747403.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Wescott CR, Beltzer JP, Sato AK;
 XX
 DR WPI; 2002-666875/71.
 XX
 PT Novel synthetic fibrin-binding moiety, useful for detecting, imaging or
 PT localizing fibrin-containing clots by magnetic resonance imaging,
 PT radioimaging and for treating diseases involving thrombus formation e.g.
 PT stroke.
 XX
 XX Claim 4; Page 55; 89pp; English.
 XX
 CC The invention relates to a synthetic fibrin binding group having affinity
 CC for fibrin. The invention is useful for detecting fibrin in a mammalian
 CC subject which involves (a) detectably labelling the binding group; (b)
 CC administering to the subject the labelled polypeptide, and (c) detecting
 CC the labelled polypeptide in the subject. The invention is useful for
 CC treating a disease involving thrombus formation eg. deep-vein thrombosis,
 CC pulmonary embolism, cardiogenic thrombosis, atherosclerosis, myocardial
 CC infarct, reperfusion ischaemia or stroke. The binding moieties are useful
 CC for detection, imaging and localisation of fibrin-containing clots by
 CC magnetic resonance imaging, radioimaging and other imaging methods and
 CC are also useful in the diagnosis and treatment of coronary conditions
 CC where fibrin plays a role. The fibrin binding moieties are useful for

CC detecting and diagnosing numerous pathophysiologicals in which fibrin plays
 CC a role eg. peritoneal adhesions which often occur after surgery or
 CC inflammatory and neoplastic processes and are comprised of a fibrin
 CC network, fibroblasts, macrophages and new blood vessels; rheumatoid
 CC arthritis, lupus or septic arthritis which often have bits of fibrin
 CC containing tissues called rice bodies in the synovial fluid of their
 CC joints; thrombocytopenic purpura, a type of anaemia in which deposits in
 CC arterioles causes turbulent blood flow resulting in stress and
 CC destruction of red blood cells. The fibrin specific agents can also be
 CC used to detect hypoxia or ischaemia of heart, kidney, liver, lung, brain
 CC or other organs, as well as the detection of tumours, diabetic
 CC retinopathy, early or high-risk atherosclerosis and other autoimmune and
 CC inflammatory disorders. Fibrin specific agents also could provide both
 CC direct or surrogate markers of disease models in which hypoxia and
 CC angiogenesis are expected to play a role. The invention is also useful
 CC for screening molecular libraries. The present sequence is a fibrin
 CC binding peptide
 XX

SQ Sequence 9 AA;

Query Match 38.9%; Score 28; DB 5; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GKSTWTC 13
 | : : |||
 Db 2 QGESRTEC 9

RESULT 15

ID AAB10895
 ID AAB10895 standard; protein; 10 AA.

AC AAB10895;

DT 26-JAN-2001 (first entry)

DE Human 9D7 protein immunogenic fragment SEQ ID NO: 54.

KW Tumor-associated antigen; 9D7; human; cytostatic; immunogenic;
 KW immunotherapy; cancer; cellular anticancer vaccine; diagnostic; kidney;
 KW lung; colon; breast; carcinoma; Hodgkin's lymphoma.

OS Homo sapiens.

PN DE19909503-A1.

PD 07-SEP-2000.

PF 04-MAR-1999; 99DE-01009503.

PR 04-MAR-1999; 99DE-01009503.

PA (BOEHR) BOEHRINGER INGELHEIM INT GMBH.

PI Klade C, Adolf G, Sommergruber W, Heider K;

DR WPI; 2000-588357/56.

PT New tumor-associated antigen 9D7, useful e.g. for immunotherapy of cancer
 PT and for producing diagnostic or therapeutic antibodies.

PS Claim 6; Page 45; 50pp; German.

XX This invention describes a novel tumor-associated antigen, designated 9D7
 CC which has cytostatic activity. The invention also describes a method for
 CC isolating (a) a polypeptide (I) that includes (SI) as part of its
 CC sequence; (b) an immunogenic protein fragment or peptide (II) derived
 CC from 9D7; (c) a pharmaceutical composition containing at least 1 of 9D7,
 CC (I) or (II) as active ingredients; (d) an isolated DNA (III) encoding a
 CC protein (IV) with the immunogenic properties of 9D7 or its fragments; (e)
 CC a recombinant DNA (IIIA) that includes (III); and (f) antibodies (Ab)
 CC directed against 9D7, (I) or (II). 9D7, or its derived immunogenic

CC peptides, are used to induce a humoral and/or cellular response for use
 CC in vivo or ex vivo immunotherapy of cancer. DNA (III) that encodes 9D7
 CC can be used similarly and cells that express 9D7 are useful in cellular
 CC anticancer vaccines. Antibodies (Ab) specific for 9D7 are useful for
 CC imaging, diagnosing and monitoring cancers, also, when conjugated to
 CC cytotoxins or radionuclide, as therapeutic agents. Peptides derived from
 CC 9D7 may also be used diagnostically to test for an immune response. 9D7-
 CC associated cancers are particularly kidney, lung, colon and breast
 CC carcinoma and Hodgkin's lymphoma. AAB10874-B10899 represent immunogenic
 CC fragments of the human tumor-associated antigen 9D7 which is described in
 CC the method of the invention
 XX

SQ Sequence 10 AA;

Query Match 38.9%; Score 28; DB 3; Length 10;
 Best Local Similarity 71.4%; Pred. No. 5.1e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELGG 7
 | : : |||
 Db 4 CGSRLLGK 10

Search completed: March 8, 2004, 11:54:09
 Job time : 55 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:55:29 ; Search time 32 Seconds
(without alignments)
85.781 Million cell updates/sec

Title: US-09-761-636A-5
Perfect score: 72
Sequence: 1 CASELCKSTNTFC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues 142886
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubaa/US06_PUBCOMB.pep.*
4: /cgn2_6/ptodata/2/pubaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubaa/US09C_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	72	100.0	13	9 US-09-761-636A-5	Sequence 5, Appl
2	69	95.8	13	9 US-09-761-636A-15	Sequence 15, Appl
3	65	90.3	13	9 US-09-761-636A-16	Sequence 16, Appl
4	65	90.3	13	9 US-09-761-636A-18	Sequence 18, Appl
5	61	84.7	13	9 US-09-761-636A-17	Sequence 17, Appl
6	30	41.7	10	14 US-10-208-304-14	Sequence 14, Appl
7	28	38.9	9	14 US-10-034-974-55	Sequence 55, Appl
8	27	37.5	10	10 US-09-573-822C-626	Sequence 626, App
9	27	37.5	10	14 US-10-271-343-19	Sequence 19, Appl
10	27	37.5	12	10 US-09-791-393-262	Sequence 262, App
11	27	37.5	12	10 US-09-791-393-262	Sequence 262, App
12	27	37.5	13	14 US-10-322-210-67	Sequence 67, Appl
13	27	37.5	13	14 US-10-304-443-67	Sequence 67, Appl
14	26	36.1	8	9 US-09-795-006A-140	Sequence 140, App
15	26	36.1	9	15 US-10-117-937-572	Sequence 572, App

16	26	36.1	9	15 US-10-044-844-70	Sequence 70, Appl
17	26	36.1	10	10 US-09-572-404B-2743	Sequence 2743, Ap
18	26	36.1	10	10 US-09-572-404B-3191	Sequence 3191, Ap
19	26	36.1	10	10 US-09-572-270A-956	Sequence 956, App
20	26	36.1	10	14 US-10-208-304-12	Sequence 12, Appl
21	26	36.1	10	14 US-10-208-304-13	Sequence 13, Appl
22	26	36.1	10	14 US-10-208-304-15	Sequence 15, Appl
23	26	36.1	10	14 US-10-208-304-16	Sequence 16, Appl
24	26	36.1	10	15 US-10-117-937-573	Sequence 573, App
25	26	36.1	13	10 US-09-792-686A-26	Sequence 26, Appl
26	26	36.1	10	14 US-10-271-343-17	Sequence 17, Appl
27	25	34.7	13	10 US-09-792-686A-28	Sequence 28, Appl
28	25	34.7	13	14 US-10-148-786A-35	Sequence 35, Appl
29	24.5	34.0	10	13 US-10-046-922-57	Sequence 57, Appl
30	24	33.3	8	14 US-10-195-142-32	Sequence 32, Appl
31	24	33.3	8	14 US-10-281-478-150	Sequence 150, App
32	24	33.3	10	15 US-10-114-669-190	Sequence 190, App
33	24	33.3	10	15 US-10-114-669-5800	Sequence 5800, Ap
34	24	33.3	10	15 US-10-114-669-5983	Sequence 5983, Ap
35	24	33.3	10	15 US-10-114-669-6053	Sequence 6053, Ap
36	24	33.3	10	15 US-10-114-669-6355	Sequence 6355, Ap
37	24	33.3	10	15 US-10-114-669-6654	Sequence 6654, Ap
38	24	33.3	10	15 US-10-114-669-6792	Sequence 6792, Ap
39	24	33.3	10	15 US-10-114-669-7062	Sequence 7062, Ap
40	24	33.3	11	15 US-10-449-659-77	Sequence 77, Appl
41	24	33.3	11	15 US-10-324-143-122	Sequence 122, App
42	24	33.3	13	10 US-09-747-802-5	Sequence 5, Appl
43	24	33.3	13	10 US-09-880-748-2991	Sequence 2991, Ap
44	23	31.9	8	14 US-10-239-313A-96	Sequence 96, Appl
45	23	31.9	8	14 US-10-348-232-224	Sequence 224, App

ALIGNMENTS

RESULT 1

US-09-761-636A-5
; Sequence 5, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-5

Query Match 100.0%; Score 72; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELCKSTNTFC 13
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DB 1 CASELCKSTNTFC 13

RESULT 2

US-09-761-636A-15
; Sequence 15, Application US/09761636A
; Patent No. US20020065218A1

GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-15

Query Match 95.8%; Score 69; DB 9; Length 13;
Best Local Similarity 92.3%; Pred. No. 1.4e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
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Db 1 CATELGKSTNTFC 13

RESULT 3
US-09-761-636A-16
; Sequence 16, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-16

Query Match 90.3%; Score 65; DB 9; Length 13;
Best Local Similarity 84.6%; Pred. No. 6.9e-05;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
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Db 1 CASELGKSTNTFC 13

RESULT 4
US-09-761-636A-18
; Sequence 18, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela

; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
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; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-18

Query Match 90.3%; Score 65; DB 9; Length 13;
Best Local Similarity 84.6%; Pred. No. 6.9e-05;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
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Db 1 CASELGKSTNTFC 13

RESULT 5
US-09-761-636A-17
; Sequence 17, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-17

Query Match 84.7%; Score 61; DB 9; Length 13;
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Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
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Db 1 CASELGKSTNTFC 13

RESULT 6
US-10-208-304-14
; Sequence 14, Application US/10208304
; Publication No. US20030124571A1
; GENERAL INFORMATION:
; APPLICANT: Larisch, Sarit
; APPLICANT: Kim, Seong-Jin
; APPLICANT: Lechleider, Robert J.
; APPLICANT: Roberts, Anita B.
; APPLICANT: Yi, Youngseuk
; TITLE OF INVENTION: NOVEL HUMAN SEPTIN AND USES THEREFOR
; FILE REFERENCE: 11613.42USW1
; CURRENT APPLICATION NUMBER: US/10/208,304
; CURRENT FILING DATE: 2002-07-29

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; PRIOR APPLICATION NUMBER: PCT/US01/02466
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/178,866
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/258,725
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Drosophila
US-10-208-304-14

Query Match 41.7%; Score 30; DB 14; Length 10;
Best Local Similarity 87.5%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
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Db 2 ASGLGKST 9

RESULT 7
US-10-034-974-55
; Sequence 55, Application US/10034974
; Publication No. US20030143158A1
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP.
; APPLICANT: Beltzer, James P.
; APPLICANT: Wescott, Charles R.
; TITLE OF INVENTION: FIBRIN BINDING MOIETIES USEFUL AS IMAGING AGENTS
; FILE REFERENCE: DYX-024.1 PCT; DYX-024.1 US
; CURRENT APPLICATION NUMBER: US/10/034,974
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 09/747,403
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 55
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fibrin binding polypeptides
US-10-034-974-55

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Best Local Similarity 50.0%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GKSTNTFC 13
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Db 2 QGESRTFC 9

RESULT 8
US-09-573-822C-626
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; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 626
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium

; PRIOR APPLICATION NUMBER: PCT/US01/02466
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/178,866
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/258,725
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Drosophila
US-10-208-304-14

Query Match 41.7%; Score 30; DB 14; Length 10;
Best Local Similarity 87.5%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
   |||||
Db 2 ASGLGKST 9

RESULT 7
US-10-034-974-55
; Sequence 55, Application US/10034974
; Publication No. US20030143158A1
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP.
; APPLICANT: Beltzer, James P.
; APPLICANT: Wescott, Charles R.
; TITLE OF INVENTION: FIBRIN BINDING MOIETIES USEFUL AS IMAGING AGENTS
; FILE REFERENCE: DYX-024.1 PCT; DYX-024.1 US
; CURRENT APPLICATION NUMBER: US/10/034,974
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 09/747,403
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 55
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fibrin binding polypeptides
US-10-034-974-55

Query Match 38.9%; Score 28; DB 14; Length 9;
Best Local Similarity 50.0%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GKSTNTFC 13
   .:|:|
Db 2 QGESRTFC 9

RESULT 8
US-09-573-822C-626
; Sequence 626, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 626
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium

; FEATURE:
; OTHER INFORMATION: Sequence located in MG309 at 847-856 and may interact with Sequ
; OTHER INFORMATION: in this patent.
US-09-573-822C-626

Query Match 37.5%; Score 27; DB 10; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

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Db 1 AKLSRTTNSF 10

RESULT 9
US-10-271-343-19
; Sequence 19, Application US/10271343
; Publication No. US2003016603A1
; GENERAL INFORMATION:
; APPLICANT: Cochran, Andrea G.
; APPLICANT: Skelton, Nicholas J.
; APPLICANT: Starovasnik, Melissa A.
; TITLE OF INVENTION: A STRUCTURED PEPTIDE SCAFFOLD FOR DISPLAYING TURN LIBRARIES
; TITLE OF INVENTION: ON PHAGE
; FILE REFERENCE: 11669.116US11
; CURRENT APPLICATION NUMBER: US/10/271,343
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/592,695
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 60/139,017
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 19
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Turn Peptide
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa is independently Trp, Tyr, Leu, Val, or Thr
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (5)..(5)
; OTHER INFORMATION: Xaa is D-pro
US-10-271-343-19

Query Match 37.5%; Score 27; DB 14; Length 10;
Best Local Similarity 55.6%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELGKST 9
   |||||
Db 1 CTXEXGKLT 9

RESULT 10
US-09-791-393-262
; Sequence 262, Application US/09791393
; Publication No. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
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; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 262
; LENGTH: 12
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-262

Query Match      37.5%; Score 27; DB 10; Length 12;
Best Local Similarity 57.1%; Pred. No. 3.4e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELKG 7
Db 6 CTTELGR 12

RESULT 11
US-09-791-389-262
; Sequence 262, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Wadiyanselage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; APPLICANT: Tarratt, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 262
; LENGTH: 12
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-262

Query Match      37.5%; Score 27; DB 10; Length 12;
Best Local Similarity 57.1%; Pred. No. 3.4e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELKG 7
Db 6 CTTELGR 12

RESULT 12
US-09-791-389-262
; Sequence 67, Application US/10322210
; Publication No. US20030147906A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Mason, Sean
; APPLICANT: Turnell, William Gordon
; APPLICANT: Van Mecheien, Marcelle Paulette
; APPLICANT: Vinals Y de Bassols, Carlotia
; TITLE OF INVENTION: Epitopes or Mimotopes Derived from the
; TITLE OF INVENTION: C-Epsilon-3 or C-Epsilon-4 Domains of IgE, Antagonists

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; TITLE OF INVENTION: Thereof, and Their Therapeutic Uses
; FILE REFERENCE: B45173
; CURRENT APPLICATION NUMBER: US/10/322,210
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/09/914,089
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: GB 9904408.3
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: GB 9917144.9
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: GB 9918598.5
; PRIOR FILING DATE: 1999-08-07
; PRIOR APPLICATION NUMBER: GB 9918599.3
; PRIOR FILING DATE: 1999-08-07
; PRIOR APPLICATION NUMBER: GB 9918601.7
; PRIOR FILING DATE: 1999-08-07
; PRIOR APPLICATION NUMBER: GB 9918604.1
; PRIOR FILING DATE: 1999-08-07
; PRIOR APPLICATION NUMBER: GB 9918606.6
; PRIOR FILING DATE: 1999-08-07
; PRIOR APPLICATION NUMBER: GB 9925618.2
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric
US-10-322-210-67

Query Match      37.5%; Score 27; DB 14; Length 13;
Best Local Similarity 38.5%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 CASELKGKSTNTFC 13
Db 1 CSRASGKPVNHC 13

RESULT 13
US-10-304-443-67
; Sequence 67, Application US/10304443
; Publication No. US20030170229A1
; GENERAL INFORMATION:
; APPLICANT: Smithkline Beecham Biologicals s.a.
; APPLICANT: Peptide Therapeutics Ltd.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45173CIP
; CURRENT APPLICATION NUMBER: US/10/304,443
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US/09/698,906A
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human peptide sequence
US-10-304-443-67

Query Match      37.5%; Score 27; DB 14; Length 13;
Best Local Similarity 38.5%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 CASELKGKSTNTFC 13
Db 1 CSRASGKPVNHC 13

RESULT 14
US-09-795-006A-140

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us-09-761-636a-5.closed.rapb

Mon Mar 8 13:10:57 2004

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; Sequence 140, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Altalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09795,006A
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 140
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
; US-09-795-006A-140
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Query Match 36.1%; Score 26; DB 9; Length 8;
Best Local Similarity 62.5%; Pred. No. 7.2e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY 4 ELGKSTNT 11
Db 1 EFGVAINT 8
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RESULT 15
US-10-117-937-572
; Sequence 572, Application US/10117937
; Publication No. US2003022039A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPIPOPE SEQUENCES
; FILE REFERENCE: CTLLM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 572
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-117-937-572
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Query Match 36.1%; Score 26; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 8 STNTEC 13
Db 2 ATNTIC 7
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Search completed: March 8, 2004, 12:00:41
Job time : 32 secs
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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:45:28 ; Search time 23 Seconds
(without alignments)

51.626 Million cell updates/sec

Title: US-09-761-636A-4
Perfect score: 133
Sequence: 1 QGQHIGEMSFLOHNCRCRPKD 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 186303

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	61.7	17	3	US-08-807-992B-25
2	73	54.9	12	3	US-08-742-243-2
3	73	54.9	12	3	US-08-742-243-63
4	73	54.9	12	3	US-08-742-243-64
5	71	53.4	12	3	US-08-742-243-62
6	70	52.6	12	3	US-08-742-243-65
7	67	50.4	12	3	US-08-742-243-61
8	66	49.6	12	3	US-08-742-243-60
9	63	47.4	12	3	US-08-742-243-59
10	56	42.1	12	3	US-08-742-243-3
11	56	42.1	12	3	US-08-742-243-66
12	54	40.6	12	3	US-08-742-243-58
13	51	38.3	14	3	US-08-807-992B-9
14	51	38.3	14	3	US-08-807-992B-12
15	51	38.3	18	1	US-08-327-709-2
16	51	38.3	18	2	US-08-464-956-2
17	51	38.3	18	3	US-08-807-992B-6
18	51	38.3	18	3	US-08-807-992B-15
19	51	38.3	18	3	US-08-807-992B-26
20	44	33.1	12	3	US-08-742-243-57
21	44	33.1	18	3	US-08-807-992B-19
22	42	31.6	12	3	US-08-742-243-67
23	36	27.1	22	1	US-08-484-635-143
24	36	27.1	22	2	US-08-484-631-143
25	36	27.1	22	2	US-08-827-570-143
26	34	25.6	12	3	US-08-742-243-56
27	33	24.8	10	1	US-08-039-137-23

28	33	24.8	15	2	US-08-752-852A-31	Sequence 31, Appl
29	33	24.8	15	2	US-08-752-852A-32	Sequence 32, Appl
30	33	24.8	15	2	US-08-752-852A-33	Sequence 33, Appl
31	33	24.8	15	2	US-08-752-852A-34	Sequence 34, Appl
32	33	24.8	15	2	US-08-752-852A-35	Sequence 35, Appl
33	33	24.8	15	2	US-08-752-852A-36	Sequence 36, Appl
34	33	24.8	15	2	US-08-752-852A-37	Sequence 37, Appl
35	33	24.8	15	2	US-08-752-852A-38	Sequence 38, Appl
36	33	24.8	20	3	US-08-786-690-5	Sequence 5, Appl
37	32	24.1	17	4	US-09-079-030-181	Sequence 181, App
38	32	24.1	22	3	US-08-782-480-25	Sequence 25, Appl
39	32	24.1	22	3	US-08-954-211-25	Sequence 25, Appl
40	32	24.1	22	4	US-09-005-167A-25	Sequence 25, Appl
41	32	24.1	22	4	US-09-176-741B-25	Sequence 25, Appl
42	31	23.3	12	2	US-08-244-496-81	Sequence 81, Appl
43	31	23.3	13	4	US-09-479-479-12	Sequence 12, Appl
44	31	23.3	13	4	US-09-297-851-12	Sequence 12, Appl
45	31	23.3	14	3	US-08-991-426-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-807-992B-25
; Sequence 25, Application US/08807992B
; Patent No. 6022541
; GENERAL INFORMATION:
; APPLICANT: Senger, Donald R
; APPLICANT: Dvorak, Harold P
; TITLE OF INVENTION: Immunological preparation for concurrent
; TITLE OF INVENTION: specific binding to spatially exposed regions of vascular
; TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated blood
; TITLE OF INVENTION: vessel
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Prashker, Esq.
; STREET: P.O. Box 5387
; CITY: Magnolia
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01930
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
; COMPUTER: IBM PS/1
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/807,992B
; FILING DATE: March 3, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: David Prashker, Esq.
; REGISTRATION NUMBER: 29,693
; REFERENCE/DOCKET NUMBER: BIS-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (978) 525-3794
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-807-992B-25

Query Match 61.7%; Score 82; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGQHIGEMSFLOHNC 15

|||||

Db 3 QGQHIGMSFLQHNK 17

RESULT 2

US-08-742-243-2
; Sequence 2, Application US/08742243A
; Patent No. 6024955
; GENERAL INFORMATION:
; APPLICANT: Asano, Makoto
; APPLICANT: Yukita, Ayako
; APPLICANT: Hanatani, Mitsuuya
; APPLICANT: Matsumoto, Tomoe
; APPLICANT: Okamoto, Masaji
; APPLICANT: Suzuki, Hideo
; TITLE OF INVENTION: Peptides And Monoclonal Antibodies
; FILE REFERENCE: 07898/005001
; CURRENT APPLICATION NUMBER: US/08/742,243A
; CURRENT FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: 308184/1995
; EARLIER FILING DATE: 1995-11-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthesized
; OTHER INFORMATION: peptide fragment
US-08-742-243-2

Query Match 54.9%; Score 73; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SFLQHNKCECRP 20

Db 1 SFLQHNKCECRP 12

RESULT 3

US-08-742-243-63
; Sequence 63, Application US/08742243A
; Patent No. 6024955
; GENERAL INFORMATION:
; APPLICANT: Asano, Makoto
; APPLICANT: Yukita, Ayako
; APPLICANT: Hanatani, Mitsuuya
; APPLICANT: Matsumoto, Tomoe
; APPLICANT: Okamoto, Masaji
; APPLICANT: Suzuki, Hideo
; TITLE OF INVENTION: Peptides And Monoclonal Antibodies
; FILE REFERENCE: 07898/005001
; CURRENT APPLICATION NUMBER: US/08/742,243A
; CURRENT FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: 308184/1995
; EARLIER FILING DATE: 1995-11-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthesized
; OTHER INFORMATION: peptide fragment
US-08-742-243-63

Query Match 54.9%; Score 73; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SFLQHNKCECRP 20

Db 1 SFLQHNKCECRP 12

RESULT 4

US-08-742-243-64
; Sequence 64, Application US/08742243A
; Patent No. 6024955
; GENERAL INFORMATION:
; APPLICANT: Asano, Makoto
; APPLICANT: Yukita, Ayako
; APPLICANT: Hanatani, Mitsuuya
; APPLICANT: Matsumoto, Tomoe
; APPLICANT: Okamoto, Masaji
; APPLICANT: Suzuki, Hideo
; TITLE OF INVENTION: Peptides And Monoclonal Antibodies
; FILE REFERENCE: 07898/005001
; CURRENT APPLICATION NUMBER: US/08/742,243A
; CURRENT FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: 308184/1995
; EARLIER FILING DATE: 1995-11-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthesized
; OTHER INFORMATION: peptide fragment
US-08-742-243-64

Query Match 54.9%; Score 73; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQHNKCECRPK 22

Db 1 LQHNKCECRPK 12

RESULT 5

US-08-742-243-62
; Sequence 62, Application US/08742243A
; Patent No. 6024955
; GENERAL INFORMATION:
; APPLICANT: Asano, Makoto
; APPLICANT: Yukita, Ayako
; APPLICANT: Hanatani, Mitsuuya
; APPLICANT: Matsumoto, Tomoe
; APPLICANT: Okamoto, Masaji
; APPLICANT: Suzuki, Hideo
; TITLE OF INVENTION: Peptides And Monoclonal Antibodies
; FILE REFERENCE: 07898/005001
; CURRENT APPLICATION NUMBER: US/08/742,243A
; CURRENT FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: 308184/1995
; EARLIER FILING DATE: 1995-11-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthesized
; OTHER INFORMATION: peptide fragment
US-08-742-243-62

Query Match 53.4%; Score 71; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EMSFLOHKNKC 18
| | | | | | | | | |
Db 1 EMSFLOHKNKC 12

RESULT 6

US-08-742-243-65
; Sequence 65, Application US/08742243A
; Patent No. 6024955
; GENERAL INFORMATION:
; APPLICANT: Asano, Makoto
; APPLICANT: Yukita, Ayako
; APPLICANT: Hanatani, Mitsuya
; APPLICANT: Matsumoto, Tomoe
; APPLICANT: Okamoto, Masaji
; APPLICANT: Suzuki, Hideo
; TITLE OF INVENTION: Peptides And Monoclonal Antibodies
; FILE REFERENCE: 07898/005001
; CURRENT APPLICATION NUMBER: US/08/742,243A
; CURRENT FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: 308184/1995
; EARLIER FILING DATE: 1995-11-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthesized
; OTHER INFORMATION: peptide fragment
US-08-742-243-65

Query Match 52.6%; Score 70; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 HNKCECRPKD 23
| | | | | | | | | |
Db 1 HNKCECRPKD 11

RESULT 7

US-08-742-243-61
; Sequence 61, Application US/08742243A
; Patent No. 6024955
; GENERAL INFORMATION:
; APPLICANT: Asano, Makoto
; APPLICANT: Yukita, Ayako
; APPLICANT: Hanatani, Mitsuya
; APPLICANT: Matsumoto, Tomoe
; APPLICANT: Okamoto, Masaji
; APPLICANT: Suzuki, Hideo
; TITLE OF INVENTION: Peptides And Monoclonal Antibodies
; FILE REFERENCE: 07898/005001
; CURRENT APPLICATION NUMBER: US/08/742,243A
; CURRENT FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: 308184/1995
; EARLIER FILING DATE: 1995-11-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthesized
; OTHER INFORMATION: peptide fragment
US-08-742-243-61

Query Match 50.4%; Score 67; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IGEMSFLOHNC 16
| | | | | | | | | |
Db 1 IGEMSFLOHNC 12

RESULT 8

US-08-742-243-60
; Sequence 60, Application US/08742243A
; Patent No. 6024955
; GENERAL INFORMATION:
; APPLICANT: Asano, Makoto
; APPLICANT: Yukita, Ayako
; APPLICANT: Hanatani, Mitsuya
; APPLICANT: Matsumoto, Tomoe
; APPLICANT: Okamoto, Masaji
; APPLICANT: Suzuki, Hideo
; TITLE OF INVENTION: Peptides And Monoclonal Antibodies
; FILE REFERENCE: 07898/005001
; CURRENT APPLICATION NUMBER: US/08/742,243A
; CURRENT FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: 308184/1995
; EARLIER FILING DATE: 1995-11-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthesized
; OTHER INFORMATION: peptide fragment
US-08-742-243-60

Query Match 49.6%; Score 66; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00064;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 OHIGEMSFLOHN 14
| | | | | | | | | |
Db 1 OHIGEMSFLOHN 12

RESULT 9

US-08-742-243-59
; Sequence 59, Application US/08742243A
; Patent No. 6024955
; GENERAL INFORMATION:
; APPLICANT: Asano, Makoto
; APPLICANT: Yukita, Ayako
; APPLICANT: Hanatani, Mitsuya
; APPLICANT: Matsumoto, Tomoe
; APPLICANT: Okamoto, Masaji
; APPLICANT: Suzuki, Hideo
; TITLE OF INVENTION: Peptides And Monoclonal Antibodies
; FILE REFERENCE: 07898/005001
; CURRENT APPLICATION NUMBER: US/08/742,243A
; CURRENT FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: 308184/1995
; EARLIER FILING DATE: 1995-11-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthesized
; OTHER INFORMATION: peptide fragment
US-08-742-243-59

Query Match 47.4%; Score 63; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0019;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGQHIGMSFLQ 12
| | | | | | | | | |
DB 1 QGQHIGMSFLQ 12

RESULT 10

US-08-742-243-3
; Sequence 3, Application US/08742243A
; Patent No. 6024955
; GENERAL INFORMATION:
; APPLICANT: Asano, Makoto
; APPLICANT: Yukita, Ayako
; APPLICANT: Hanatani, Mitsuya
; APPLICANT: Matsumoto, Tomoe
; APPLICANT: Okamoto, Masaji
; APPLICANT: Suzuki, Hideo
; TITLE OF INVENTION: Peptides And Monoclonal Antibodies
; FILE REFERENCE: 07898/005001
; CURRENT APPLICATION NUMBER: US/08/742,243A
; CURRENT FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: 308184/1995
; EARLIER FILING DATE: 1995-11-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthesized
; OTHER INFORMATION: peptide fragment
US-08-742-243-3

Query Match 42.1%; Score 56; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 KCECRPKD 23
| | | | | | | | | |
DB 1 KCECRPKD 9

RESULT 11

US-08-742-243-66
; Sequence 66, Application US/08742243A
; Patent No. 6024955
; GENERAL INFORMATION:
; APPLICANT: Asano, Makoto
; APPLICANT: Yukita, Ayako
; APPLICANT: Hanatani, Mitsuya
; APPLICANT: Matsumoto, Tomoe
; APPLICANT: Okamoto, Masaji
; APPLICANT: Suzuki, Hideo
; TITLE OF INVENTION: Peptides And Monoclonal Antibodies
; FILE REFERENCE: 07898/005001
; CURRENT APPLICATION NUMBER: US/08/742,243A
; CURRENT FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: 308184/1995
; EARLIER FILING DATE: 1995-11-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthesized
; OTHER INFORMATION: peptide fragment
US-08-742-243-66

Query Match 42.1%; Score 56; DB 3; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 KCECRPKD 23
| | | | | | | | | |
DB 1 KCECRPKD 9

RESULT 12

US-08-742-243-58
; Sequence 58, Application US/08742243A
; Patent No. 6024955
; GENERAL INFORMATION:
; APPLICANT: Asano, Makoto
; APPLICANT: Yukita, Ayako
; APPLICANT: Hanatani, Mitsuya
; APPLICANT: Matsumoto, Tomoe
; APPLICANT: Okamoto, Masaji
; APPLICANT: Suzuki, Hideo
; TITLE OF INVENTION: Peptides And Monoclonal Antibodies
; FILE REFERENCE: 07898/005001
; CURRENT APPLICATION NUMBER: US/08/742,243A
; CURRENT FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: 308184/1995
; EARLIER FILING DATE: 1995-11-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthesized
; OTHER INFORMATION: peptide fragment
US-08-742-243-58

Query Match 40.6%; Score 54; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGQHIGMSF 10
| | | | | | | | | |
DB 3 QGQHIGMSF 12

RESULT 13

US-08-807-992B-9
; Sequence 9, Application US/08807992B
; Patent No. 6022541
; GENERAL INFORMATION:
; APPLICANT: Senger, Donald R
; APPLICANT: Dvorak, Harold F
; TITLE OF INVENTION: Immunological preparation for concurrent
; TITLE OF INVENTION: specific binding to spatially exposed regions of vascular
; TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated blood
; TITLE OF INVENTION: vessel
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Prashker, Esq.
; STREET: P.O. Box 5387
; CITY: Magnolia
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01930
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
; COMPUTER: IBM PS/1
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/807,992B
; FILING DATE: March 3, 1997
; CLASSIFICATION: 424


```
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: David Prashker, Esq.
/ REGISTRATION NUMBER: 29,693
/ REFERENCE/DOCKET NUMBER: BIS-033
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (978) 525-3794
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-08-807-992B-9
Query Match 38.3%; Score 51; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CECRPKDD 23
DB 1 CECRPKDD 8

RESULT 14
US-08-807-992B-12
/ Sequence 12, Application US/08807992B
/ Patent No. 6022541
/ GENERAL INFORMATION:
/ APPLICANT: Senger, Donald R
/ APPLICANT: Dvorak, Harold F
/ TITLE OF INVENTION: Immunological preparation for concurrent
/ TITLE OF INVENTION: specific binding to spatially exposed regions of vascular
/ TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated blood
/ TITLE OF INVENTION: vessel
/ NUMBER OF SEQUENCES: 31
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: David Prashker, Esq.
/ STREET: P.O. Box 5387
/ CITY: Magnolia
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 01930
/
COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
/ COMPUTER: IBM PS/1
/ OPERATING SYSTEM: MS DOS
/ SOFTWARE: WordPerfect version 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/807,992B
/ FILING DATE: March 3, 1997
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: David Prashker, Esq.
/ REGISTRATION NUMBER: 29,693
/ REFERENCE/DOCKET NUMBER: BIS-033
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (978) 525-3794
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-08-807-992B-12
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```
Query Match 38.3%; Score 51; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 16 CECRPKDD 23
DB 1 CECRPKDD 8
```

```
RESULT 15
US-08-327-709-2
/ Sequence 2, Application US/08327709
/ Patent No. 5659013
/ GENERAL INFORMATION:
/ APPLICANT: Donald R. Senger and Harold F.
/ APPLICANT: Dvorak
/ TITLE OF INVENTION: VASCULAR PERMEABILITY FACTOR
/ TITLE OF INVENTION: TARGETED COMPOUNDS
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/
COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ COMPUTER: IBM PS/2 Model 502 or 55SX
/ OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
/ SOFTWARE: WordPerfect (Version 5.0)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/327,709
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/779,384
/ FILING DATE: October 18, 1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 01948/024001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18
/ TYPE: amino acid
/ TOPOLOGY: linear
/
US-08-327-709-2
```

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Query Match 38.3%; Score 51; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 16 CECRPKDD 23
DB 1 CECRPKDD 8
```

```
Search completed: March 8, 2004, 11:48:48
Job time : 24 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:15:17 ; Search time 13 Seconds
(without alignments)
66.594 Million cell updates/sec

Title: US-09-761-636A-14

Perfect score: 52

Sequence: 1 CISVPLVPC 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 790

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	42.3	6	2	I65546
2	19	36.5	5	2	A60521
3	19	36.5	9	2	A60356
4	18	34.6	9	2	A61620
5	17	32.7	8	2	S10783
6	17	32.7	9	2	S66419
7	16	30.8	4	2	I51049
8	16	30.8	9	2	S13636
9	15	28.8	6	2	H48394
10	15	28.8	8	2	G33098
11	15	28.8	8	4	I54017
12	15	28.8	9	2	FT0080
13	14	26.9	7	2	I48105
14	14	26.9	8	2	S21288
15	14	26.9	9	2	D48186
16	14	26.9	9	2	PH0943
17	13	25.0	5	2	E42364
18	13	25.0	7	2	S42620
19	13	25.0	8	2	B39745
20	13	25.0	8	2	A42689
21	13	25.0	9	2	B28495
22	13	25.0	9	2	PT0247
23	13	25.0	9	2	PT0268
24	13	25.0	9	2	S26508
25	12	23.1	5	2	B22565
26	12	23.1	6	2	B34835
27	12	23.1	6	2	B26206
28	12	23.1	6	4	A35039
29	12	23.1	7	2	ECMUOR

30 12 23.1 7 2 E61491
31 12 23.1 7 2 PH1602
32 12 23.1 7 2 PH0932
33 12 23.1 8 2 S16324
34 12 23.1 8 2 A35180
35 12 23.1 8 2 PH0934
36 12 23.1 9 2 S19329
37 12 23.1 9 2 G58502
38 12 23.1 9 2 S55696
39 12 23.1 9 2 A53797
40 12 23.1 9 2 PH0935
41 12 23.1 9 2 PH0937
42 12 23.1 9 2 PH0902
43 12 23.1 9 2 PH0917
44 12 23.1 9 2 PH0918
45 12 23.1 9 2 PH0921

ALIGNMENTS

RESULT 1

I65546
MHC H2-L antigen - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I65546
R;Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
Cell 44, 261-272, 1986
A;Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and the
A;Reference number: I52778; MUID:86106202; PMID:3510743
A;Accession: I65546
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-6 <RES>
A;Cross-references: GB:M12483; NID:gl99565; PIDN:AAA39663.1; PID:G554234

Query Match 42.3%; Score 22; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LVPC 9
Db :|||
1 MVPC 4

RESULT 2

A60521
glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N;Alternate names: glycogen phosphorylase b
C;Species: Liza ramada
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003
C;Accession: A60521
R;Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A;Title: Purification and characterization of glycogen phosphorylase B from skeletal mu
A;Reference number: A60521; MUID:90227907; PMID:2109669
A;Accession: A60521
A;Molecule type: protein
A;Residues: 1-5 <BON>
C;Superfamily: glucan phosphorylase
C;Keywords: Glycosyltransferase; hexosyltransferase; phosphoprotein
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experi

Query Match 36.5%; Score 19; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ISVP 5
Db :|||
2 ISVP 5

```
RESULT 3
A60356
118K stomach cancer antigen - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 17-Mar-1999
C:Accession: A60356
R:Shiraishi, Y.
Int. J. Cancer 45, 783-787, 1990
A:Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens fr
A:Reference number: A60356; MUID:90216080; PMID:2323853
A:Accession: A60356
A:Molecule type: protein
A:Residues: 1-9 <SH1>
C:Keywords: glycoprotein

Query Match 36.5%; Score 19; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPLVP 8
DB 1 IPLKP 5

RESULT 4
A61620
locustamyotropin III - migratory locust
C:Species: Locusta migratoria (migratory locust)
C>Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jul-1997
C:Accession: A61620
R:Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.
Insect Biochem. Mol. Biol. 22, 447-452, 1992
A:Title: Isolation, identification and synthesis of locustamyotropin III and IV, two add
A:Reference number: A61620
A:Accession: A61620
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <SCH>
C:Keywords: amidated carboxyl end; neuropeptide
F:9/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 34.6%; Score 18; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLVP 8
DB 4 PFVP 7

RESULT 5
S10783
enamelin f - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C:Accession: S10783
R:Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu
A:Reference number: S10780; MUID:90336641; PMID:2379503
A:Accession: S10783
A:Molecule type: protein
A:Residues: 1-8 <STR>
C:Keywords: enamel; phosphoprotein

Query Match 32.7%; Score 17; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPLVP 8
DB 1 MPLPP 5

RESULT 6
S66419
tetrameric proteinase precursor, 60K, dithiothreitol-sensitive - spinach (fragment)
C:Species: Spinacia oleracea (spinach)
C>Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997
C:Accession: S66419
R:Kuwabara, T.
FEBS Lett. 371, 195-198, 1995
A:Title: The 60-kDa precursor to the dithiothreitol-sensitive tetrameric protease of sp
A:Reference number: S66419; MUID:95402209; PMID:7672127
A:Accession: S66419
A:Molecule type: protein
A:Residues: 1-9 <KOW>

Query Match 32.7%; Score 17; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLVP 8
DB 2 PILP 5

RESULT 7
I51049
metallothionein-A - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51049
R:Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.
Eur. J. Biochem. 230, 344-349, 1995
A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) m
A:Reference number: I51049; MUID:95324545; PMID:7601121
A:Accession: I51049
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <OLS>
A:Cross-references: EMBL:X80181; NID:G1019799; PIDN:CAA56466.1; PID:G4379328

Query Match 30.8%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PC 9
DB 3 PC 4

RESULT 8
S13636
coat protein beta chain, Golgi-derived - rabbit (fragment)
N:Alternate names: beta-COP protein
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C:Accession: S13636
R:Serafini, T.; Stenbeck, G.; Brecht, A.; Lottspeich, F.; Orzi, L.; Rothman, J.E.; Wiel
Nature 349, 215-220, 1991
A:Title: A coat subunit of Golgi-derived non-clathrin-coated vesicles with homology to
A:Reference number: S13636; MUID:91101693; PMID:1898984
A:Accession: S13636
A:Molecule type: protein
A:Residues: 1-9 <SER>
C:Superfamily: coatmer complex beta chain
C:Keywords: Golgi apparatus; protein transport

Query Match 30.8%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPLVP 7
DB 5 IPIV 8
```

```

      Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 PLVP 8
Db      3 PLGP 6

RESULT 12
PT0080
60K Ca binding protein - edible frog (fragment)
C:Species: Rana esculenta (edible frog)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PT0080
R:Treves, S.; Zorzato, F.; Chiozzi, P.; Melandri, P.; Volpe, P.; Pozzan, T.
Biochem. Biophys. Res. Commun. 175, 444-450, 1991
A:Title: Frog brain expresses a 60 kDa Ca2+ binding protein similar to mammalian calret
A:Reference number: PT0080; MUID:91207333; PMID:2018493
A:Accession: PT0080
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <TRE>

      Query Match      28.8%; Score 15; DB 2; Length 9;
      Best Local Similarity 100.0%; Pred. No. 2.8e+05;
      Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PLV 7
Db      2 PLV 4

RESULT 13
I48105
dihydrofolate reductase - Chinese hamster (fragment)
C:Species: Crictetus griseus (Chinese hamster)
C>Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
C:Accession: I48105
R:Aizkhan, J.C.; Vaughn, J.P.; Christy, R.J.; Hamlin, J.L.
Biochemistry 25, 6228-6236, 1986
A:Title: Nucleotide sequence and nuclease hypersensitivity of the Chinese hamster dihyd
A:Reference number: I48105; MUID:87076541; PMID:3024702
A:Accession: I48105
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7 <RES>
A:Cross-references: GB:M14771; NID:g191055; PIDN:AAA36975.1; PID:g191056

      Query Match      26.9%; Score 14; DB 2; Length 7;
      Best Local Similarity 66.7%; Pred. No. 2.8e+05;
      Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      5 PLV 7
Db      4 PLI 6

RESULT 14
S21288
lectin - potato (fragment)
C:Species: Solanum tuberosum (potato)
C>Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 05-Dec-1998
C:Accession: S21288
R:Miller, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.
Biochem. J. 283, 813-821, 1992
A:Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterizati
A:Reference number: S21288; MUID:92272683; PMID:1590771
A:Accession: S21288
A:Molecule type: protein
A:Residues: 1-8 <ML>
A:Experimental source: var. Ulster Sceptre
C:Function:
A:Description: may be involved in defence mechanism of the plant
C:Keywords: hydroxyproline, lectin

glycoprotein component 16/major fat-globule membrane protein/MFG-B8 homolog - bovine (fr
C:Species: Bos primigenius taurus (cattle)
C>Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C:Accession: H48394
R:Mather, I.H.; Baughart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
A:Reference number: A48394; MUID:93250576; PMID:8485470
A:Accession: H48394
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-6 <MAT>
A:Experimental source: milk
A>Note: sequence extracted from NCBI backbone (NCBIP:131518)
C:Keywords: glycoprotein

      Query Match      28.8%; Score 15; DB 2; Length 6;
      Best Local Similarity 50.0%; Pred. No. 2.8e+05;
      Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 VPLWPC 9
Db      1 VELLGC 6

RESULT 10
G33098
205K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C>Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C:Accession: G33098
R:Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A:Reference number: A33098
A:Accession: G33098
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <NIC>

      Query Match      28.8%; Score 15; DB 2; Length 8;
      Best Local Similarity 100.0%; Pred. No. 2.8e+05;
      Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 VPL 6
Db      2 VPL 4

RESULT 11
I54017
granulocyte-colony stimulating factor precursor - synthetic (fragment)
C:Species: synthetic
A>Note: human gene engineered and expressed in Escherichia coli
C>Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 28-Jan-2000
C:Accession: I54017
R:Devlin, P.E.; Drummond, R.J.; Toy, P.; Mark, D.F.; Watt, K.W.; Devlin, J.J.
Gene 65, 13-22, 1988
A:Title: Alteration of amino-terminal codons of human granulocyte-colony-stimulating fac
A:Reference number: I54017; MUID:88284374; PMID:2456256
A:Accession: I54017
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-8 <DEV>
A:Cross-references: GB:M20922; NID:g806638; PIDN:AAA66353.1; PID:g183043

      Query Match      28.8%; Score 15; DB 4; Length 8;
      Best Local Similarity 75.0%; Pred. No. 2.8e+05;

```

Query Match 26.9%; Score 14; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 SVPLVP 8
 | | |
 DB 3 STPSFP 8

RESULT 15

D48186
 ATPase R1 subunit - wood tobacco (fragment)
 C:Species: Nicotiana sylvestris (wood tobacco)
 C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 23-Feb-1997
 C:Accession: D48186
 R:De Paeppe, R.; Porchioni, A.; Chetrit, P.; Vedel, F.
 Proc. Natl. Acad. Sci. U.S.A. 90, 5934-5938, 1993
 A>Title: Specific mitochondrial proteins in pollen: presence of an additional ATP synthase
 A:Reference number: A48186; MUID:93317598; PMID:8327463
 A:Accession: D48186
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9 <DEI>
 A:Experimental source: pollen
 A>Note: sequence extracted from NCBI backbone (NCBIP:134871)

Query Match 26.9%; Score 14; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 VPLVP 8
 | | |
 DB 3 VDLAP 7

Search completed: March 8, 2004, 12:20:25
 Job time : 14 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:11:57 ; Search time 10 Seconds
(without alignments)
46.863 Million cell updates/sec

Title: US-09-761-636A-14

Perfect score: 52

Sequence: 1 CISVLPVC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 251

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	38.5	9	1 MGMT_BOVIN	P29177 bos taurus
2	18	34.6	8	1 COM2_CONFU	P58785 conus purpur
3	18	34.6	9	1 LMT3_LOCFI	P41489 locusta mig
4	17	32.7	9	1 UP43_HUMAN	P30089 homo sapien
5	16	30.8	8	1 PPK3_PERAM	P82692 periplaneta
6	15	28.8	8	1 PPK3_PERAM	P82618 periplaneta
7	15	28.8	9	1 UP47_HUMAN	P30093 homo sapien
8	13	25.0	6	1 E101_LITRU	P82096 litoria rub
9	13	25.0	9	1 CONO_CONST	P05487 conus stria
10	12	23.1	7	1 CARP_MYTED	P10420 mytilus edu
11	12	23.1	8	1 ALL6_CYPDO	P82157 cydia pomon
12	12	23.1	8	1 FUS3_FUSO	P81010 fusarium so
13	12	23.1	8	1 UP41_HUMAN	P30087 homo sapien
14	12	23.1	9	1 FAR5_PENMO	P83320 penaeus mon
15	12	23.1	9	1 FLA2_TREHY	P80159 treponema h
16	12	23.1	9	1 OXYT_BUPRE	P24995 bufo regula
17	12	23.1	9	1 SAP_STOVA	P24047 scompreute
18	11	21.2	6	1 VP19_HSV1K	P23210 herpes simp
19	11	21.2	7	1 CCF1_ENTFA	P20104 enterococcu
20	11	21.2	7	1 MNPI_LRPDE	P42984 leptinotars
21	11	21.2	7	1 TPFX_PACDA	P83455 pacymedusa
22	11	21.2	8	1 VOLIG_HSV2B	P81780 herpes simp
23	11	21.2	9	1 COXE_THOUB	P80975 thunnus obe
24	11	21.2	9	1 DNFI_LOCFI	P16339 locusta mig
25	11	21.2	9	1 FAR9_ASCSU	P43172 ascaris suu
26	11	21.2	9	1 OXYA_SQUAC	P42999 squalus aca
27	11	21.2	9	1 OXYT_RABIT	P32878 oryctolagus
28	11	21.2	9	1 RT33_BOVIN	P82926 bos taurus
29	10	19.2	7	1 TY51_LITRU	P82065 litoria rub
30	10	19.2	7	1 UP04_MOUSE	P38642 mus musculu
31	10	19.2	7	1 COM_CONVE	P83047 conus ventr
32	10	19.2	9	1 PPK1_PERAM	P82691 periplaneta
33	10	19.2	9	1 TALI_PICJA	P17440 pichia jadi

34	10	19.2	9	1 TAL3_PICJA	P17441 pichia jadi
35	9	17.3	5	1 E103_LITRU	P82099 litoria rub
36	9	17.3	5	1 E104_LITRU	P82100 litoria rub
37	9	17.3	6	1 CIP1_MYTED	P13736 mytilus edu
38	9	17.3	6	1 CIP2_MYTED	P13737 mytilus edu
39	9	17.3	7	1 BRHP_CONIM	P58803 conus imper
40	9	17.3	7	1 UN06_PINPS	P81675 pinus pinas
41	9	17.3	7	1 WWA1_ACHFU	P35919 achatina fu
42	9	17.3	7	1 WWA2_ACHFU	P35920 achatina fu
43	9	17.3	7	1 WWA3_ACHFU	P35921 achatina fu
44	9	17.3	8	1 ACT_CARMA	P80709 carcinus ma
45	9	17.3	8	1 AKH_LIBAU	P25418 libellula a

ALIGNMENTS

RESULT 1

ID	MGMT_BOVIN	STANDARD	PRT	9 AA
AC	P29177			
DT	01-DEC-1992 (Rel. 24, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DT	01-OCT-1996 (Rel. 34, Last annotation update)			
DE	Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-methylguanine-DNA methyltransferase) (fragment).			
GN	MGMT			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.			
CC	NCBI_TaxID=9913			
RN	[1]			
RP	SEQUENCE			
RC	TISSUE=Thymus;			
EX	MEDLINE=90174912; PubMed=2308822;			
RA	Rydyberg B., Hall J., Karran P.;			
RT	"Active site amino acid sequence of the bovine O6-methylguanine-DNA methyltransferase."			
RL	Nucleic Acids Res. 18:17-21(1990).			
CC	-I- FUNCTION: Repair of alkylated guanine in DNA by stoichiometrically transferring the alkyl group at the O-6 position to a cysteine residue in the enzyme. This is a suicide reaction: the enzyme is irreversibly inactivated.			
CC	-I- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) + [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein S-methyl-L-cysteine.			
CC	-I- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OGT METHYLTRANSFERASE WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.			
DR	InterPro: IPR001497; Methyltransf_1.			
DR	PROSITE: PS00374; MGMT; PARTIAL.			
KW	DNA repair; transferase; Methyltransferase.			
FT	NON_TER	1	1	
FT	ACT_SITE	9	9	ALKYL GROUP ACCEPTOR (BY SIMILARITY).
FT	NON_TER	9	9	
SQ	SEQUENCE	9 AA; 967 MW; 325171A720476047 CRC64;		

Query Match 38.5%; Score 20; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 LVPC 9

DB 6 LTFC 9

RESULT 2

ID	COM2_CONFU	STANDARD	PRT	8 AA
AC	P58785			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			

DE Leu-contryphan-P.
 OS Conus purpurascens (Purple cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=41690;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC STRAIN=Clipperton Island; TISSUE=Venom;
 RX MEDLINE=9938839; PubMed=10461743;
 RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
 RA Olivera B.M.;
 RT "A novel D-leucine-containing Conus peptide: diverse conformational
 RT dynamics in the contryphan family.";
 RL J. Pept. Res. 54:93-99(1999).
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -|- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
 CC -|- SIMILARITY: Belongs to the contryphan family.
 KW Toxin; Hydroxylation; D-amino acid.
 FT DISULFID 2 8
 FT MOD_RES 4 4 D-LEUCINE.
 FT SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;
 SQ
 Query Match 34.6%; Score 18; DB 1; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CISPVP 5
 Db | : |
 2 CULLP 6
 RESULT 3
 LMT3_LOCM
 ID LMT3 LOCM1 STANDARD; PRT; 9 AA.
 AC P41489;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Locustamytropin 3 (LOM-WT-3).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
 RA de Loof A.;
 RT "Isolation, identification and synthesis of locustamytropin III and
 RT IV, two additional neuropeptides of Locusta migratoria: members of the
 RT locustamytropin peptide family.";
 RL Insect Biochem. Mol. Biol. 22:447-452(1992).
 CC -|- FUNCTION: Potent mediator of visceral muscle contractile activity
 CC (myotropic activity).
 CC -|- SIMILARITY: Belongs to the pyrokinin family.
 DR PIR: A61620; A61620.
 DR InterPro: IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 9 9 AMIDATION.
 FT SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;
 SQ
 Query Match 34.6%; Score 18; DB 1; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 PLVP 8
 Db | : |
 4 PFVP 7

RESULT 4
 UPA3 HUMAN
 ID UPA3 HUMAN STANDARD; PRT; 9 AA.
 AC P30089;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
 DE Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RL Electrophoresis 13:707-714(1992).
 CC -|- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 4.6, its MW is: 46 kDa.
 DR SWISS-2DPAGE; P30089; HUMAN.
 FT NON_TER 1 1
 FT NON_TER 9 9
 FT SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;
 SQ
 Query Match 32.7%; Score 17; DB 1; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 PLVP 8
 Db | : |
 2 PLFP 5
 RESULT 5
 PPK2 PERAM
 ID PPK2 PERAM STANDARD; PRT; 8 AA.
 AC P82632;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-2 (Pea-PK-2) (FXPRIL-amide).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Blattodea; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=97353923; PubMed=9210163;
 RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of two pyrokinins from the
 RT retrocerebral complex of the American cockroach.";
 RL Peptides 18:473-478(1997).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tegma-specific distribution of FXPRILamides in the nervous system of
 RT the American cockroach.";
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -|- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 CC activity).
 CC -|- TISSUE SPECIFICITY: Corpora cardiaca.
 CC -|- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
 CC -|- SIMILARITY: Belongs to the pyrokinin family.
 DR InterPro: IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; FALSE_NEG.

```
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match 30.8%; Score 16; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 SVPLVP 8
Db 1 SPFPAP 6

RESULT 6
PPK3 PERAM STANDARD; PRT; 8 AA.
AC P82618;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-3 (Pea-PK-3) (FXPL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RP TISSUE=Retrocerebral complex;
RX MEDLINE=99212469; PubMed=10196736;
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
RT "Differential distribution of pyrokinin-isoforms in cerebral and
RL abdominal neurohemal organs of the American cockroach.";
RN [2]
RN TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Rckert M.;
RT "Tagma-specific distribution of FXPLamides in the nervous system of
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -!- TISSUE SPECIFICITY: Corpora cardiaca.
CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=WALDI.
CC -!- SIMILARITY: Belongs to the pyrokinin family.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 28.8%; Score 15; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LVP 8
Db 1 LVP 3

RESULT 7
UPA7 HUMAN STANDARD; PRT; 9 AA.
AC P30093;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 18) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE.
```

```
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochrasser D.P.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.05, its MW is: 37 kDa.
DR SWISS-2DPAGE; P30093; HUMAN.
FT MOD RES 1 1
FT UNSURE 5 5
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1042 MW; SC14477AEB0772C7 CRC64;

Query Match 28.8%; Score 15; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LVP 8
Db 2 LVP 4

RESULT 8
EI01 LITRU STANDARD; PRT; 6 AA.
AC P82096;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Electrin 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RN TISSUE=Skin secretion;
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 6 6
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 25.0%; Score 13; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPL 6
Db 2 VPI 4

RESULT 9
CONO CONST STANDARD; PRT; 9 AA.
AC P05487;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Arg-conopressin S.
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6493;
```



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RN SEQUENCE
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
RT peptides from Conus geographus and Conus straitus venoms.";
RL J. Biol. Chem. 262:15821-15824 (1987).
RN [2]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700 (1988).
CC -1- FUNCTION: Targets vasopressin-oxytocin related receptors.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR PIR; B28495; B28495.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4.1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1031 MW; 17EB176EB4540050 CRC64;
SQ SEQUENCE 9 AA; 1031 MW; 17EB176EB4540050 CRC64;

Query Match 25.0%; Score 13; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CI 2
Db 1 CI 2

RESULT 10
CARP MYTED STANDARD; PRT; 7 AA.
ID _CARP_MYTED STANDARD; PRT; 7 AA.
AC P10420;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Catch-relaxing peptide (CARP).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
OC Mytiloides; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RX MEDLINE=88052022; PubMed=3676797;
RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
RA Muneoka Y.;
RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
RL Brain Res. 422:374-376 (1987).
CC -1- FUNCTION: This peptide exhibits both potentiating (contraction)
CC and inhibitory (relaxation) effects on the anterior byssus
CC retractor muscle.
DR PIR; A29342; ECMUCR.
KW Hormone; Amidation.
FT MOD_RES 7 7
FT SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;
SQ SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;

Query Match 23.1%; Score 12; DB 1; Length 7;
Best Local Similarity 20.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLV 7
Db 1 AMPML 5

RESULT 11

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ALL6 CYDPO STANDARD; PRT; 8 AA.
ID ALL6_CYDPO STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 6.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricoides; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=62600;
RN [1]
RP SEQUENCE.
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309 (1997).
CC -1- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8
FT SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 23.1%; Score 12; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPL 6
Db 1 LPL 3

RESULT 12
FUSS FUSSO STANDARD; PRT; 8 AA.
ID _FUSS_FUSSO STANDARD; PRT; 8 AA.
AC P81010;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Allergen Fus s I3596* (Fragment).
OS Fusarium solani (subsp. pisi) (Nectria haematococca).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=70791;
RN [1]
RP SEQUENCE.
RC STRAIN=IARI 3596; TISSUE=Mycelium;
RA Verma J., Gangal S.V.;
RL Submitted (JUL-1997) to Swiss-Prot.
CC -1- ALLERGEN: Causes an allergic reaction in human.
KW Allergen.
FT NON_TER 8 8
FT SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;
SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 23.1%; Score 12; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVP 5
Db 6 NVP 8

RESULT 13
UPAL HUMAN STANDARD; PRT; 8 AA.
ID _UPAL_HUMAN STANDARD; PRT; 8 AA.
AC P30087;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RC TISSUE=Plasma;
RA MEDLINE=93092937; PubMed=1459097;
RX Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 4.9, its MW is: 65 kDa.
DR SWISS-2DPAGE; P30087; HUMAN.
FT NON_TER 1 1
FT UNSURE 8 8
FT NON_TER 8 8
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 944 MW; C01772C455B806DA CRC64;

Query Match 23.1%; Score 12; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVP 5
Db :||
5 NVP 7

RESULT 14
FAR5_PENNO STANDARD; PRT; 9 AA.
AC P83320;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP5 (SMPSLRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupem J., Krungkassam C., Longyant S.,
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1121.1; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
DR GO:0007218; P-neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1106 MW; B60B07340735A766 CRC64;

Query Match 23.1%; Score 12; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVP 5
Db :||
1 SMP 3

RESULT 15
FLA2_TREHY STANDARD; PRT; 9 AA.
ID FLA2_TREHY

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AC P80159;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Flagellar filament outer layer protein flaa2 (35 kDa sheath protein)
DE (Fragment).
GN FLAA2.
OS Treponema hyodysenteriae (Serpulina hyodysenteriae).
OC Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspira.
OX NCBI_TaxID=159;
RN [1]
RP SEQUENCE
RC STRAIN=C5;
RX MEDLINE=93139764; PubMed=1487733;
RA Koopman M.B.H., Baats B., van Vorstenbosch C.J.A.H.V.,
RA van der Zeijst B.A.M., Kusters J.G.;
RT "The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are
composed of two sheath proteins and three core proteins.";
RL J. Gen. Microbiol. 138:2697-2706(1992).
CC -1- FUNCTION: Component of the outer layer of the flagella.
CC -1- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO
CC SHEATH PROTEINS, FLAA1 (44 kDa) AND FLAA2 (35 kDa) AROUND A CORE
CC THAT CONTAINS THREE PROTEINS FLAB1 (37 kDa), FLAB2 (34 kDa) AND
CC FLAB3 (32 kDa).
CC -1- SUBCELLULAR LOCATION: Periplasmic flagellum.
KW Flagellum; Periplasmic.
FT UNSURE 2 2
FT UNSURE 8 9
FT NON_TER 9 9
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1129 MW; 855A19C68B4772D1 CRC64;

Query Match 23.1%; Score 12; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVP 5
Db :||
2 TYP 4

Search completed: March 8, 2004, 12:18:24
Job time : 11 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:14:57 ; Search time 34.5 Seconds
(without alignments)
82.309 Million cell updates/sec

Title: US-09-761-636A-14
Perfect score: 52
Sequence: 1 CISVLPVC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 840

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*

1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mbc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	38.5	9	3 Q9P8E5	Q9P8E5 kluyveromyc
2	19	36.5	7	13 O42564	O42564 figu rubrip
3	19	36.5	8	2 Q56140	Q56140 streptococc
4	18	34.6	9	13 Q8AYL5	Q8AYL5 carassius a
5	18	34.6	9	13 Q8AUM7	Q8AUM7 carassius a
6	17	32.7	9	10 Q7X6A3	Q7X6A3 zea mays su
7	16	30.8	7	10 P93233	P93233 lycopersico
8	16	30.8	8	6 O02831	O02831 oryctolagus
9	16	30.8	8	6 Q9TRY3	Q9TRY3 sus sp. ins
10	16	30.8	9	4 Q16220	Q16220 homo sapien
11	16	30.8	9	4 Q9UMF3	Q9UMF3 homo sapien
12	16	30.8	9	12 Q8QVD3	Q8QVD3 ovine respi
13	15	28.8	7	15 Q07624	Q07624 rous sarcom
14	15	28.8	9	7 Q78225	Q78225 mus musculu
15	15	28.8	9	10 Q958J8	Q958J8 oryza sativ
16	15	28.8	9	11 Q35953	Q35953 mus musculu

17	14	26.9	7	2 O07354	O07354 synchococc
18	14	26.9	8	2 Q9X3K1	Q9X3K1 prochloroco
19	14	26.9	8	2 P83532	P83532 lactobacill
20	14	26.9	8	6 Q9TRX8	Q9TRX8 bos taurus
21	13	25.0	6	5 P83569	P83569 sepia offic
22	13	25.0	7	12 Q67113	Q67113 influenzavi
23	13	25.0	8	2 Q49534	Q49534 mycoplasma
24	13	25.0	8	2 Q32560	Q32560 escherichia
25	13	25.0	8	8 Q8WFR5	Q8WFR5 diadema pau
26	13	25.0	8	11 Q8K3Z7	Q8K3Z7 mus musculu
27	13	25.0	8	11 Q99P40	Q99P40 mus musculu
28	13	25.0	8	11 P82598	P82598 rattus norv
29	13	25.0	8	12 Q9E805	Q9E805 beet soil-b
30	13	25.0	8	12 Q9E8Q2	Q9E8Q2 beet soil-b
31	13	25.0	8	12 Q9E8P9	Q9E8P9 beet soil-b
32	13	25.0	8	12 Q9E8Q3	Q9E8Q3 beet soil-b
33	13	25.0	8	12 Q9E8Q1	Q9E8Q1 beet soil-b
34	13	25.0	8	12 Q9DSN2	Q9DSN2 beet soil-b
35	13	25.0	8	12 Q9E8Q4	Q9E8Q4 beet soil-b
36	13	25.0	8	12 Q9DSN5	Q9DSN5 beet soil-b
37	13	25.0	8	12 Q9E8P7	Q9E8P7 beet soil-b
38	13	25.0	8	12 Q9DSN1	Q9DSN1 beet soil-b
39	13	25.0	8	12 Q9DSN3	Q9DSN3 beet soil-b
40	13	25.0	8	12 Q9DSN4	Q9DSN4 beet soil-b
41	13	25.0	8	12 Q9E8Q0	Q9E8Q0 beet soil-b
42	13	25.0	8	12 Q9E8Q7	Q9E8Q7 beet soil-b
43	13	25.0	8	12 Q9DSN6	Q9DSN6 beet soil-b
44	13	25.0	8	12 Q9DSN0	Q9DSN0 beet soil-b
45	13	25.0	8	12 Q9E8Q6	Q9E8Q6 beet soil-b

ALIGNMENTS

RESULT 1
ID Q9P8E5 PRELIMINARY; PRT; 9 AA.
AC Q9P8E5
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
DE HIS4 protein (Fragment).
GN HIS4.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRL-V1140;
RX MEDLINE=99448392; PubMed=10518937;
RA Lamas-Maceiras M., Esperanza Cerdan E., Freire-Picos M.A.;
RT "Kluyveromyces lactis HIS4 transcriptional regulation: similarities
RT and differences to Saccharomyces cerevisiae HIS4 gene."
RL FEBS Lett. 458:72-76(1999).
DR EMBL: AJ238494; CAB87125.1; -.
FT NON_TER
SQ SEQUENCE 9 AA; 1015 MW; 5770D2D772D2D767 CRC64;
Query Match 38.5%; Score 20; DB 3; Length 9;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 4 VPLVP 8
Db 2 LPVVP 6
RESULT 2
ID Q42564 PRELIMINARY; PRT; 7 AA.
AC Q42564
DT 01-JAN-1998 (TREMELrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 GN Truncated voltage-gated sodium channel alpha subunit (Fragment).
 OS SCN8A.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97442476; PubMed=9295353;
 RX Plummer N.W., McBurney M.W., Weisler M.H.;
 RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
 RT two-domain protein in fetal brain and non-neuronal cells.";
 RL J. Biol. Chem. 272:24008-24015(1997).
 DR EMBL; U97673; AAB80916.1; --
 DR GO; GO:0005216; P:ion channel activity; IEA.
 KW Ionic channel.
 FT NON TER 1 1
 SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;
 Query Match 36.5%; Score 19; DB 13; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 VPLV 7
 Db ||||
 1 VPLV 4
 RESULT 3
 Q56140 PRELIMINARY; PRT; 8 AA.
 AC Q56140;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE STP6 protein (Fragment).
 GN STP6
 OS Streptococcus thermophilus.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1308;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ST1;
 RX MEDLINE=95047254; PubMed=7958782;
 RA Constable A., Mollet B.;
 RT "Isolation and characterisation of promoter regions from Streptococcus
 RT thermophilus.";
 RL FEMS Microbiol. Lett. 122:85-90(1994).
 DR EMBL; X78210; CAA55045.1; --
 FT NON TER 8 8
 SQ SEQUENCE 8 AA; 846 MW; ED086772DSB045B6 CRC64;
 Query Match 36.5%; Score 19; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ISVP 5
 Db ||||
 3 ISVP 6
 RESULT 4
 Q8AYL5 PRELIMINARY; PRT; 9 AA.
 AC Q8AYL5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Cytochrome P450 aromatase (Fragment).
 GN CYP19A.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 OX NCBI_TaxID=7957;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;
 RT "Promoter characteristics of two CYP19 genes differentially expressed
 RT in the brain and ovary of teleost fish.";
 RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).
 DR EMBL; AF324897; AAN32618.1; --
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 1060 MW; C49E76D7272B040D CRC64;
 Query Match 34.6%; Score 18; DB 13; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 LVPC 9
 Db ||||
 6 LVPC 9
 RESULT 5
 Q8AUM7 PRELIMINARY; PRT; 9 AA.
 AC Q8AUM7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Cytochrome P450 aromatase (Fragment).
 GN CYP19A.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 OX NCBI_TaxID=7957;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;
 RT "Promoter characteristics of two CYP19 genes differentially expressed
 RT in the brain and ovary of teleost fish.";
 RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).
 DR EMBL; AF324895; AAN32616.1; --
 DR EMBL; AF324896; AAN32617.1; --
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 961 MW; C49E76D7272B187D CRC64;
 Query Match 34.6%; Score 18; DB 13; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 LVPC 9
 Db ||||
 6 LVPC 9
 RESULT 6
 Q7X6A3 PRELIMINARY; PRT; 9 AA.
 AC Q7X6A3;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Isoamylase (Fragment).
 GN SUL.
 OS Zea mays subsp. mays (maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.

OX NCBI_TaxID=4578;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. 38-11, and cv. A632;
 RA Wilson L.M., Whitt S.R., Ibanez A.M., Rocheford T.R., Goodman M.M.,
 RA Buckler E.S., IV.,
 RA "Dissection of maize starch production by candidate gene
 RT association."
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY290305; AAP45331.1; -.
 DR EMBL; AY290311; AAP45337.1; -.
 FT NON TER
 SQ SEQUENCE 9 AA; 976 MW; DF9BCEA76736CGDD CRC64;

Query Match 32.7%; Score 17; DB 10; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 VPC 9
 :||
 Db 5 LPC 7

RESULT 7

P93233
 ID P93233 PRELIMINARY; PRT; 7 AA.
 AC P93233;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
 DE (Fragment).
 GN LE-ACS1B.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97351561; PubMed=9207843;
 RA Oetiker J.H., Olson D.C., Shiu O.Y., Yang S.P.;
 RT "Differential induction of seven 1-aminocyclopropane-1-carboxylate
 RT synthase genes by elicitor in suspension cultures of tomato
 RT (Lycopersicon esculentum).";
 RL Plant Mol. Biol. 34:275-286(1997).
 DR GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 KW Lyase.
 FT NON TER
 SQ SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;

Query Match 30.8%; Score 16; DB 10; Length 7;
 Best Local Similarity 80.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SVPLV 7
 :|||
 Db 1 SRPLV 5

RESULT 8

O02831
 ID O02831 PRELIMINARY; PRT; 8 AA.
 AC O02831;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Pro alpha 1 type III collagen protein (Fragment).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96377339; PubMed=8783186;
 RA Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
 RA Vuorio E.;
 RA "Evidence for insufficient chondrocytic differentiation during repair
 RT of full-thickness defects of articular cartilage."
 RL Matrix Biol. 15:39-47(1996).
 DR EMBL; S83371; AAD14433.1; -.
 KW Collagen.
 FT NON TER
 SQ SEQUENCE 8 AA; 1028 MW; B859C7272EA77371 CRC64;

Query Match 30.8%; Score 16; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PC 9
 :||
 Db 3 PC 4

RESULT 9

O9TRV3
 ID O9TRV3 PRELIMINARY; PRT; 8 AA.
 AC O9TRV3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Insulin-like growth factor-binding protein-6, IGFBP-6 (Fragment).
 OS Sus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9826;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92049376; PubMed=1719383;
 RA Shimasaki S., Gao L., Shimonaka M., Ling N.;
 RT "Isolation and molecular cloning of insulin-like growth factor-binding
 RT protein-6."
 RL Mol. Endocrinol. 5:938-948(1991).
 FT NON TER
 SQ SEQUENCE 8 AA; 850 MW; 9FB2CEA37EA7687D CRC64;

Query Match 30.8%; Score 16; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PC 9
 :||
 Db 3 PC 4

RESULT 10

Q16220
 ID Q16220 PRELIMINARY; PRT; 9 AA.
 AC Q16220;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE HGRP protein (Fragment).
 GN HGRP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94320083; PubMed=8044796;
 RA Nagalla S.R., Spindel E.R.;
 RT "Functional analysis of the 5'-flanking region of the human gastrin-

RT releasing peptide gene in small cell lung carcinoma cell lines.";

RL Cancer Res. 54:4461-4467(1994).

DR EMBL; S73265; AAD14116.1; -.

DR GO; GO:0005634; C:nucleus; NAS.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.

FT NON_TER 9 9

SQ SEQUENCE 9 AA; 1070 MW; 77FE37672B040864 CRC64;

Query Match 30.8%; Score 16; DB 4; Length 9;

Best Local Similarity 75.0%; Pred. No. 1e+06;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPLV 7

DB 6 LPLV 9

RESULT 11

Q9UMF3 PRELIMINARY; PRT; 9 AA.

ID Q9UMF3

AC Q9UMF3

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE PD-1 protein (Fragment).

GN PD-1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RA MEDLINE=97479511; PubMed=9332365;

RA Finger L.R., Pu J., Wasserman R., Vibhakar R., Louie E., Hardy R.R.,

RA Burrows P.D., Billips L.G.

RT "The human PD-1 gene: complete cDNA, genomic organization, and

developmentally regulated expression in B cell progenitors.";

RL Gene 197:177-187(1997).

DR EMBL; U64864; AAC51774.1; -.

FT NON_TER 9 9

SQ SEQUENCE 9 AA; 1067 MW; DDAA676DC6C76046 CRC64;

Query Match 30.8%; Score 16; DB 4; Length 9;

Best Local Similarity 28.8%; Pred. No. 1e+06;

Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISVPLVP 8

DB 1 MOIPQAP 7

RESULT 12

Q8QVD3

ID Q8QVD3

AC Q8QVD3

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Matrix protein 2 (Fragment).

GN M2.

OS Ovine respiratory syncytial virus.

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Paramyxoviridae; Pneumovirinae; Pneumovirus.

OX NCBI_TaxID=28869;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=21580659; PubMed=11724134;

RA Eleraky N.Z., Kania S.A., Porcileter L.N.;

RT "The ovine respiratory syncytial virus F gene sequence and its

diagnostic application.";

RL J. Vet. Diagn. Invest. 13:455-461(2001).

DR EMBL; AF334398; AAL91343.1; -.

FT NON_TER 9 9

SQ SEQUENCE 9 AA; 1154 MW; 8B6A3EA764541415 CRC64;

Query Match 30.8%; Score 16; DB 12; Length 9;

Best Local Similarity 100.0%; Pred. No. 1e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PC 9

DB 6 PC 7

RESULT 13

Q07624

ID Q07624

AC Q07624

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE UORF1.

OS Rous sarcoma virus (strain Prague C).

OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.

OX NCBI_TaxID=11888;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93010967; PubMed=1327749;

RA Donze O., Spahr P.P.;

RT "Role of the open reading frames of Rous sarcoma virus leader RNA in

translation and genome packaging.";

RL EMBO J. 11:3747-3757(1992).

DR EMBL; X67587; CAA47862.1; -.

SQ SEQUENCE 7 AA; 672 MW; 776045A7687DD6F0 CRC64;

Query Match 28.8%; Score 15; DB 15; Length 7;

Best Local Similarity 50.0%; Pred. No. 1e+06;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLVP 8

DB 4 PSIP 7

RESULT 14

078225

ID 078225

AC 078225

DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Lymphocyte antigen (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CRO435; TISSUE=Kidney;

RX MEDLINE=88084418; PubMed=3632165;

RA Golubic M., Budimir O., Schoepfer R., Kasahara M., Mayer W.E.,

RA Figueroa F., Klein J.;

RT "Nucleotide sequence analysis of class II genes borne by mouse t

chromosomes.";

RL Genet. Res. 50:137-146(1987).

DR EMBL; L38589; AAA57293.1; -.

FT NON_TER 1 1

FT NON_TER 9 9

SQ SEQUENCE 9 AA; 1143 MW; 9E68177C729C33A CRC64;

Query Match 28.8%; Score 15; DB 7; Length 9;

Best Local Similarity 100.0%; Pred. No. 1e+06;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LVP 8

Db |||
5 LVP 7

RESULT 15

Q9S8J8 PRELIMINARY; PRT; 9 AA.
AC Q9S8J8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORYZATENSIN=BIOACTIVE peptide.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RX MEDLINE=95102521; PubMed=7804141;
RA Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R.;
RT "Isolation and characterization of oryzatensin: a novel bioactive
RT peptide with ileum-contracting and immunomodulating activities derived
RT from rice albumin.";
RL Biochem. Mol. Biol. Int. 33:1151-1158(1994).
DR Gramene; Q9S8J8;
SQ SEQUENCE 9 AA; 1093 MW; 0E8C67377B56877B CRC64;

Query Match 28.8%; Score 15; DB 10; Length 9;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLVP 8
Db | : |
3 PMYP 6

Search completed: March 8, 2004, 12:19:47
Job time : 35.5 secs

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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:11:17 ; Search time 48.5 Seconds
(without alignments)
52.431 Million cell updates/sec

Title: US-09-761-636A-14

Perfect score: 52

Sequence: 1 CITSVPLVPC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 231240

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq 29Jan04: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	9	4	Aau04533
2	27	51.9	9	5	ABG35134
3	27	51.9	9	5	ABG35134 Pancreati
4	27	51.9	9	5	ABG46931
5	27	51.9	9	5	ABG60522 Selective
6	26	50.0	7	3	ABR56920
7	26	50.0	7	3	ABR56920 Pancreati
8	26	50.0	7	3	ADG44293 Endotheli
9	26	50.0	7	3	ADG44293 Endotheli
10	26	50.0	9	4	AAE07204
11	26	50.0	9	4	AAE07204 Modified
12	25	48.1	5	2	ABG35050 Endostati
13	25	48.1	5	2	AAE95843 IGF-1 mut
14	25	48.1	5	3	AAE95843
15	24	46.2	6	2	ADG44308 Endotheli
16	24	46.2	9	1	AAE10098
17	24	46.2	9	4	ABP21743
18	24	46.2	9	5	AAU94456 Human nov
19	24	46.2	9	5	AAU94456 Human nov
20	24	46.2	9	7	AAU94653 Human nov
21	24	46.2	9	7	ADG44488 Endotheli
22	23	44.2	6	2	AAE59359
23	23	44.2	6	2	AAE59359 GST bindi
24	23	44.2	6	6	ABP99702
25	23	44.2	7	4	AAE64710
			7	4	AAU04530 VEGF base

26	23	44.2	8	2	AAE58417
27	23	44.2	8	2	AAE58416
28	23	44.2	8	2	AAE58415
29	23	44.2	8	2	AAE58418
30	23	44.2	9	2	AAW99327 Human IGG
31	23	44.2	9	2	AAV10322 T cell ep
32	23	44.2	9	2	AAW9853 HIV-1 gp1
33	23	44.2	9	2	AAV47758 Immunogen
34	23	44.2	9	2	AAV45765 Immunogen
35	23	44.2	9	2	AAV45766 Immunogen
36	23	44.2	9	2	AAV48998 Membrane
37	23	44.2	9	3	AAV51358 MHC type
38	23	44.2	9	3	AAE36017 Human bet
39	23	44.2	9	3	AAE27093 Plasmodiu
40	23	44.2	9	4	AAE1826 Human Ig
41	23	44.2	9	5	AAE26894 Linker pe
42	23	44.2	9	5	ABG35060 Angiostat
43	23	44.2	9	5	ABG35128 Pancreati
44	23	44.2	9	5	ABG60516 Selective
45	23	44.2	9	5	ABG80004 MHC class

ALIGNMENTS

RESULT 1
AAU04533
ID AAU04533 standard; peptide; 9 AA.
XX AC AAU04533;
XX AC
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 11.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX Synthetic.
XX Key Location/Qualifiers
PH Disulfide-bond 1..9
FT /note= "This bond cyclises the peptide"
XX
XX WO200152875-A1.
XX
XX 26-JUL-2001.
XX
XX 18-JAN-2001; 2001WO-US001533.
XX
XX 18-JAN-2000; 2000US-0176293P.
XX 16-MAY-2000; 2000US-0204590P.
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Achen MG, Hughes RA, Stacker S, Cendron A;
XX WPI; 2001-442248/47.
XX
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
XX from an exposed loop of a growth factor protein by oxidizing the cysteine
XX residues.
XX Claim 49; Page 32; 102pp; English.
XX
XX The sequence represents a monomeric monocyclic peptide of the invention,
XX whose 3-dimensional structure is modelled on the expose loop of human
XX VEGF (vascular endothelial growth factor). The invention relates to a
XX method of producing a monomeric monocyclic peptide by a measuring beta-
XX beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
 |||||
 Db 1 CISVPLVPC 9

RESULT 2
 ABG35134
 ID ABG35134 standard; peptide; 9 AA.

AC ABG35134;
 XX
 DT 15-JUL-2002 (first entry)
 DE Desmocollin-2 CAR cyclic peptide #10.
 XX
 DE Targeting peptide; cancer; Hodgkin's disease; cytostatic;
 KW immunosuppressive; anti-inflammatory; antiarthritic; antiviral;
 KW antithrombotic; antidiabetic; antibacterial; diabetes mellitus;
 KW inflammatory disease; arthritis; atherosclerosis; cancer;
 KW autoimmune disease; bacterial infection; viral infection.

XX Unidentified.
 XX WO200220722-A2.
 XX 14-MAR-2002.
 XX 07-SEP-2001; 2001WO-US027702.
 XX 08-SEP-2000; 2000US-0231266P.
 XX 17-JAN-2001; 2001US-00765101.
 XX (TEXA) UNIV TEXAS SYSTEM.

XX Arap W, Pasqualini R;
 XX WPI; 2002-383050/41.
 XX Identifying targeting peptides useful for treating e.g. diabetes
 PT mellitus, inflammatory diseases, cancer, or autoimmune diseases,
 PT comprises exposing a sample to a phase display library and recovering
 PT phase bound to the sample.
 XX
 PS Claim 56; Page 288; 298pp; English.

XX
 CC This invention relates to a novel method for identifying disease
 CC targeting peptides. The method comprises exposing a sample from an organ,
 CC tissue or cell type of interest, to a phase display library and
 CC recovering phase bound to the sample (the phase expresses targeting
 CC peptides). The peptides identified by the method of the invention may
 CC have cytostatic, immunosuppressive, anti-inflammatory, antiarthritic,
 CC antithrombotic, antidiabetic, antibacterial and antiviral
 CC activities. The methods and composition are useful for identifying
 CC targeting peptides and one or more receptors for a targeting peptide. The
 CC targeting peptides are used for selective delivery of therapeutic agents,
 CC including gene therapy vectors and fusion proteins, to specific organs,
 CC tissues, or cell types in subject. The targeting peptide may also be used
 CC for treating diseases such as diabetes mellitus, inflammatory diseases,
 CC arthritis, atherosclerosis, cancer, autoimmune diseases, bacterial and
 CC viral infections and Hodgkin's disease. The present sequence represents a
 CC targeting peptide of the invention
 XX
 SQ Sequence 9 AA;

Query Match 51.9%; Score 27; DB 5; Length 9;
 Best Local Similarity 55.6%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
 |||||
 Db 1 CMSSPGVAC 9

RESULT 3
 ABB46931
 ID ABB46931 standard; peptide; 9 AA.

XX ABB46931;
 XX
 DT 30-JAN-2002 (first entry)
 DE Desmocollin-2 CAR cyclic peptide 13.

XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;
 KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
 XX Synthetic.

XX WO2000172956-A2.
 XX 04-OCT-2001.

XX 27-MAR-2001; 2001WO-IB001400.
 XX 27-MAR-2000; 2000US-00535852.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OM, Symonds JM, Gour BJ;

XX WPI; 2002-025778/03.

XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis.

XX Claim 23; Page 111; 127pp; English.

XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have

CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer (e.g.
 CC carcinoma, leukaemia or melanoma) and induce apoptosis
 XX
 SQ Sequence 9 AA;

Query Match 51.9%; Score 27; DB 5; Length 9;
 Best Local Similarity 44.4%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTSVPLVPC 9
 | : | | |
 Db 1 CIAPATTTC 9

RESULT 4
 ABG60522
 ID ABG60522 standard; peptide; 9 AA.
 XX
 AC ABG60522;
 XX
 DT 30-JUL-2002 (first entry)
 XX
 DE Selective targeting peptide #197.
 XX
 XX Targeting peptide; cancer; arthritis; diabetes; inflammatory disease;
 KW atherosclerosis; autoimmune disease; bacterial infection; apoptosis;
 KW viral infection; cardiovascular disease; degenerative disease; ischaemia;
 KW inflammation; macular degeneration; antiinflammatory; antidiabetic;
 KW cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;
 KW gene therapy.
 XX
 OS Synthetic.
 XX
 PN WO200220769-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 07-SEP-2001; 2001WO-US027692.
 XX
 PR 08-SEP-2001; 2000US-0231266P.
 PR 17-JAN-2001; 2001US-00765101.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Arap W, Pasqualini R;
 XX
 DR WPI; 2002-415731/44.
 XX
 PT Targeting peptides identified by phage display, useful for targeting
 PT delivery to an organ or tissue, particularly for treating a disease, e.g.
 PT cancer, inflammatory or autoimmune diseases, infections or cardiovascular
 PT disease.
 XX
 PS Claim 22; Page 121; 317pp; English.
 XX
 CC The invention relates to an isolated peptide of 100 amino acids or less
 CC in size useful for targeting delivery to an organ or tissue, particularly
 CC for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory
 CC disease, atherosclerosis, autoimmune disease, bacterial infection, viral
 CC infection, cardiovascular disease or degenerative disease. The peptide is
 CC also useful for inducing apoptosis, particularly to a subject with
 CC ischaemia, cancer, arthritis, diabetes, cardiovascular disease,
 CC inflammation or macular degeneration. Furthermore, the peptide is useful
 CC for diagnosing the diseases cited above. Targeting peptides of the
 CC invention can also be used to deliver an agent to a foetus, by attaching
 CC a peptide to the agent and administering the peptide to a pregnant
 CC subject. Sequences ABG60326-ABG60574 represent selective targeting
 CC peptides of the invention
 XX
 SQ Sequence 9 AA;

Query Match 51.9%; Score 27; DB 5; Length 9;
 Best Local Similarity 55.6%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTSVPLVPC 9
 | : | | |
 Db 1 CMSSPGVAC 9

RESULT 5
 ABR56920
 ID ABR56920 standard; peptide; 9 AA.
 XX
 AC ABR56920;
 XX
 DT 30-JUL-2003 (first entry)
 XX
 DE Pancreatic targeting peptide SEQ ID NO:137.
 XX
 KW Targeting peptide; obesity; lipodystrophy; anorectic; antilipaeamic;
 KW peptide therapy; gene therapy; infection; human immunodeficiency virus;
 KW HIV; placental delivery; teratogenic; placenta; adipose; pancreatic;
 KW beta-3 integrin; beta-5 integrin; spleen; aminopeptidase A.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 PN WO2003022991-A2.
 XX
 PD 20-MAR-2003.
 XX
 PF 30-AUG-2002; 2002WO-US027836.
 XX
 PR 07-SEP-2001; 2001WO-US027692.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Pasqualini R, Arap W, Kolonin MG;
 XX
 DR WPI; 2003-371749/35.
 XX
 PT Treating obesity or a lipodystrophy comprises obtaining a targeting
 PT peptide selective for adipose tissue, attaching the peptide to a
 PT therapeutic agent to form a complex, and administering the complex to a
 PT subject.
 XX
 PS Example 9; Page 114; 247pp; English.
 XX
 CC The present invention describes a method for treating obesity or a
 CC lipodystrophy, which comprises: (a) obtaining a targeting peptide
 CC selective for adipose tissue; (b) attaching the peptide to a therapeutic
 CC agent to form a complex; (c) administering the complex to a subject; and
 CC (d) inducing weight loss in the subject or treating lipodystrophy. The
 CC adipose targeting peptides have anorectic and antilipaeamic activities,
 CC and can be used in peptide and gene therapy. The method is used for
 CC treating obesity or a lipodystrophy that is related to infection with
 CC human immunodeficiency virus (HIV). The peptides used in the method can
 CC also be used for targeting delivery to an organ or tissue, such as
 CC placental delivery. A receptor that binds to a placenta targeting peptide
 CC is used to screen compounds for teratogenic activity. ABR56806 to
 CC ABR56927 and ACC79106 to ACC79111 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 9 AA;

Query Match 51.9%; Score 27; DB 6; Length 9;
 Best Local Similarity 55.6%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTSVPLVPC 9
 | : | | |
 Db 1 CMSSPGVAC 9

```

RESULT 6
AAV84998
ID AAV84998 standard; peptide; 7 AA.
XX
XX
AC AAV84998;
XX
XX
DT 21-AUG-2000 (first entry)
XX
XX
DE Amino acid sequence of an endothelial cell-binding peptide motif.
XX
XX
KW Endothelial cell-binding peptide; Genetic display package;
KW peptide display library; affinity selection; population display package;
KW cell proliferation; cell differentiation; cell death; cell migration;
KW angiogenic activity; infective peptide; anti-fungal; anti-bacterial;
KW receptor protein effector.
XX
XX
OS Unidentified.
XX
XX
PN WO200023465-A2.
XX
XX
PD 27-APR-2000.
XX
XX
PF 19-OCT-1999; 99WO-US024276.
XX
XX
PR 19-OCT-1998; 98US-00174943.
XX
XX
PA (MITO-) MITOTIX INC.
XX
XX
PI Gyuris J, Morris AJ;
XX
XX
DR WPI; 2000-339649/29.
XX
XX
PT Generating a peptide with a selected biological activity useful for
PT identifying endothelial inhibitors and peptides with anti-angiogenic
PT activity by combining peptide display libraries in a display and a
PT secretion mode.
XX
XX
FS Disclosure; Page 42; 86pp; English.
XX
XX
CC The present sequence represents an endothelial cell-binding peptide
CC motif. The peptide may be identified using the method of the invention.
CC The specification describes a method for generating a peptide having a
CC selected biological activity. The method comprises displaying the
CC peptides on the outer surface of a genetic display package to create a
CC peptide display library, and using affinity selection to enrich the
CC population display packages for those containing peptides which have
CC desired specificity to the target cell. The method may be used in the
CC selection of peptides having effects on cell proliferation,
CC differentiation, death and migration, as well as in the identification of
CC peptides which have anti-proliferative activity with respect to one or
CC more types of cells, peptides with (anti-)angiogenic activity, anti-
CC infective peptides (e.g. which are active as anti-fungal or anti-
CC bacterial), receptor protein effectors, and ligands for orphan receptors
CC for which no ligand is known. Moreover, the method may be used to test
CC functional ligand-receptor or ligand-ion channel interactions for cell
CC surface-localized receptors and channels
XX
SQ
Query Match 50.0%; Score 26; DB 3; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVPLVP 8
Db 2 AIPLVP 7
:::|

RESULT 7
ADC44293
ID ADC44293 standard; peptide; 7 AA.

```

```

XX
AC ADC44293;
XX
XX
DT 18-DEC-2003 (first entry)
XX
XX
DE Endothelial cell binding peptide SEQ ID NO:21.
XX
XX
KW endothelial cell binding protein; EGBP; anti-tumour; cytostatic;
KW vasotropic; antiapoptotic; dermatological; ophthalmological;
KW antidiabetic; antiarthritic; vulnary; antitumor; antiinflammatory;
KW antibacterial; gynaecological; angiogenesis.
XX
XX
OS Synthetic.
XX
XX
PN WO2003037172-A2.
XX
XX
PD 08-MAY-2003.
XX
XX
PF 01-NOV-2002; 2002WO-US035258.
XX
XX
PR 01-NOV-2001; 2001US-0334822P.
XX
XX
PA (GPCB-) GPC BIOTECH INC.
XX
XX
PI Gyuris J, Lamphere L, Morris AJ, Tsaion K;
XX
XX
DR WPI; 2003-482072/45.
XX
XX
PT Novel synthetic or recombinant polypeptide useful for promoting, reducing
PT proliferation and/or migration of endothelial cells, and for modulating
PT angiogenesis, has endothelial cell binding protein sequences.
XX
XX
FS Claim 3; SEQ ID NO 21; 126pp; English.
XX
XX
CC The invention relates to a novel isolated, synthetic or recombinant
CC peptide or polypeptide which includes one or more endothelial cell
CC binding protein (ECBP) sequences. A peptide of the invention has anti-
CC tumour, cytostatic, vasotropic, antipsoiatic, dermatological,
CC ophthalmological, antidiabetic, antiarthritic, vulnary, antitumor,
CC antiinflammatory, antibacterial, and gynaecological activity. The peptide
CC is useful for promoting, reducing the proliferation and/or migration of
CC endothelial cells, by treating the cells with an ECBP agonist, which is
CC preferably the peptide, to promote proliferation and/or migration of the
CC treated cells, and for reducing or promoting angiogenesis, by treating
CC the cells with an ECBP antagonist, which is preferably the peptide of the
CC invention. A peptide of the invention is also useful for manufacturing a
CC medicament for promoting angiogenesis, by admixing an ECBP agonist or
CC ECBP antagonist to promote or reduce angiogenesis at one or more sites in
CC a treated mammal. The medicament is useful for promoting or reducing
CC angiogenesis. ECBP sequences are useful to alter the infectivity spectrum
CC of a viral particle. The present sequence represents an ECBP of the
XX
XX
SQ Sequence 7 AA;
Query Match 50.0%; Score 26; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVPLVP 8
Db 2 AIPLVP 7
:::|

RESULT 8
AAV63242
ID AAV63242 standard; peptide; 9 AA.
XX
XX
AC AAV63242;
XX
XX
DT 02-MAR-2000 (first entry)
XX
XX
DE Protocadherin cell adhesion recognition cyclic peptide SEQ ID NO:2726.

```

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..9
 XX WO9957149-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 05-MAY-1999; 99WO-CA000363.
 XX
 PR 05-MAY-1998; 98US-00073040.
 PR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-00234395.
 PR 08-MAR-1999; 99US-00264516.
 XX
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 XX Blaschuk OW, Gour BJ, Byers S;
 XX WPI; 2000-038791/03.
 DR
 XX New cadherin modulating agents, used for modulating nonclassical cadherin
 PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX
 XX Claim 84; Page 201; 252pp; English.
 XX
 CC The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MAs can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC -related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC
 CC RAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in
 CC the exemplification of the present invention
 XX
 SQ Sequence 9 AA;

Query Match 50.0%; Score 26; DB 3; Length 9;
 Best Local Similarity 44.4%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 C1SVPLVPC 9
 Db 1 CFALDLVTC 9

RESULT 9
 AAE07204
 ID AAE07204 standard; peptide; 9 AA.
 XX
 AC AAE07204;
 DT 06-NOV-2001 (first entry)
 XX
 XX Modified colostrinin cyclic peptide #10.
 XX
 XX Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 KW central nervous system disorder; neurodegenerative disorder; weight loss;
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 KW acquired immunological deficiency; neurological disorder; dementia;
 KW antiviral; cyclic.
 XX
 XX Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl; this residue forms a cyclic
 FT linkage with Ser found at the C-terminal end"
 XX
 PN WO200155199-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 26-JAN-2001; 2001WO-GB000329.
 XX
 PR 26-JAN-2000; 2000GB-00001825.
 XX
 XX (REG-) REGEN THERAPEUTICS PLC.
 XX
 XX Georgiades JA;
 XX WPI; 2001-488775/53.
 XX
 PT Peptide useful as an interalia in the treatment of e.g. disorders of the
 PT immune system and the central nervous system comprises ten amino-terminal
 PT amino acid sequence derived from peptides present in colostrinin.
 XX
 PS Example 2; Page 9; 40pp; English.
 XX
 CC The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxiliary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child. The
 CC present sequence is modified colostrinin cyclic peptide #10 related to
 CC the invention
 XX
 SQ Sequence 9 AA;

Query Match 50.0%; Score 26; DB 4; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 C1SVPLV 7

Db 1 CLPLPLV 7

RESULT 10
 ID AM24655 standard; peptide; 9 AA.
 AC AM24655;
 DT 04-DEC-2001 (first entry)
 DE Human MHC class I molecule HLA-A2 binding 83P5G4 peptide #32.
 KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
 KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
 KW cystostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
 KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
 KW chromosome 1q31-q32.

OS Homo sapiens.
 XX WO200159115-A2.
 PN 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US004426.
 XX 09-FEB-2000; 2000US-0181261P.
 XX (UROC-) UROGENESYS INC.
 XX Hubert RS, Afar DEH, Challita-Eid PM, Faris M, Levin E;
 XX Mitchell SC, Jakobovits A;
 XX WPI; 2001-514669/56.
 XX An isolated 83P5G4-related protein useful as a diagnostic and/or
 XX therapeutic agent in multiple cancers such as prostate, bladder and bone
 XX cancer.
 XX Example 15; Page 77; 112pp; English.

CC The polypeptide sequences represent the 83P5G4-related protein and
 CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
 CC expression in normal adult tissue, but it is also aberrantly expressed in
 CC many cancers including tumours of the prostate, testis, bladder, kidney,
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
 CC peptide fragments and specific PCR primers are therefore useful for
 CC diagnosing and treating cancer. A vector comprising a polynucleotide
 CC which encodes a single chain monoclonal antibody, that immunospecifically
 CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
 CC preparation of a composition for treating a patient with a cancer that
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and
 CC tissue and to thereby detect the presence of cancerous cells

XX Sequence 9 AA;
 Query Match 50.0%; Score 26; DB 4; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 ISVPLVPC 9
 Db 2 LPLPLRPC 9

RESULT 11
 ID ABG35050 standard; peptide; 9 AA.

XX ABG35050;
 XX 15-JUL-2002 (first entry)
 XX Endostatin targeting peptide #49.
 XX Targeting peptide; cancer; Hodgkin's disease; cytostatic;
 KW immunosuppressive; anti-inflammatory; antiarthritic; antiviral;
 KW antithrombotic; antidiabetic; antibacterial; diabetes mellitus;
 KW inflammatory disease; arthritis; atherosclerosis; cancer;
 KW autoimmune disease; bacterial infection; viral infection.
 XX Unidentified.
 XX WO200220722-A2.
 XX 14-MAR-2002.
 XX 07-SEP-2001; 2001WO-US027702.
 XX 08-SEP-2000; 2000US-0231266P.
 XX 17-JAN-2001; 2001US-00765101.
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX Arap W, Pasqualini R;
 XX WPI; 2002-383050/41.
 XX Identifying targeting peptides useful for treating e.g. diabetes
 XX mellitus, inflammatory diseases, cancer, or autoimmune diseases,
 XX comprises exposing a sample to a phage display library and recovering
 XX phage bound to the sample.
 XX Claim 56; Page 252; 298pp; English.

CC This invention relates to a novel method for identifying disease
 CC targeting peptides. The method comprises exposing a sample from an organ,
 CC tissue or cell type of interest, to a phage display library and
 CC recovering phage bound to the sample (the phage expresses targeting
 CC peptides). The peptides identified by the method of the invention may
 CC have cytostatic, immunosuppressive, anti-inflammatory, antithrombotic,
 CC antithrombotic, antidiabetic, antibacterial and antiviral
 CC activities. The methods and composition are useful for identifying
 CC targeting peptides and one or more receptors for a targeting peptide. The
 CC targeting peptides are used for selective delivery of therapeutic agents,
 CC including gene therapy vectors and fusion proteins, to specific organs,
 CC tissues, or cell types in subject. The targeting peptide may also be used
 CC for treating diseases such as diabetes mellitus, inflammatory diseases,
 CC arthritis, atherosclerosis, cancer, autoimmune diseases, bacterial and
 CC viral infections and Hodgkin's disease. The present sequence represents a
 CC targeting peptide of the invention

XX Sequence 9 AA;
 Query Match 50.0%; Score 26; DB 5; Length 9;
 Best Local Similarity 55.6%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CUSVPLVPC 9
 Db 1 CRSLPPVRC 9

RESULT 12
 ID AAR95843 standard; peptide; 5 AA.
 XX AAR95843;
 XX 26-JUN-1996 (first entry)

DE IGF-1 mutin C67 residues 63-67.
XX
KW Insulin-like growth factor-1; IGF-1; polyethylene glycol; PEG; triflate;
KW IGF-1/PEG conjugate; maleimide; sulphydryl; thiol; tresylate; aziride;
KW exirane; 5-pyridyl; therapy; dwarfism; diabetes; periodontal disease;
KW osteoporosis.
XX
OS Synthetic.
XX
XX
XX Key Location/Qualifiers
FT Misc-difference 5
FT /note= "A5C"
XX
XX W09532003-AL.
XX
XX 30-NOV-1995.
XX
XX 24-MAY-1995; 95WO-US006540.
XX
XX 24-MAY-1994; 94US-00248273.
XX
XX (AMGE-) AMGEN BOULDER INC.
XX
XX Cox GN, Modermott MJ, Ko C;
XX
XX WPI; 1996-020360/02.
XX
XX Conjugates for treatment of, e.g. dwarfism, diabetes, or osteoporosis -
XX comprising polyethylene glycol attached to mutin of IGF at free
XX cysteine.
XX
XX Example 2; Page 22; 48pp; English.
XX
XX AAR59832-R95844 represent the altered fragments of the insulin-like
XX growth factor-1 (IGF-1) mutins of the invention. This sequence
XX represents the N-terminal residues 63-67 of the IGF-1 mutin C67. The
XX wild type IGF-1 sequence is represented by AAR87744. These mutins
XX contain a non-naive cysteine residue substituted for one of the first (or
XX last) four amino acid residues of this sequence. Polyethylene glycol
XX (PEG) conjugates are then created from the mutins, where the PEG is
XX attached to the non-native cysteine residue. The PEG is attached to the
XX free cysteine through an activating group selected from maleimide,
XX sulphydryl, thiol, triflate, tresylate, aziride, exirane or 5-pyridyl.
XX The conjugates can also comprise a second polypeptide attached to the
XX PEG. The conjugates may be used for the treatment of IGF associated
XX conditions, such as dwarfism, diabetes, periodontal disease or
XX osteoporosis. Advantages associated with these conjugates are that they
XX have a higher molecular weight, and an extended circulating half life in
XX comparison to wild type IGF
XX
XX Sequence 5 AA;
Query Match 48.1%; Score 25; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 PLVPC 9
DB 1 PLKPC 5
RESULT 13
AAY84999
ID AAY84999 standard; peptide; 5 AA.
XX
XX AC AAY84999;
XX
XX 21-AUG-2000 (first entry)
DT
XX Amino acid sequence of an endothelial cell-binding peptide motif.
DE
XX Endothelial cell-binding peptide; Genetic display package;
KW
KW peptide display library; affinity selection; population display package;
XX

KW cell proliferation; cell differentiation; cell death; cell migration;
KW angiogenic activity; infective peptide; anti-fungal; anti-bacterial;
KW receptor protein effector.
XX
OS Unidentified.
XX
XX W0200023465-A2.
XX
XX 27-APR-2000.
XX
XX 19-OCT-1999; 99WO-US024276.
XX
XX 19-OCT-1998; 98US-00174943.
XX
XX (MITO-) MITOTIX INC.
XX
XX Gyuris J, Morris AJ;
XX
XX WPI; 2000-339649/29.
XX
XX Generating a peptide with a selected biological activity useful for
XX identifying endothelial inhibitors and peptides with anti-angiogenic
XX activity by combining peptide display libraries in a display and a
XX secretion mode.
XX
XX Disclosure; Page 42; 86pp; English.
XX
XX The present sequence represents an endothelial cell-binding peptide
XX motif. The peptide may be identified using the method of the invention.
XX The specification describes a method for generating a peptide having a
XX selected biological activity. The method comprises displaying the
XX peptides on the outer surface of a genetic display package to create a
XX peptide display library, and using affinity selection to enrich the
XX population display packages for those containing peptides which have
XX desired specificity to the target cell. The method may be used in the
XX selection of peptides having effects on cell proliferation,
XX differentiation, death and migration, as well as in the identification of
XX peptides which have anti-proliferative activity with respect to one or
XX more types of cells, peptides with (anti-)angiogenic activity, anti-
XX infective peptides (e.g. which are active as anti-fungal or anti-
XX bacterial), receptor protein effectors, and ligands for orphan receptors
XX for which no ligand is known. Moreover, the method may be used to test
XX functional ligand-receptor or ligand-ion channel interactions for cell
XX surface-localized receptors and channels
XX
XX Sequence 5 AA;
Query Match 48.1%; Score 25; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 VPLVP 8
DB 1 IPLVP 5
RESULT 14
ADC44308
ID ADC44308 standard; peptide; 5 AA.
XX
XX AC ADC44308;
XX
XX 18-DEC-2003 (first entry)
DT
XX Endothelial cell binding peptide SEQ ID NO:36.
DE
XX
XX Endothelial cell binding protein; EGBP; anti-tumour; cytostatic;
KW vasotropic; antipsoriatic; dermatological; ophthalmological;
KW antidiabetic; antiarthritic; vulnerary; antitumor; antiinflammatory;
KW antibacterial; gynaecological; angiogenesis.
XX
XX Synthetic.
XX

PN WO2003037172-A2.
 XX 08-MAY-2003.
 PD
 XX
 PF 01-NOV-2002; 2002WO-US035258.
 XX
 XX 01-NOV-2001; 2001US-0334822P.
 PR
 XX (GFCB-) GPC BIOTECH INC.
 PA
 XX Gyuris J, Lamphere L, Morris AJ, Tsaloun K;
 PI WPI; 2003-482072/45.
 DR
 XX Novel synthetic or recombinant polypeptide useful for promoting, reducing
 PT proliferation and/or migration of endothelial cells, and for modulating
 PT angiogenesis, has endothelial cell binding protein sequences.
 XX
 PS Claim 3; SEQ ID NO 36; 126pp; English.
 XX
 CC The invention relates to a novel isolated, synthetic or recombinant
 CC peptide or polypeptide which includes one or more endothelial cell
 CC binding protein (ECBP) sequences. A peptide of the invention has anti-
 CC tumour, cytostatic, vasotropic, antipsoriatic, dermatological,
 CC ophthalmological, antidiabetic, antiarthritic, vulnary, antiulcer,
 CC antiinflammatory, antibacterial, and gynaecological activity. The peptide
 CC is useful for promoting, reducing the proliferation and/or migration of
 CC endothelial cells, by treating the cells with an ECBP agonist, which is
 CC preferably the peptide, to promote proliferation and/or migration of the
 CC treated cells, and for reducing or promoting angiogenesis, by treating
 CC the cells with an ECBP antagonist, which is preferably the peptide of the
 CC invention. A peptide of the invention is also useful for manufacturing a
 CC medicament for promoting angiogenesis, by administering an ECBP agonist or
 CC ECBP antagonist to promote or reduce angiogenesis at one or more sites in
 CC a treated mammal. The medicament is useful for promoting or reducing
 CC angiogenesis. ECBP sequences are useful to alter the infectivity spectrum
 CC of a viral particle. The present sequence represents an ECBP of the
 CC invention.
 XX
 SQ Sequence 5 AA;
 Query Match 48.1%; Score 25; DB 7; Length 5;
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 VPLVP 8
 Db :|||||
 1 IPLVP 5
 RESULT 15
 AAY03909
 ID AAY03909 standard; peptide; 6 AA.
 XX
 AC AAY03909;
 XX
 DT 08-JUN-1999 (first entry)
 XX
 DE Hepatitis C inhibitor peptide.
 XX
 KW Hepatitis C; inhibitor; NS3 protease; NS4A cofactor.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-Ac-Asp"
 XX
 PN WO9907733-A2.
 XX
 PD 18-FEB-1999.
 XX
 PF 10-AUG-1998; 98WO-CA000765.

XX 11-AUG-1997; 97US-0055186P.
 PR
 XX (BOEH) BOEHRINGER INGELHEIM CANADA LTD.
 PA
 XX Llinas-Brunet M, Poupart M, Rancourt J, Simoneau B, Tsantrizos Y;
 PI Wernic D;
 PI
 XX WPI; 1999-167361/14.
 DR
 XX New peptides inhibitors of NS3 protease - useful for treatment of
 PT hepatitis C infections.
 PT
 XX Disclosure; Page 108; 158pp; English.
 PS
 XX New generically described peptides are disclosed which are NS3 protease
 CC inhibitors useful for treating hepatitis C virus (HCV) infection. The
 CC present sequence represents a specific example of these peptides. In a
 CC test to determine inhibition in a NS3 protease/NS4A cofactor peptide
 CC radiometric assay, this peptide had an IC50 value of 92 micromolar
 CC
 XX Sequence 6 AA;
 SQ
 Query Match 46.2%; Score 24; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 LVPC 9
 Db :|||||
 3 LVPC 6
 Search completed: March 8, 2004, 12:17:53
 Job time : 50.5 secs

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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:19:53 ; Search time 26 Seconds
(without alignments)
73.092 Million cell updates/sec

Title: US-09-761-636A-14

Perfect score: 52

Sequence: 1 C1SVPLVPC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 90760

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PTCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	52	100.0	9	US-09-761-636A-14	Sequence 14, Appl
2	27	51.9	9	US-10-154-884B-11221	Sequence 11221, A
3	27	51.9	9	US-10-154-884B-11228	Sequence 11228, A
4	27	51.9	9	US-10-154-884B-11250	Sequence 11250, A
5	27	51.9	9	US-10-154-884B-11254	Sequence 11254, A
6	27	51.9	9	US-10-154-884B-11258	Sequence 11258, A
7	27	51.9	9	US-10-154-884B-11259	Sequence 11259, A
8	27	51.9	9	US-10-154-884B-11265	Sequence 11265, A
9	27	51.9	9	US-10-154-884B-11275	Sequence 11275, A
10	27	51.9	9	US-10-154-884B-11280	Sequence 11280, A
11	26	50.0	7	US-10-286-457-21	Sequence 21, Appl
12	26	50.0	9	US-09-780-053-148	Sequence 148, Appl
13	26	50.0	9	US-10-006-869-2726	Sequence 2726, Ap
14	26	50.0	9	US-10-395-032-2726	Sequence 2726, Ap
15	25	48.1	5	US-10-286-457-36	Sequence 36, Appl

16	24.5	47.1	9	15	US-10-428-335-52	Sequence 52, Appl
17	24	46.2	9	10	US-09-932-165-439	Sequence 439, App
18	24	46.2	9	10	US-09-932-165-636	Sequence 636, App
19	24	46.2	9	14	US-10-286-457-216	Sequence 216, App
20	24	46.2	9	15	US-10-428-335-90	Sequence 90, Appl
21	23	44.2	7	9	US-09-761-636A-11	Sequence 11, Appl
22	23	44.2	9	9	US-09-997-579-19	Sequence 19, Appl
23	23	44.2	9	14	US-10-038-407-29	Sequence 29, Appl
24	23	44.2	9	14	US-10-254-446A-123	Sequence 123, App
25	23	44.2	9	14	US-10-286-457-165	Sequence 165, App
26	23	44.2	9	14	US-10-286-457-500	Sequence 500, App
27	23	44.2	9	14	US-10-164-279-15	Sequence 15, Appl
28	22	42.3	4	9	US-09-947-387-69	Sequence 69, Appl
29	22	42.3	4	15	US-10-138-375-69	Sequence 69, Appl
30	22	42.3	5	9	US-09-947-387-68	Sequence 68, Appl
31	22	42.3	5	9	US-09-947-387-116	Sequence 116, App
32	22	42.3	5	15	US-10-138-375-68	Sequence 68, Appl
33	22	42.3	5	15	US-10-138-375-116	Sequence 116, App
34	22	42.3	6	9	US-09-947-387-67	Sequence 67, Appl
35	22	42.3	6	9	US-09-947-387-115	Sequence 115, App
36	22	42.3	6	14	US-10-010-184A-2	Sequence 2, Appl
37	22	42.3	6	15	US-10-138-375-67	Sequence 67, Appl
38	22	42.3	6	15	US-10-138-375-115	Sequence 115, App
39	22	42.3	7	9	US-09-947-387-114	Sequence 114, App
40	22	42.3	7	15	US-10-138-375-114	Sequence 114, App
41	22	42.3	8	9	US-09-947-387-113	Sequence 113, App
42	22	42.3	8	15	US-10-138-375-113	Sequence 113, App
43	22	42.3	9	9	US-09-918-243-39	Sequence 39, Appl
44	22	42.3	9	9	US-09-918-243-74	Sequence 74, Appl
45	22	42.3	9	9	US-09-905-083-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-09-761-636A-14
; Sequence 14, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761.636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-14

Query Match 100.0%; Score 52; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C1SVPLVPC 9
|||
Db 1 C1SVPLVPC 9

RESULT 2
US-10-154-884B-11221
; Sequence 11221, Application US/10154884B
; Publication No. US20040005561A1


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; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11221
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11221

Query Match 51.9%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C1SVPL 6
Db 2 CLSVPV 7

RESULT 3
US-10-154-884B-11228
; Sequence 11228, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11221
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11221

Query Match 51.9%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C1SVPL 6
Db 2 CLSVPV 7

RESULT 4
US-10-154-884B-11250
; Sequence 11250, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11250
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11250
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Query Match          51.9%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 C1SVPL 6
Db 4 CLSVPV 9

RESULT 5
US-10-154-884B-11254
; Sequence 11254, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US 60/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11254
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11254

Query Match          51.9%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 C1SVPL 6
Db 4 CLSVPV 9

RESULT 6
US-10-154-884B-11258
; Sequence 11258, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
```

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; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11258
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11258

Query Match          51.9%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 C1SVPL 6
Db 4 CLSVPV 9

RESULT 7
US-10-154-884B-11259
; Sequence 11259, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
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; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11259
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11259

Query Match      51.9%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 C1SVPL 6
Db      4 CLSVPV 9

RESULT 8
US-10-154-884B-11265
; Sequence 11265, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11265
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11265

Query Match      51.9%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 C1SVPL 6
Db      4 CLSVPV 9

RESULT 9
US-10-154-884B-11275
; Sequence 11275, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11275
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11275

Query Match      51.9%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 C1SVPL 6
Db      4 CLSVPV 9

RESULT 10
US-10-154-884B-11280
; Sequence 11280, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479

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; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11280
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11280

Query Match 51.9%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 C1SVPL 6
|:|:|:
Db 4 C1SVPV 9

RESULT 11
US-10-286-457-21
; Sequence 21, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-21

Query Match 50.0%; Score 26; DB 14; Length 7;
Best Local Similarity 56.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLVP 8
|:|:|:
Db 2 AIPLVP 7

RESULT 12
US-09-780-053-148
; Sequence 148, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert

; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Chailita-Bid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 8395G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.SUSUI
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-148

Query Match 50.0%; Score 26; DB 9; Length 9;
Best Local Similarity 50.0%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISVPLVPC 9
|:|:|:
Db 2 LPLPLRPC 9

RESULT 13
US-10-006-869-2726
; Sequence 2726, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 2726
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-10-006-869-2726

Query Match 50.0%; Score 26; DB 14; Length 9;
Best Local Similarity 44.4%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 C1SVPLVPC 9
|:|:|:
Db 1 CFALDLVTC 9

RESULT 14
US-10-395-032-2726
; Sequence 2726, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2726
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-10-395-032-2726

Query Match 50.0%; Score 26; DB 15; Length 9;
Best Local Similarity 44.4%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
Db 1 CFALDLVTC 9

RESULT 15
US-10-286-457-36
; Sequence 36, Application US/10286457
; Publication No. US2003016004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-36

Query Match 48.1%; Score 25; DB 14; Length 5;
Best Local Similarity 80.0%; Pred. No. 7.2e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPLVP 8
Db 1 IPLVP 5

Search completed: March 8, 2004, 12:28:23
Job time : 27 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:41:37 ; Search time 20 Seconds
(without alignments)
110.620 Million cell updates/sec

Title: US-09-761-636a-4
Perfect score: 133
Sequence: 1 QGQHIGMSFLOHKNCECRPKD 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 4494

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	24.8	23	B38671	peptidylglycine mo
2	31	23.3	23	S60565	homeodomain protei
3	26	19.5	22	B90996	probable transcrip
4	26	19.5	22	H86433	protein T17H7.9 [i
5	25.5	19.2	19	T37096	small hypothetical
6	25.5	19.2	22	1 MXKN1	mu-conotoxin GIIIA
7	25.5	19.2	22	1 MXKN2	mu-conotoxin GIIIB
8	25	18.8	13	A61210	antibiotic GR2270
9	25	18.8	23	S23637	hypothetical prote
10	25	18.8	23	AF0535	hypothetical prote
11	24.5	18.4	22	1 MXKN3	mu-conotoxin GIIIC
12	24	18.0	5	A33882	cadmium-binding pe
13	24	18.0	7	B33882	cadmium-binding he
14	24	18.0	14	PA0104	protein QF200070 -
15	24	18.0	19	A31252	metallothionein I
16	24	18.0	20	2 DIRT	dental fluid tra
17	24	18.0	20	B60365	chymotrypsin inhib
18	24	18.0	21	A59048	T-cell receptor J-
19	23.5	17.7	23	A59048	convulsant peptide
20	23	17.3	9	S66636	alpha-2-macroglobu
21	23	17.3	10	A13687	caerulein-like pep
22	23	17.3	12	JQ2308	hypothetical 1.4K
23	23	17.3	12	JQ2318	hypothetical 1.4K
24	23	17.3	13	S39413	tubulin beta chain
25	23	17.3	14	1 QMWAPP	polistes mastopara
26	23	17.3	14	S41601	interferon alpha r
27	23	17.3	16	D45193	zinc finger protei
28	23	17.3	16	JN0264	translation initia
29	23	17.3	18	S57520	T cell receptor be

30 23 17.3 19 2 D49404 T-cell receptor be
31 23 17.3 22 2 PC7072 H+-transporting tw
32 22 16.5 8 2 S59622 metallothionein is
33 22 16.5 10 1 RHLNGS gonadoliberin - se
34 22 16.5 12 2 T46794 hypothetical prote
35 22 16.5 13 2 JH0460 corticostatic pept
36 22 16.5 13 2 PH0799 T-cell receptor al
37 22 16.5 14 2 PA0015 seed storage prote
38 22 16.5 15 2 PH1443 T-cell receptor al
39 22 16.5 16 2 A45133 casein kinase II (
40 22 16.5 16 2 B49255 T-cell receptor be
41 22 16.5 16 2 F49039 T-cell receptor be
42 22 16.5 17 2 E40442 integrase homolog
43 22 16.5 17 2 I78870 gene RBI protein -
44 22 16.5 18 2 I40062 shikimate 5-dehydr
45 22 16.5 18 2 C59089 theta defensin-1 -

ALIGNMENTS

RESULT 1

B38671
peptidylglycine monooxygenase (EC 1.14.17.3) form 4 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 05-Nov-1999
C:Accession: B38671
R:Stoffers, D.A.; Ouafik, L.; Bippier, B.A.
J. Biol. Chem. 266, 1701-1707, 1991
A:Title: Characterization of novel mRNAs encoding enzymes involved in peptide alpha-am
A:Reference number: A38671; MUID:91107670; PMID:1988445
A:Accession: B38671
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-23 <STO>
A:Cross-references: GB:M63662; NID:g206719; PIDN:AAA42068.1; PID:g206720
C:Keywords: oxidoreductase

Query Match 24.8%; Score 33; DB 2; Length 23;
Best Local Similarity 46.7%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

Qy 8 MSFLOHKNK--ECRP 20
Db 8 ISFTQKKCKVHCNP 22

RESULT 2

S60565
homeodomain protein hrox3 - California red abalone (fragment)
C:Species: Haliotis rufescens (California red abalone)
C>Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 15-Oct-1999
C:Accession: S60565
R:Degnan, B.M.; Morse, D.E.
Mol. Marine Biol. Biotechnol. 2, 1-9, 1993
A:Title: Identification of eight homeobox-containing transcripts expressed during larv
A:Reference number: S60564; MUID:93372986; PMID:7689904
A:Accession: S60565
A:Molecule type: mRNA
A:Residues: 1-23 <DEG>
A:Cross-references: EMBL:X79372; NID:g495110; PIDN:CAA55917.1; PID:g495111
C:Genetics:
A:Gene: hrox3
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 23.3%; Score 31; DB 2; Length 23;
Best Local Similarity 55.68; Pred. No. 3.3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 14 NKCECRPKK 22
Db 2 NKVLCRRR 10

```

Query Match          19.2%   Score 25.5;   DB 1;   Length 22;
Best Local Similarity 36.4%;   Pred: No. 2.3e+03;
Matches 4;   Conservative 4;   Mismatches 0;   Indels 3;   Gaps 1;
QY      15 KC--ECRPKK 22
      ||| :||:

```

Db 9 KCXDRCKPQR 19

RESULT 7
MXKN2
mu-conotoxin GIIIB [validated] - cone shell (Conus geographus)
N;Alternate names: geographotoxin II (GTX II); myotoxin II
C;Species: Conus geographus (geography cone)
C;Date: 14-Nov-1993 #sequence_revision 14-Nov-1993 #text_change 15-Sep-2000
C;Accession: A01787; B23579
R;Sato, S.; Nakamura, H.; Ohizumi, Y.; Kobayashi, J.; Hirata, Y.
FEBS Lett. 155, 277-280, 1983
A;Title: The amino acid sequences of homologous hydroxyproline-containing myotoxins from
A;Reference number: A91309; PMID:83240170; PMID:6852238
A;Accession: A01787
A;Molecule type: protein
A;Residues: 1-22 <SAT>
R;Cruz, L.J.; Gray, W.R.; Olivera, B.M.; Zeikus, R.D.; Kerr, L.; Yoshikami, D.; Moczydl
J. Biol. Chem. 260, 9280-9288, 1985
A;Title: Conus geographus toxins that discriminate between neuronal and muscle sodium ch
A;Reference number: A23579; PMID:85261316; PMID:2410412
A;Accession: B23579
A;Molecule type: protein
A;Residues: 1-22 <CRU>
R;Hill, J.M.; Alewood, P.F.; Craik, D.J.
submitted to the Brookhaven Protein Data Bank, April 1996
A;Reference number: A65705; PDB:1GIB
A;Contents: annotation; conformation by (1)H-NMR, residues 1-22
R;Hill, J.M.; Alewood, P.F.; Craik, D.J.
Biochemistry 35, 8824-8835, 1996
A;Title: Three-dimensional solution structure of mu-conotoxin GIIIB, a specific blocker
A;Reference number: A58590; PMID:96280640; PMID:8688418
A;Contents: annotation; conformation by (1)H-NMR
C;Superfamily: mu-conotoxin
C;Keywords: amidated carboxyl end; hydroxyproline; myotoxin; sodium channel inhibitor; v
F;3-15,4-20,10-21/Diulfide bonds: #status experimental
F;6.7/Modified site: 4-hydroxyproline (Pro) #status experimental
F;17/Modified site: 4-hydroxyproline (Pro) #status experimental
F;22/Modified site: amidated carboxyl end (Ala) #status experimental

Query Match 19.2%; Score 25.5; DB 1; Length 22;
Best Local Similarity 45.5%; Pred. No. 2.3e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 15 KCE--CRPKK 22
||| : |||
Db 9 KCXDRCKPKM 19

RESULT 8
A61210
antibiotic GE2270 - Planobispora rosea (ATCC 53773)
C;Species: Planobispora rosea
C;Date: 13-May-1994 #sequence_revision 05-Apr-1995 #text_change 07-May-1999
C;Accession: A61210
R;Kettenring, J.; Colombo, L.; Ferrari, P.; Tavecchia, P.; Nebuloni, M.; Vekey, K.; Gall
J. Antibiot. 44, 702-715, 1991
A;Title: Antibiotic GE2270 A: a novel inhibitor of bacterial protein synthesis. II. Stru
A;Reference number: A61210; PMID:91349090; PMID:1880060
A;Accession: A61210
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <KE>
C;Keywords: amidated carboxyl end; methylated amino acid; oxazole/thiazole ring
F;1-10/Cross-link: thiazole amino end (Cys-Lys) (by 10-C6) #status experimental
F;2-3/Cross-link: 5-methoxythiazole (Val-Cys) #status experimental
F;4-5/Cross-link: 5-methylthiazole (Asn-Cys) #status experimental
F;4/Modified site: N4-methylasparagine (Asn) #status experimental
F;7-8/Cross-link: thiazole (Phe-Cys) #status experimental
F;7/Modified site: 3-hydroxyphenylalanine (Phe) #status experimental
F;8-9/Cross-link: thiazole (Cys-Cys) #status experimental
F;9-10/Cross-link: pyridine (Cys-Lys) #status experimental
F;10-11/Cross-link: thiazole (Lys-Cys) #status experimental

F;11-12/Cross-link: 2-oxazoline (Cys-Ser) #status experimental
F;13/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 18.8%; Score 25; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 16 CECRP 20
||| : |||
Db 9 CKCGP 13

RESULT 9
S23637
hypothetical protein - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C;Accession: S23637
R;Huber, C.; Klobbeck, H.G.; Zachau, H.G.
Eur. J. Immunol. 22, 1561-1565, 1992
A;Title: Ongoing V(kappa)-J(kappa) recombination after formation of a productive V(kap
A;Reference number: S23637; PMID:92289816; PMID:1601042
A;Accession: S23637
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-23 <HUB>
A;Cross-references: EMBL:X63370

Query Match 18.8%; Score 25; DB 2; Length 23;
Best Local Similarity 46.2%; Pred. No. 2.8e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 11 LQHNKC--ECRPK 21
||| : |||
Db 4 LQHNKPRDVRPR 16

RESULT 10
AF0535
hypothetical protein STV0293 [imported] - Salmonella enterica subsp. enterica serovar
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: This species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AF0535
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
S.; Conington, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farra
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica ser
A;Reference number: AB0502; PMID:21534947; PMID:11677608
A;Accession: AF0535
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-23 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08726.1; PID:g16501549; GSPDB:GN00176
C;Genetics:
A;Gene: STV0293

Query Match 18.8%; Score 25; DB 2; Length 23;
Best Local Similarity 83.3%; Pred. No. 2.8e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 FLQHNK 15
||| : |||
Db 16 FLQHNK 21

RESULT 11
MXKN3
mu-conotoxin GIIIC - cone shell (Conus geographus)
C;Species: Conus geographus (geography cone)
C;Date: 31-Mar-1989 #sequence_revision 04-Nov-1994 #text_change 23-May-1997

C;Accession: C23579
R;Cruz, L.J.; Gray, W.R.; Olivera, B.M.; Zeikus, R.D.; Kerr, L.; Yoshikami, D.; Moczyldo
J. Biol. Chem. 260, 9280-9288, 1985
A;Title: Conus geographus toxins that discriminate between neuronal and muscle sodium ch
A;Reference number: A23579; MUID:85261316; PMID:2410412
A;Accession: C23579
A;Molecule type: protein
A;Residues: 1-22 <CRU>
C;Superfamily: mu-conotoxin
C;Keywords: amidated carboxyl end; hydroxyproline; myotoxin; sodium channel inhibitor; v
F;3-15,4-20,10-21/Disulfide bonds: #status predicted
F;6,7,17/Modified site: 4-hydroxyproline (Pro) #status experimental
F;22/Modified site: amidated carboxyl end (Ala) #status experimental

Query Match 18.4%; Score 24.5; DB 1; Length 22;
Best Local Similarity 45.5%; Pred. No. 3.3e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

Qy 15 KCE---CRPKK 22
Db 9 KCKDRRCCKLK 19

RESULT 12
A33882
cadmium-binding pentapeptide - downy thornapple
C;Species: Datura innoxia (downy thornapple)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993
C;Accession: A33882
R;Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987
A;Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plant c
A;Reference number: A94182; MUID:88016144; PMID:3477793
A;Accession: A33882
A;Molecule type: protein
A;Residues: 1-5 <JAC>

Query Match 18.0%; Score 24; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 15 KCCE 18
Db 1 ECEC 4

RESULT 13
B33882
cadmium-binding heptapeptide - downy thornapple
C;Species: Datura innoxia (downy thornapple)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993
C;Accession: B33882
R;Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987
A;Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plant c
A;Reference number: A94182; MUID:88016144; PMID:3477793
A;Accession: B33882
A;Molecule type: protein
A;Residues: 1-7 <JAC>

Query Match 18.0%; Score 24; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 15 KCEC 18
Db 1 ECEC 4

RESULT 14
PA0104
protein QF200070 - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0104
R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JTPID, October 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotric
A;Reference number: PA0051
A;Accession: PA0104
A;Molecule type: protein
A;Residues: 1-14 <CHO>

Query Match 18.0%; Score 24; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 IGEMSF 10
Db 1 LGEMXF 6

RESULT 15
A31252
metallothionein I - yeast (Candida glabrata) (fragment)
C;Species: Candida glabrata
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C;Accession: A31252
R;Mehra, R.K.; Tarbet, E.B.; Gray, W.R.; Winge, D.R.
Proc. Natl. Acad. Sci. U.S.A. 85, 8815-8819, 1988
A;Title: Metal-specific synthesis of two metallothioneins and gamma-glutamyl peptides
A;Reference number: A94212; MUID:89057829; PMID:3194392
A;Accession: A31252
A;Molecule type: protein
A;Residues: 1-19 <MEH>
C;Superfamily: metallothionein

Query Match 18.0%; Score 24; DB 2; Length 19;
Best Local Similarity 60.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 14 NKCEC 18
Db 2 NDKCK 6

Search completed: March 8, 2004, 11:48:13
Job time : 21 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:15:07 ; Search time 11 Seconds
(without alignments)
108.874 Million cell updates/sec

Title: US-09-761-636A-4

Sequence: 1 QQQHIGEMFLQHNKCEPRPKD 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 1457

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	31	23.3	22	1 HCY4_HOMAM	P82299 homarus ame
2	25.5	19.2	22	1 CXM1_CONGE	P01523 conus geogr
3	25.5	19.2	22	1 CXM2_CONGE	P01524 conus geogr
4	25	18.8	19	1 PHLC_STAIN	P80324 staphylococ
5	25	18.8	20	1 TL14_SPIOL	P82862 spinacia ol
6	24.5	18.4	22	1 CXM3_CONGE	P05482 conus geogr
7	24	18.0	20	1 DPTS_RAT	P07448 rattus norv
8	23.5	17.7	23	1 CXCV_CONTE	P58845 conus texti
9	23	17.3	14	1 MAST_POLJA	P01517 polistes ja
10	23	17.3	15	1 NKSO_PSSTE	P59073 pseudonaja
11	22	16.5	10	1 GON1_PETMA	P04378 petromyzon
12	22	16.5	12	1 UKA2_HUMAN	F31144 homo sapien
13	22	16.5	21	1 SRD2_ATREN	P13211 atractaspis
14	22	16.5	23	1 SK11_TITCA	P83243 titiys camb
15	21.5	16.2	23	1 ACHG_ELEEL	P09692 electrophor
16	21	15.8	20	1 PSRF_CAPAN	Q03367 capiscum an
17	21	15.8	12	1 RSL9_TOBBP	Q56251 tomato big
18	21	15.8	17	1 LCK_RAT	Q01621 rattus norv
19	21	15.8	20	1 FRE3_LITIN	P56249 litoria inf
20	21	15.8	20	1 KORA_METTM	P80904 methanobact
21	21	15.8	23	1 PAP2_MANSE	P30254 manduca sex
22	20	15.0	18	1 MIA_HORSE	P01202 equus cabal
23	20	15.0	18	1 TAMF_STRMB	P83543 streptomyc
24	20	15.0	20	1 LYC_FELCA	F37155 felis silve
25	20	15.0	20	1 TXV2_PHONI	Q9TWR5 phoneutria
26	20	15.0	21	1 BTX_ATRBI	P80163 atractaspis
27	20	15.0	21	1 MISG_MISAN	P81474 misgurnus a
28	20	15.0	22	1 ANFC_CHICK	P21805 gallus gall
29	20	15.0	23	1 BRIB_RANES	F40836 rana escul
30	20	15.0	23	1 DEF4_SPIOL	P81569 spinacia ol
31	20	15.0	23	1 NUO5_SOLTU	P80262 solanum tub
32	19	14.3	8	1 FAR1_PENMO	P83316 penaeus mon
33	19	14.3	10	1 BPP8_BOVIN	P30426 bothrops in

34 19 14.3 10 1 PAR7_MACRS
35 19 14.3 10 1 LSK2_LEUNA
36 19 14.3 11 1 TKN_ELEMO
37 19 14.3 13 1 AFN_CALVI
38 19 14.3 13 1 FARB_ASCSU
39 19 14.3 15 1 PC20_BRANA
40 19 14.3 16 1 FIBA_PABIT
41 19 14.3 17 1 ITHB_HIRME
42 19 14.3 18 1 ALI3_CARMA
43 19 14.3 19 1 NS2_MYCTU
44 19 14.3 20 1 BRA_BASAL
45 19 14.3 21 1 FIBB_RANTA

ALIGNMENTS

RESULT 1
HCY4_HOMAM
ID HCY4_HOMAM STANDARD; PRT; 22 AA.
AC P82299;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hemocyanin subunit 4 (Fragment).
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_TaxID=6706;
RN [1]
RP SEQUENCE.
RX MEDLINE=9959579; PubMed=10327595;
RA Stoeva S., Dolashka P., Kristova R., Genov N., Voelter W.;
RT "Subunit composition and N-terminal analysis of arthropod
hemocyanins.";
RL Comp. Biochem. Physiol. 122B:69-75(1999).
CC -!- FUNCTION: Hemocyanins are copper-containing oxygen carriers
occurring freely dissolved in the hemolymph of many mollusks and
arthropods.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Hemolymph.
CC -!- SIMILARITY: Belongs to the tyrosinase family. Hemocyanin
subfamily.
DR InterPro; IPR000896; Hemocyanin.
DR InterPro; IPR002227; Tyrosinase.
DR PROSITE; P500209; HEMOCYANIN_1; PARTIAL.
DR PROSITE; P500210; HEMOCYANIN_2; PARTIAL.
DR PROSITE; P500497; TYROSINASE_1; PARTIAL.
DR PROSITE; P500498; TYROSINASE_2; PARTIAL.
KW Transport; Oxygen transport; Copper; Hemolymph.
FT NON TER 22
SQ SEQUENCE 22 AA; 2476 MW; 0C47D4D98E12FDB6 CRC64;

Query Match 23.3%; Score 31; DB 1; Length 22;
Best Local Similarity 62.5%; Pred. No. 74;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQQHIGEM 8
|||:::
Db 5 QQQNIGQL 12

RESULT 2
CXM1_CONGE
ID CXM1_CONGE STANDARD; PRT; 22 AA.
AC P01523;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mu-conotoxin GIITa (Myotoxin I) (Geographutoxin I) (GTx-I).
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
RN [1] NCBI_TaxID=6491;
RP SEQUENCE.
RX MEDLINE=85261316; PubMed=2410412;
RA Cruz L.J., Gray W.R., Olivera B.M., Zeikus R.D., Kerr L.,
RA Yoshikami D., Moczydlowski E.;
RT "Conus geographus toxins that discriminate between neuronal and
RT muscle sodium channels.";
RL J. Biol. Chem. 260:9280-9288(1985).
RN [2]
RP SEQUENCE.
RX MEDLINE=83210170; PubMed=6852238;
RA Sato S., Nakamura H., Ohizumi Y., Kobayashi J., Hirata Y.;
RA "The amino acid sequences of homologous hydroxyproline-containing
RT myotoxins from the marine snail Conus geographus venom.";
RL FEBS Lett. 155:277-280(1983).
RN [3]
RP DISULFIDE BONDS.
RX MEDLINE=90249506; PubMed=2338142;
RA Hidaka Y., Sato K., Nakamura H., Kobayashi J., Ohizumi Y.,
RA Simonishi Y.;
RT "Disulfide pairings in geographutoxin I, a peptide neurotoxin from
RT Conus geographus.";
RL FEBS Lett. 284:29-32(1990).
RN [4]
RP STRUCTURE BY NMR.
RX MEDLINE=91122275; PubMed=1991506;
RA Ott K.-H., Becker S., Gordon R.D., Rueterjans H.;
RT "Solution structure of mu-conotoxin GIIIA analysed by 2D-NMR and
RT distance geometry calculations.";
RL FEBS Lett. 278:160-166(1991).
RN [5]
RP STRUCTURE BY NMR.
RX MEDLINE=91299744; PubMed=2069951;
RA Lancelin J.-M., Kohda D., Tate S.-I., Yanagawa Y., Abe T., Satake M.,
RA Inagaki F.;
RT "Tertiary structure of conotoxin GIIIA in aqueous solution.";
RL Biochemistry 30:6908-6916(1991).
CC -1- FUNCTION: Mu-conotoxins bind and block voltage-sensitive sodium
CC channel (VSSC).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS. MU-TYPE
CC FAMILY.
DR PIR; A01786; MXXN1.
DR PDB; 1TCG; 31-JAN-94.
DR PDB; 1TCG; 31-JAN-94.
DR PDB; 1TCG; 31-JAN-94.
DR PDB; 1TCG; 31-JAN-94.
DR InterPro; IPR008036; Mu-conotoxin.
DR Pfam; PF05374; Mu-conotoxin; 1.
KW Toxin; Sodium channel inhibitor; Hydroxylation; Amidation;
KW 3D-structure.
FT DISULFID 3 15
FT DISULFID 4 20
FT DISULFID 10 21
FT MOD RES 6 6
FT MOD RES 7 7
FT MOD RES 17 17
FT MOD RES 22 22
FT MOD RES 13 16
FT HELIX 19 21
FT TURN 19 21
SQ SEQUENCE 22 AA; 2568 MW; F6CB02ADB359813C CRC64;
Query Match 19.2%; Score 25.5; DB 1; Length 22;
Best Local Similarity 36.4%; Pred. No. 5.9e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 3; Gaps 1;
QY 15 KC---ECRPK 22
DB 9 KCKDRQCKPQR 19

RESULT 3
CXM2_CONGE STANDARD; PRT; 22 AA.
AC P01524;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mu-conotoxin GIIIB (Myotoxin II) (Geographutoxin II) (GTx-II).
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
RN [1] NCBI_TaxID=6491;
RP SEQUENCE.
RX MEDLINE=85261316; PubMed=2410412;
RA Cruz L.J., Gray W.R., Olivera B.M., Zeikus R.D., Kerr L.,
RA Yoshikami D., Moczydlowski E.;
RT "Conus geographus toxins that discriminate between neuronal and
RT muscle sodium channels.";
RL J. Biol. Chem. 260:9280-9288(1985).
RN [2]
RP SEQUENCE.
RX MEDLINE=83210170; PubMed=6852238;
RA Sato S., Nakamura H., Ohizumi Y., Kobayashi J., Hirata Y.;
RA "The amino acid sequences of homologous hydroxyproline-containing
RT myotoxins from the marine snail Conus geographus venom.";
RL FEBS Lett. 155:277-280(1983).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=96280640; PubMed=8688418;
RA Hill J.M., Alewood P.F., Craik D.J.;
RT "Three-dimensional solution structure of mu-conotoxin GIIIB, a
RT specific blocker of skeletal muscle sodium channels.";
RL Biochemistry 35:8824-8835(1996).
CC -1- FUNCTION: Mu-conotoxins bind and block voltage-sensitive sodium
CC channel (VSSC).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS. MU-TYPE
CC FAMILY.
DR PIR; A01787; MXXN2.
DR PDB; 1GIB; 08-NOV-96.
DR InterPro; IPR008036; Mu-conotoxin.
DR Pfam; PF05374; Mu-conotoxin; 1.
KW Toxin; Sodium channel inhibitor; Hydroxylation; Amidation;
KW 3D-structure.
FT DISULFID 3 15
FT DISULFID 4 20
FT DISULFID 10 21
FT MOD RES 6 6
FT MOD RES 7 7
FT MOD RES 17 17
FT MOD RES 22 22
FT MOD RES 22 22
SQ SEQUENCE 22 AA; 2599 MW; F50402BA93199E01 CRC64;
Query Match 19.2%; Score 25.5; DB 1; Length 22;
Best Local Similarity 45.5%; Pred. No. 5.9e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 3; Gaps 1;
QY 15 KCE---CRPK 22
DB 9 KCKDRCKPKM 19

RESULT 4
PHLC_STAIN STANDARD; PRT; 19 AA.
ID PHLC_STAIN
AC P80924;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Spingomyelinase C (EC 3.1.4.12) (Beta-toxin) (Beta-hemolysin)
 DE (Neutral sphingomyelinase) (nSMase) (Fragment).
 OS Staphylococcus intermedius.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1285;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=94-072594;
 RX MEDLINE=97072006; PubMed=8914839;
 RA Dziekanowska K., Edwards V.M., Deringer J.R., Bohach G.A.,
 RA Guerra D.J.;
 RT "Comparison of the beta-toxins from Staphylococcus aureus and
 RT Staphylococcus intermedius.";
 RL Arch. Biochem. Biophys. 335:102-108(1996).
 CC -!- FUNCTION: REQUIRED, WITH SPHINGOMYELINASE TO EFFECT TARGET CELL
 CC LYSIS (HEMOLYSIS). THE PH OPTIMUM IS 6.0-7.5. IT HAS A HIGH
 CC SPECIFICITY FOR SPHINGOMYELIN. HYDROLYSES LYSOPHOSPHATIDYLCHOLINE
 CC AT A MUCH LOWER RATE, BUT HAS NO ACTIVITY TOWARDS
 CC PHOSPHATIDYLCHOLINE, PHOSPHATIDYLETHANOLAMINE, OR
 CC PHOSPHATIDYLSELINE.
 CC -!- CATALYTIC ACTIVITY: Sphingomyelin + H(2)O = N-acylsphingosine +
 CC choline phosphate.
 CC -!- COFACTOR: Magnesium.
 CC -!- SUBUNIT: Monomer.
 CC -!- SIMILARITY: Belongs to the neutral sphingomyelinase family.
 KW Hemolysis; Hydrolase; Toxin; Magnesium.
 FT NON TER 19 19
 SQ SEQUENCE 19 AA; 2089 MW; A50753FCF500F80E CRC64;

 QY Query Match 18.8%; Score 25; DB 1; Length 19;
 Best Local Similarity 30.8%; Pred. No. 6.1e+02;
 Matches 4; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

 Db 2 GQHIGEMSFQHN 14
 ||:|:|:
 3 GENQELKLATHN 15

 RESULT 5
 ID TL14_SPTOL STANDARD; PRT; 20 AA.
 AC P82682;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thylakoid lumenal 14.7 kDa protein (P14.7) (Fragment).
 OS Spinacia oleracea (Spinach)
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Amaranthaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RA Kieselbach T., Pettersson U., Bystedt M., Schroeder W.P.;
 RL Submitted (JUL-2000) to Swiss-Prot.
 CC -!- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
 KW Chloroplast; Thylakoid.
 FT NON TER 20 20
 SQ SEQUENCE 20 AA; 2211 MW; 984B7E4C52F5E3E0 CRC64;

 QY Query Match 18.8%; Score 25; DB 1; Length 20;
 Best Local Similarity 50.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

 Db 14 NKCECRPKKD 23
 ||:|:|:
 5 NKPELLPREE 14

 RESULT 6
 ID CXM3_CONGE STANDARD; PRT; 22 AA.

AC P05482;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mu-conotoxin GIIC.
 OS Conus geographus (Geography cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6491;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85261316; PubMed=2410412;
 RA Cruz L.J., Gray W.R., Olivera B.M., Zeikus R.D., Kerr L.,
 RA Yoshikami D., Moczydlowski E.;
 RT "Conus geographus toxins that discriminate between neuronal and
 RT muscle sodium channels.";
 RL J. Biol. Chem. 260:9280-9288(1985).
 CC -!- FUNCTION: Mu-conotoxins bind and block voltage-sensitive sodium
 CC channel (VSSC).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS. MU-TYPE
 CC FAMILY.
 DR PIR; C23579; MXN3.
 DR HSSP; P01524; IGIB.
 DR InterPro; IPR008036; Mu-conotoxin.
 DR Pfam; PF05374; Mu-conotoxin; 1.
 KW Toxin; Sodium channel inhibitor; Hydroxylation; Amidation.
 FT DISULFID 3 15 BY SIMILARITY.
 FT DISULFID 4 20 BY SIMILARITY.
 FT DISULFID 10 21 BY SIMILARITY.
 FT MOD_RES 6 6 HYDROXYLATION.
 FT MOD_RES 7 7 HYDROXYLATION.
 FT MOD_RES 17 17 HYDROXYLATION.
 FT MOD_RES 22 22 AMIDATION.
 SQ SEQUENCE 22 AA; 2553 MW; F50402BA92A9813C CRC64;

 Query Match 18.4%; Score 24.5; DB 1; Length 22;
 Best Local Similarity 45.5%; Pred. No. 8.6e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

 QY 15 KCE---CRPKK 22
 ||:|:|:
 9 KCQRRCKCKPLK 19

 Db 15 KCE---CRPKK 22
 ||:|:|:
 9 KCQRRCKCKPLK 19

 RESULT 7
 ID DFTS_RAT STANDARD; PRT; 20 AA.
 AC P07448;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-MAR-1989 (Rel. 10, Last annotation update)
 DE Dentine fluid transport-stimulating peptide (DFT-stimulating
 DE peptide).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Parotid gland;
 RX MEDLINE=87131231; PubMed=3815601;
 RA Yamamoto T., Kobayashi M., Kobayashi M., Yamamoto M., Nomura M.,
 RA Aonuma S.;
 RT "Isolation and amino acid sequence of dentinal fluid transport-
 RT stimulating peptide from rat parotid glands.";
 RL Chem. Pharm. Bull. 34:3803-3811(1986).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=67131708; PubMed=5297832;
 RA Steinman R.R.;

RT "The movement of acriflavine hydrochloride through molars of rats on
 RT a cariogenic and non-cariogenic diet.";
 RL J. South. Calif. Dent. Assoc. 35:151-157(1967).
 CC -!- FUNCTION: This peptide stimulates the transport of dentinal fluid,
 CC which is important for the prevention of dental caries.
 CC PIR: J30001; DIRT.

KW Dental caries; Parotid gland; Hormone.
 SQ SEQUENCE 20 AA; 2165 MW; FA164F2B6AF80D5A CRC64;

Query Match 18.0%; Score 24; DB 1; Length 20;

Best Local Similarity 80.0%; Pred. No. 9.4e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 LOHNS 15
 ||||
 Db 7 LOHNS 11

RESULT 8

CXCV CONTE STANDARD; PRT; 23 AA.
 ID CXCV CONTE STANDARD; PRT; 23 AA.

AC P58845;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Textile convulsant peptide.
 OS Conus textile (Cloth-of-gold cone).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 CC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 CC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6494;
 RN [1]

RP SEQUENCE.
 RA Cruz L.J., Ramilo C.A., Corpuz G.P., Olivera B.M.;

RT "Conus peptides: phylogenetic range of biological activity.";

RL Biol. Bull. 183:159-164(1992).

CC -!- FUNCTION: Causes convulsions mice.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.

CC -!- SIMILARITY: Belongs to the conotoxin O-superfamily.

KW Toxin; Amidation.

FT DISULFID 2 10 PROBABLE.

FT DISULFID 5 15 PROBABLE.

FT DISULFID 9 20 PROBABLE.

FT MOD RES 23 23 AMIDATION.

SQ SEQUENCE 23 AA; 2496 MW; AE99BDBB7DC8AD56 CRC64;

Query Match 17.7%; Score 23.5; DB 1; Length 23;

Best Local Similarity 62.5%; Pred. No. 1.3e+03;

Matches 5; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 16 CE---CRP 20
 ||||
 Db 15 CEASGCRP 22

RESULT 9

MAST POLJA STANDARD; PRT; 14 AA.
 ID MAST POLJA STANDARD; PRT; 14 AA.

AC P01517;
 DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Polistes mastoparan.

OS Polistes mastoparan.

CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

CC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;

CC Vespidae; Polistinae; Polistes.

OX NCBI_TaxID=7457;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RA Hirai Y., Ueno Y., Yasuhara T., Yoshida H., Nakajima T.;

RT "A new mast cell degranulating peptide, polistes mastoparan, in the

RT venom of Polistes jadwigae.";

RL Biomed. Res. 1:185-187(1980).

CC -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins

CC that couple to phospholipase C.

DR PIR: A01780; QMWAPP.

KW Mast cell degranulation; Amidation.

FT MOD RES 14 14 AMIDATION.

SQ SEQUENCE 14 AA; 1636 MW; 26472A53BF4778D8 CRC64;

Query Match 17.3%; Score 23; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 9.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GQHI 5
 ||||
 Db 7 GQHI 10

RESULT 10

NXSO PSETE STANDARD; PRT; 15 AA.
 ID NXSO PSETE STANDARD; PRT; 15 AA.

AC P59073;
 DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Short neurotoxin N2 (Alpha neurotoxin) (Fragment).

OS Pseudonaja textilis (Eastern brown snake).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

CC Elapidae; Acanthophiinae; Pseudonaja.

OX NCBI_TaxID=8673;

RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Venom;

RX MEDLINE=99449602; PubMed=10518793;

RA Gong N.L., Armugam A., Jeyaseelan K.;

RT "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA

cloning, expression and protein characterization.";

RL Eur. J. Biochem. 265:982-989(1999).

CC -!- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic

CC acetylcholine receptors (nAChR).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -!- MASS SPECTROMETRY: MW=6345; METHOD=Electrospray.

CC -!- MISCELLANEOUS: LD(50) is 0.80 mg/kg by intravenous injection.

CC -!- SIMILARITY: Belongs to the snake toxin family.

DR InterPro: IPR003571; Snake toxin.

DR PROSITE: PS00272; SNAKE_TOXIN; PARTIAL.

KW Toxin; Neurotoxin; Postsynaptic neurotoxin;

KW Acetylcholine receptor inhibitor; Multigene family.

FT UNSURE 3 3

FT UNSURE 13 13

FT NON TER 15 15

SQ SEQUENCE 15 AA; 1727 MW; E149FD4BF01EF0DD CRC64;

Query Match 17.3%; Score 23; DB 1; Length 15;

Best Local Similarity 37.5%; Pred. No. 1e+03;

Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 13 HNKCCRP 20
 ||:|:|
 Db 8 HDTVCKP 15

RESULT 11

GONI_PETWA STANDARD; PRT; 10 AA.
 ID GONI_PETWA STANDARD; PRT; 10 AA.

AC P04378;

DT 20-MAR-1987 (Rel. 04, Created)

DT 20-MAR-1987 (Rel. 04, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

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Db          |||:
            4 GOHW 7

RESULT 13
SRPD_ATREN
ID  SRPD_ATREN  STANDARD;  PRT;  21 AA.
AC  P13211;
DT  01-JAN-1990 (Rel. 13, Created)
DT  01-JAN-1990 (Rel. 13, Last sequence update)
DT  15-MAR-2004 (Rel. 43, Last annotation update)
DE  Sarafotoxin-D (S6D) (SRTX-D)
DE  Atractaspis engaddensis (Israeli burrowing asp).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC  Atractaspididae; Atractaspis.
OX  NCBI_TaxID=8600;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Venom;
RX  MEDLINE=90033283; PubMed=2509240;
RA  Bdoiah A., Wollberg Z., Fleminger G.;
RT  "SRTX-d, a new native peptide of the endothelin/sarafotoxin family.";
RL  FEBS Lett. 256:1-3(1989).
CC  -!- FUNCTION: Vasoconstrictor activity. These toxins cause cardiac
CC  arrest probably as a result of coronary vasospasm.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- MISCELLANEOUS: LD(50) is 0.35 mg/kg by intravenous injection.
CC  -!- SIMILARITY: Belongs to the endothelin/sarafotoxin family.
DR  HSSP; P13208; 1SRB.
DR  InterPro; IPR001928; Endothln tox.
DR  InterPro; IPR003642; Sara/bib_toxin.
DR  Pfam; PF00322; endothelin; 1.
DR  PRINTS; PR00365; ENDOTHELIN.
DR  ProDom; PD004740; Sara/bib_toxin; 1.
DR  SMART; SM00272; END; 1.
DR  PROSITE; PS00270; ENDOTHELIN; 1.
KW  Vasoconstrictor; Toxin.
FT  DISULFID 1 15  BY SIMILARITY.
FT  DISULFID 3 11  BY SIMILARITY.
SQ  SEQUENCE  21 AA; 2596 MW;  83A8A04D1D536AE2 CRC64;

Query Match      16.5%; Score 22; DB 1; Length 21;
Best Local Similarity 37.5%; Pred. No. 2.1e+03;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY  16 CECRPKDD 23
    |||:
    1 CTKQWTD 8

Db          |||:
            4 GOHW 7

RESULT 14
SCKL_TITCA
ID  SCKL_TITCA  STANDARD;  PRT;  23 AA.
AC  P83243;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  15-MAR-2004 (Rel. 43, Last annotation update)
DE  Toxin Tc1 (Alpha-KTx 13.1).
OS  Tityus cambridgei (Amazonian scorpion).
OC  Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC  Buthoidea; Buthidae; Tityus.
OX  NCBI_TaxID=184226;
RN  [1]
RP  SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC  TISSUE=Venom;
RX  MEDLINE=20565534; PubMed=11113450;
RA  Batista C.V.F., Gomez-Lagunas F., Lucas S., Possani L.D.;
RT  "Tc1, from Tityus cambridgei, is the first member of a new subfamily
RL  of scorpion toxin that blocks K(+-)channels.";
RL  FEBS Lett. 486:117-120(2000).
CC  -!- FUNCTION: Blocks reversibly Shaker B potassium channels. Also
CC  displaces binding of nortuxrovin to mouse brain synaptosome

```

CC CC
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MASS SPECTROMETRY: MW=2446.4; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the short scorpion toxin family. Potassium
CC channel inhibitor subfamily.
DR GO: GO:0005576; Cerebral cellular; NAS.
DR GO: GO:0019870; F:potassium channel inhibitor activity; IDA.
DR GO: GO:0015070; F:toxin activity; IDA.
DR InterPro: IPR001947; Scorpion toxins.
DR PROSITE: PS01138; SCORP SHORT TOXIN; FALSE NEG.
KW Toxin; Neurotoxin; Ionic channel inhibitor;
KW Potassium channel inhibitor.
FT DISULFID 2 15 BY SIMILARITY.
FT DISULFID 5 20 BY SIMILARITY.
FT DISULFID 9 22 BY SIMILARITY.
FT SITE 13 20 INTERACTION WITH CA(2+)-ACTIVATED K(+) CHANNELS (POTENTIAL).
SQ SEQUENCE 23 AA; 2454 MW; D59BPD8C9F31700 CRC64;

Query Match 16.5%; Score 22; DB 1; Length 23;
Best Local Similarity 33.3%; Pred. No. 2.3e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 13 HNKCEC 18
Db 17 NGRCKC 22

RESULT 15
ACHG_ELEEL STANDARD; PRT; 23 AA.
AC P09652;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acetylcholine receptor protein, gamma chain (Fragment).
OS Electrophorus electricus (Electric eel).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
CC Electrophoridae; Electrophorus.
OX NCBI_TaxID=8005;
RN [1]
RP SEQUENCE
RX MEDLINE=83065199; PubMed=6959131;
RA Conti-Tronconi B.M., Hunkapiller M.W., Lindstrom J.M., Raftery M.A.;
RT "Subunit structure of the acetylcholine receptor from Electrophorus
RT electricus.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6489-6493(1982).
CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an
CC extensive change in conformation that affects all subunits and
CC leads to opening of an ion-conducting channel across the plasma
CC membrane.
CC -!- SUBUNIT: Pentamer of two alpha chains, and one each of the beta,
CC delta, and gamma chains.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
DR FIR; C27262; C27262.
DR InterPro: IPR006202; Neur chan LBD.
DR InterPro: IPR006201; Neur channel.
DR Pfam: PF02931; Neur chan LBD; 1.
DR PROSITE: PS00236; NEUROTR ION CHANNEL; PARTIAL.
KW Receptor; Postsynaptic membrane; Ionic channel; Transmembrane.
FT NON_TER 23 23
SQ SEQUENCE 23 AA; 2717 MW; DA88F7E9900C024B CRC64;

Query Match 16.2%; Score 21.5; DB 1; Length 23;
Best Local Similarity 46.2%; Pred. No. 2.8e+03;
Matches 6; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 10 FLOHNKCECRPKK 22
Db 11 FTNYNKL-IRPAK 22

Search completed: March 8, 2004, 11:46:49
Job time : 12 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:40:47 ; Search time 38 Seconds
(without alignments)
190.972 Million cell updates/sec

Title: US-09-761-636A-4
Perfect score: 133
Sequence: 1 QGQHIGMSFLOHKNCEPRKDK 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 9533

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 25:*
1: sp_arChaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	38	28.6	23	7	Q95376	Q95376 homo sapien
2	31	23.3	23	5	Q25134	Q25134 hallois ru
3	30	22.6	23	3	Q8TCM6	Q8TCM6 microsporium
4	29	21.8	23	11	Q99LQ2	Q99LQ2 mus musculu
5	28	21.1	21	5	Q25086	Q25086 hermania m
6	28	21.1	21	15	Q12066	Q12066 caprine art
7	28	21.1	22	8	Q85WB3	Q85WB3 hylocium
8	28	21.1	22	8	Q85WB1	Q85WB1 plagiotheci
9	28	21.1	22	8	Q85WA9	Q85WA9 bartramia p
10	28	21.1	23	5	Q86WN6	Q86WN6 ensis ensis
11	28	21.1	23	5	Q86WN2	Q86WN2 mytilus gal
12	28	21.1	23	5	Q86WM0	Q86WM0 yoidia eigh
13	27	20.3	18	8	Q8SKY0	Q8SKY0 cuscata ref
14	27	20.3	19	8	Q63058	Q63058 lathraea cl
15	26	19.5	11	2	Q9RBV0	Q9RBV0 pseudomonas
16	26	19.5	18	6	Q97668	Q97668 equus cabal

17 26 19.5 22 10 Q9SY23
18 26 19.5 22 16 Q8X365
19 26 19.5 23 12 Q91CX8
20 26 19.5 23 12 Q91CX2
21 25.5 19.2 19 16 Q9SLW0
22 25.5 19.2 20 4 Q81ZX0
23 25 18.8 14 10 Q7X9S0
24 25 18.8 18 4 Q16053
25 25 18.8 20 13 Q42534
26 25 18.8 22 2 Q9KK60
27 25 18.8 22 11 Q9EQS7
28 25 18.8 22 13 Q91102
29 25 18.8 23 5 P90716
30 25 18.8 23 16 Q8Z974
31 24.5 18.4 21 2 Q9R567
32 24 18.0 12 15 Q12036
33 24 18.0 13 13 Q7ZZN7
34 24 18.0 15 4 Q9HCX8
35 24 18.0 16 5 Q9TWN2
36 23 17.3 15 2 Q9R4M6
37 23 17.3 16 6 Q9TRQ9
38 23 17.3 18 3 Q06711
39 23 17.3 19 2 Q57012
40 23 17.3 19 5 Q86H04
41 23 17.3 20 4 Q9Y3G6
42 23 17.3 20 11 Q9QV27
43 23 17.3 21 2 Q9X3E5
44 22.5 16.9 12 13 Q8UWV0
45 22 16.5 9 12 Q82622

ALIGNMENTS

RESULT 1
Q95376 PRELIMINARY; PRT; 23 AA.
AC Q95376;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II antigen HLA-DRB4*0201N (Fragment).
GN HLA-DRB4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=9306279; PubMed=9162096;
RA Robbins F., Hurley C.K., Tang T., Yao H., Lin Y.S., Wade J.,
Goeken N., Hartzman R.J.;
RT "Diversity associated with the second expressed HLA-DRB locus in the
human population."
RL Immunogenetics 46:104-110(1997).
DR EMBL; US0061; AAB63532.1; -;
FT NON_TER
SQ SEQUENCE 23 AA; 2729 MW; AD6B35DC3A259EBF CRC64;
Query Match 28.6%; Score 38; DB 7; Length 23;
Best Local Similarity 66.7%; Pred.No. 26;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 10 FLEQNKCEC 18
Db 2 FLEQAKCEC 10
RESULT 2
Q25134 PRELIMINARY; PRT; 23 AA.
ID Q25134
AC Q25134;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE HroX3 protein (Fragment).
GN HROX3.
OS Haliotis rufescens (California red abalone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Vetigastropoda; Haliotidae; Haliotis.
OX NCBI_TaxID=6454;
RN [1]
RP SEQUENCE FROM N.A.
RA Degnan B.M.;
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93372986; PubMed=7689904;
RA Degnan B.M., Morse D.E.;
RT "Identification of eight homeobox-containing transcripts expressed during larval development and at metamorphosis in the gastropod mollusc Haliotis rufescens.";
RT Mol. Mar. Biol. Biotechnol. 2:1-9(1993).
RL EMBL; X79372; CAA55917.1; -
DR FIR; S60565; S60565.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
FT NON_TER 1 1
FT NON_TER 23 23
SQ SEQUENCE 23 AA; 2793 MW; CC387AE7BDA6C44D CRC64;

Query Match 23.3%; Score 31; DB 5; Length 23;
Best Local Similarity 55.6%; Pred. No. 4.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 14 NKCECRPKK 22
Db 2 NKVLCRPR 10

RESULT 3
Q8TGW6 PRELIMINARY; PRT; 23 AA.
AC Q8TGW6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Metallothionein.
OS Microsporium canis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Onygenales; Arthrodermataceae; mitosporic Arthrodermataceae;
OC Microsporium.
OX NCBI_TaxID=82078;
RN [1]
RP SEQUENCE FROM N.A.
RA Uchman A., Dockal M., Ban J., Rezaie S., Soeltz-Szoets J.,
RA Techachler E.;
RT "Isolation and characterization of metallothionein from Microsporium canis by differential display and its regulation with fluconazole.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF408429; AAU76232.1; -
SQ SEQUENCE 23 AA; 2257 MW; 4693AD5D51A60975 CRC64;

Query Match 22.6%; Score 30; DB 3; Length 23;
Best Local Similarity 80.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 15 KCECR 19
Db 18 KCECK 22

RESULT 4
Q99LQ2 PRELIMINARY; PRT; 23 AA.
AC Q99LQ2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002276; AAH02276.1; -
KW Hypothetical protein.
SQ SEQUENCE 23 AA; 2223 MW; 2A4C872213B58B01 CRC64;

Query Match 21.8%; Score 29; DB 11; Length 23;
Best Local Similarity 43.8%; Pred. No. 9.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 6; Gaps 1;

Qy 2 GQHIGMSFLQNKCE 17
Db 5 GQFGEI-----KCE 14

RESULT 5
Q25086 PRELIMINARY; PRT; 21 AA.
AC Q25086;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Clone AHox4 homeobox protein (Fragment).
OS Herdmania momus (Brown sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Herdmania.
OX NCBI_TaxID=7733;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Kennett C.V.D.;
RT "Cloning and Sequencing of Homeoboxes from the Ascidian Herdmania momus.";
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U09939; AAA18629.1; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1 1
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2650 MW; AB7FF3AF1FA659C3 CRC64;

Query Match 21.1%; Score 28; DB 5; Length 21;
Best Local Similarity 44.4%; Pred. No. 1.3e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 14 NKCECRPKK 22
Db 1 NKVLCRPR 9

RESULT 6
O12066 PRELIMINARY; PRT; 21 AA.
ID O12066
AC O12066;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Envlope glycoprotein (Fragment).
 GN ENV.
 OS Caprine arthritis encephalitis virus (CAEV).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11660;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97296261; PubMed=9151845;
 RX Turelli P., Guiguen F., Mornex J.F., Vigne R., Querat G.;
 RT "DUTPase-minus caprine arthritis-encephalitis virus is attenuated for
 RT pathogenesis and accumulates G-to-A substitutions.";
 RL J. Virol. 71:4522-4530(1997).
 DR EMBL; U81420; AAC57935.1; -.
 FT NON_TER 1
 SQ SEQUENCE 21 AA; 2497 MW; A377E2451CCEFA4 CRC64;

 Query Match 21.1%; Score 28; DB 15; Length 21;
 Best Local Similarity 36.4%; Pred. No. 1.3e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

 QY 12 QHNKCECPKK 22
 : : : : :
 Db 5 BSNKWTCAPEP 15

 RESULT 7
 Q85WB3 PRELIMINARY; PRT; 22 AA.
 ID Q85WB3
 AC Q85WB3;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Ribosomal protein S11 (Fragment).
 GN RPS11.
 OS Hyalomium splendens (Mountain fern moss).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Bryopsida; Bryidae; Hypnales; Hylocomiaceae; Hylocomium.
 OX NCBI_TaxID=53007;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sugita M.;
 RT "The intergenic region between rps11 and petD of the moss chloroplast
 RT DNA.";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB098724; BAC64957.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 KW Chloroplast; Ribosomal protein.
 FT NON_TER 1
 SQ SEQUENCE 22 AA; 2638 MW; 130D2ADC3C3D2C04 CRC64;

 Query Match 21.1%; Score 28; DB 8; Length 22;
 Best Local Similarity 33.3%; Pred. No. 1.3e+03;
 Matches 6; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

 QY 5 IGEMSFLOHKNCECPKK 22
 : : : : :
 Db 3 VRDVTMPFHN--GCRPPK 18

 RESULT 8
 Q85WB1 PRELIMINARY; PRT; 22 AA.
 ID Q85WB1
 AC Q85WB1;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Ribosomal protein S11 (Fragment).
 GN RPS11.
 OS Plagiothecium eurphyllum.

OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Bryopsida; Bryidae; Hypnales; Plagiotheciaceae; Plagiothecium.
 OX NCBI_TaxID=90297;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sugita M.;
 RT "The intergenic region between rps11 and petD of the moss chloroplast
 RT DNA.";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB098725; BAC64959.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 KW Chloroplast; Ribosomal protein.
 FT NON_TER 1
 SQ SEQUENCE 22 AA; 2638 MW; 130D2ADC3C3D2C04 CRC64;

 Query Match 21.1%; Score 28; DB 8; Length 22;
 Best Local Similarity 33.3%; Pred. No. 1.3e+03;
 Matches 6; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

 QY 5 IGEMSFLOHKNCECPKK 22
 : : : : :
 Db 3 VRDVTMPFHN--GCRPPK 18

 RESULT 9
 Q85WA9 PRELIMINARY; PRT; 22 AA.
 ID Q85WA9
 AC Q85WA9;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Ribosomal protein S11 (Fragment).
 GN RPS11.
 OS Bartramia pomiformis.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Bryopsida; Bryidae; Bryales; Bartramiaceae; Bartramia.
 OX NCBI_TaxID=52976;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sugita M.;
 RT "The intergenic region between rps11 and petD of the moss chloroplast
 RT DNA.";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB098726; BAC64961.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 KW Chloroplast; Ribosomal protein.
 FT NON_TER 1
 SQ SEQUENCE 22 AA; 2638 MW; 130D2ADC3C3D2C04 CRC64;

 Query Match 21.1%; Score 28; DB 8; Length 22;
 Best Local Similarity 33.3%; Pred. No. 1.3e+03;
 Matches 6; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

 QY 5 IGEMSFLOHKNCECPKK 22
 : : : : :
 Db 3 VRDVTMPFHN--GCRPPK 18

 RESULT 10
 Q86MN6 PRELIMINARY; PRT; 23 AA.
 ID Q86MN6
 AC Q86MN6;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hox3 homeodomain protein (Fragment).
 GN Hox3.
 OS Ensis ensis.
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;

OC Solenoidea; Phariidae; Ensis.
OX NCBI_TaxID=120427;
RN [1]
RP SEQUENCE FROM N.A.
RA Barucca M., Olmo E., Canapa A.;
RT "Hox and ParaHox genes in bivalve molluscs.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ534448; CAD5897.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
KW Homeobox; DNA-binding; Nuclear protein.
FT NON_TER 1
FT NON_TER 23
SQ SEQUENCE 23 AA; 2864 MW; 0F387FF3AF1FD45F CRC64;
Query Match 21.1%; Score 28; DB 5; Length 23;
Best Local Similarity 44.4%; Pred. No. 1.4e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 14 NKCECRPKK 22
|: |||:
Db 2 NRYLCRPR 10
RESULT 11
Q86MN2 PRELIMINARY; PRT; 23 AA.
AC Q86MN2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hox3 homeodomain protein (Fragment).
GN HOX3.
OS Mytilus galloprovincialis (Mediterranean mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
OC Mytiloidae; Mytilidae; Mytilus.
OX NCBI_TaxID=29158;
RN [1]
RP SEQUENCE FROM N.A.
RA Barucca M., Olmo E., Canapa A.;
RT "Hox and ParaHox genes in bivalve molluscs.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ534452; CAD58901.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
KW Homeobox; DNA-binding; Nuclear protein.
FT NON_TER 1
FT NON_TER 23
SQ SEQUENCE 23 AA; 2864 MW; 0F387FF3AF1FD45F CRC64;
Query Match 21.1%; Score 28; DB 5; Length 23;
Best Local Similarity 44.4%; Pred. No. 1.4e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 14 NKCECRPKK 22
|: |||:
Db 2 NRYLCRPR 10
RESULT 12
Q86MN2 PRELIMINARY; PRT; 23 AA.
AC Q86MN2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hox3 homeodomain protein (Fragment).

GN HOX3.
OS Yoldia eightai.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Protobranchia; Nuculoida;
OC Nuculanoidea; Sareptidae; Yoldia.
OX NCBI_TaxID=177101;
RN [1]
RP SEQUENCE FROM N.A.
RA Barucca M., Olmo E., Canapa A.;
RT "Hox and ParaHox genes in bivalve molluscs.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ534462; CAD58911.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
KW Homeobox; DNA-binding; Nuclear protein.
FT NON_TER 1
FT NON_TER 23
SQ SEQUENCE 23 AA; 2864 MW; 0F387FF3AF1FD45F CRC64;
Query Match 21.1%; Score 28; DB 5; Length 23;
Best Local Similarity 44.4%; Pred. No. 1.4e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 14 NKCECRPKK 22
|: |||:
Db 2 NRYLCRPR 10
RESULT 13
Q8SKY0 PRELIMINARY; PRT; 18 AA.
AC Q8SKY0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein S11 (Fragment).
GN RPS11.
OS Cuscuta reflexa (Southern Asian dodder).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Convolvulaceae; Cuscuta.
OX NCBI_TaxID=4129;
RN [1]
RP SEQUENCE FROM N.A.
RA Berg S.;
RT "Sequence analysis and coding potential of the holoparasitic flowering
plant genus Cuscuta.";
RL Thesis (2002), Department of Institute of Botany, .
DR EMBL; AJ439611; CAD28796.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR001971; Ribosomal S11.
DR Pfam; PF00411; Ribosomal_S11; 1.
KW Chloroplast.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2088 MW; 130D427BFE680B24 CRC64;
Query Match 20.3%; Score 27; DB 8; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 3; Indels 2; Gaps 1;
QY 11 LOHKKCRPKK 22
|: |||:
Db 5 MPHN--GCRPPK 14
RESULT 14

063058
ID O63058 PRELIMINARY; PRT; 19 AA.
AC O63058;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein S11 (Fragment).
GN RPS11.
OS Lathraea clandestina (Purple toothwort).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Orobanchaceae; Orobanchaceae incertae sedis;
OC Lathraea.
OX NCBI_TaxID=41911;
RN [1]
RP SEQUENCE FROM N.A.
RA Lussan N., Delavault P., Tholouarn P.;
RT "The rbcL gene from Lathraea (holoparasitic) is not transcribed by a
RL plastid-encoded RNA polymerase.";
DR Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF030983; AAC16521.1; -
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR001971; Ribosomal_S11.
DR Pfam; PF00411; Ribosomal_S11; 1.
KW Chloroplast.
FT NON TER 1 1
SQ SEQUENCE 19 AA; 2245 MW; 130D2AB3FE680B24 CRC64;

Query Match 20.3%; Score 27; DB 8; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 6; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 11 LQHNKCECPKK 22
Db : || || || ||
6 MPHN--GCRPK 15

RESULT 15
Q9RBV0
ID Q9RBV0 PRELIMINARY; PRT; 11 AA.
AC Q9RBV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Resolvase (Fragment).
OS Pseudomonas sp. R9.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=101164;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R9; TRANSPOSON=Tn1404;
RX MEDLINE=20011227; PubMed=10543801;
RA Schnabel E.L., Jones A.L.;
RT "Distribution of tetracycline resistance genes and transposons among
RT phyloplane bacteria in Michigan apple orchards.";
RL Appl. Environ. Microbiol. 65:4898-4907 (1999).
DR EMBL; AF157800; RAD4802.1; -
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1307 MW; D00B18E258704416 CRC64;

Query Match 19.5%; Score 26; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QGQHIG 6
Db || || || ||
2 QGQRIG 7

Search completed: March 8, 2004, 11:47:40
Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:13:12 ; Search time 52 Seconds
(without alignments)
124.973 Million cell updates/sec

Title: US-09-761-636A-4

Perfect score: 133
Sequence: 1 QGQHIGMSFLOHNCCECRPKD 23

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 532682

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	133	100.0	23	AAU04523	AAU04523 Human VEG
2	79	59.4	13	AAU08454	AAU08454 Peptide A
3	75	56.4	21	AAU10862	AAU10862 ScVEGF2 c
4	75	56.4	21	AAU10860	AAU10860 ScVEGF2 c
5	73	54.9	12	AAW23802	AAW23802 VEGF/VPF
6	73	54.9	12	AAW53383	AAW53383 Tumour me
7	73	54.9	12	AAW53444	AAW53444 Vascular
8	73	54.9	12	AAW74627	AAW74627 Amino aci
9	73	54.9	12	AAW74688	AAW74688 Amino aci
10	73	54.9	12	AAW55950	AAW55950 Human vas
11	73	54.9	12	AAW55949	AAW55949 Human vas
12	73	54.9	12	AAW97382	AAW97382 A VEGF/VP
13	73	54.9	12	AAV57613	AAV57613 Human VEG
14	73	54.9	12	AAV57674	AAV57674 Human vas
15	73	54.9	12	AAV59616	AAV59616 Vascular
16	73	54.9	12	AAV58055	AAV58055 Vascular
17	73	54.9	12	AAW74566	AAW74566 VEGF VPF
18	73	54.9	12	AAW74567	AAW74567 VEGF VPF
19	73	54.9	12	AAW74575	AAW74575 VEGF VPF
20	73	54.9	12	AAW97893	AAW97893 Human VEG
21	73	54.9	12	AAW97894	AAW97894 Human VEG
22	71	53.4	12	AAW53443	AAW53443 Vascular
23	71	53.4	12	AAW74687	AAW74687 Amino aci
24	71	53.4	12	AAW55948	AAW55948 Human vas
25	71	53.4	12	AAV57673	AAV57673 Human vas

26	71	53.4	12	3	AAV59615	AAV59615 Vascular
27	71	53.4	12	4	AAW74565	AAW74565 VEGF VPF
28	71	53.4	12	4	AAW97892	AAW97892 Human VEG
29	70	52.6	12	2	AAW53445	AAW53445 Vascular
30	70	52.6	12	2	AAW74689	AAW74689 Amino aci
31	70	52.6	12	2	AAW55951	AAW55951 Human vas
32	70	52.6	12	3	AAV57675	AAV57675 Human vas
33	70	52.6	12	3	AAV59617	AAV59617 Vascular
34	70	52.6	12	4	AAW74568	AAW74568 VEGF VPF
35	70	52.6	12	4	AAW97895	AAW97895 Human VEG
36	67	50.4	12	2	AAW53442	AAW53442 Vascular
37	67	50.4	12	2	AAW74686	AAW74686 Amino aci
38	67	50.4	12	2	AAW55947	AAW55947 Human vas
39	67	50.4	12	3	AAV57672	AAV57672 Human vas
40	67	50.4	12	3	AAV59614	AAV59614 Vascular
41	67	50.4	12	4	AAW74564	AAW74564 VEGF VPF
42	67	50.4	12	4	AAW97891	AAW97891 Human VEG
43	66	49.6	12	2	AAW53441	AAW53441 Vascular
44	66	49.6	12	2	AAW74685	AAW74685 Amino aci
45	66	49.6	12	2	AAW55946	AAW55946 Human vas

ALIGNMENTS

RESULT 1
AAU04523
ID AAU04523 standard; peptide; 23 AA.
XX
AC AAU04523;
XX
DT 26-SRP-2001 (first entry)
XX
DE Human VEGF amino acids Gln113-Asp135.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation.
XX
OS Homo sapiens.
XX
PN WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
XX
PA 16-MAY-2000; 2000US-0204590P.
XX
(LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR WPI; 2001-442248/47.
XX
PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
PS Example 1; Page 91; 102pp; English.
XX
CC The sequence represents Human VEGF (vascular endothelial growth factor)
CC amino acids Gln113-Asp135, used to replace the C-terminal 23 residues of
CC VEGF-D to make a hybrid theoretical molecule for 3 dimensional modelling.
CC The sequence is used in a method of producing a monomeric monocyclic
CC peptide by a measuring beta-beta carbon separation distances on opposite
CC antiparallel strands of a peptide loop fragment from an exposed loop of a
CC growth factor protein and cyclising the peptide by oxidising the cysteine
CC residues. The monocyclic peptides, dimeric bicyclic peptides (comprising
CC 2 linked monocyclic peptides) and a cyclic peptide with at least one

CC amino acid deleted prior to cyclisation are used to interfere with
 CC angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a
 CC condition characterised by angiogenesis, neovascularisation or
 CC lymphangiogenesis. The condition is diabetic retinopathy, psoriasis,
 CC arthropathy, hemangioma, vascularised malignant or benign tumour, post-
 CC recovery cerebrovascular accident, post-angioplasty restenosis, head,
 CC heat or cold trauma, substance-induced neovascularisation of the liver,
 CC excessive hormone-related angiogenic dysfunction, diabetes induced
 CC neovascular sequelae, hypertension induced neovascular sequelae, or
 CC chronic liver infection. The peptides are also used to modulate vascular
 CC permeability in a mammal (the mammal has a condition characterised by
 CC fluid accumulation in peripheral limbs or in lungs, peritoneal cavity,
 CC pleura, or brain. The peptides are used to image blood vessels and
 CC lymphatic vasculature. The monomeric and bicyclic peptides are used to
 CC interfere with at least one biological activity induced by VEGF, VEGF-C
 CC or -D and are also used in combination with an anti-inflammatory agent,
 CC to treat a chronic inflammation, especially rheumatoid arthritis,
 CC psoriasis and diabetic retinopathy
 XX
 SQ Sequence 23 AA;

Query Match 100.0%; Score 133; DB 4; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.1e-13;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGQHIGEMSFLOHKKCECRPKD 23
 DB 1 QGQHIGEMSFLOHKKCECRPKD 23

RESULT 2
 AAU08454
 ID AAU08454 standard; peptide; 13 AA.

XX AAU08454;
 DT 21-NOV-2001 (first entry)
 XX
 DE Peptide A9 encoded by human VEGF-A forward primer A9-F.
 XX
 KW Human; vascular endothelial growth factor; VEGF-A; vasculogenesis;
 KW angiogenesis; blood vessel; cancer; proliferative retinopathy; psoriasis;
 KW age-related macular degeneration; rheumatoid arthritis; cardiovascular;
 KW primer; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200162942-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 26-FEB-2001; 2001WO-US006113.
 XX
 PR 25-FEB-2000; 2000US-0185205P.
 PR 18-MAY-2000; 2000US-0205331P.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (LICN) LICENTIA OY.
 XX
 PI Alitalo K, Jeltsch MM;
 XX
 DR WPI; 2001-536640/59.
 DR N-PSDB; AAS12810.
 XX
 XX Polypeptides that bind cellular receptors for vascular endothelial growth
 PT factors, polynucleotides encoding them.
 PT
 XX Claim 9; Fig 7b; 26pp; English.
 PS
 XX The present invention relates to polypeptides that bind cellular
 CC receptors for vascular endothelial growth factors (VEGFs), the
 CC polynucleotides encoding them, and their use for identifying agents that

CC modulate interactions between VEGFs and their receptors. VEGFs and their
 CC receptors play an important role in vasculogenesis, the development of
 CC the embryonic vasculature from early differentiating endothelial cells
 CC and angiogenesis, the process of forming new blood vessels from pre-
 CC existing ones. Modulators of interactions between VEGF and its receptors
 CC may be used to treat dysfunction of the endothelial cell regulatory
 CC system. Such disorders include cancers, abnormal angiogenesis,
 CC proliferative retinopathies, age-related macular degeneration, rheumatoid
 CC arthritis and psoriasis. The polypeptides of the invention exhibit unique
 CC receptor binding profiles compared to known naturally occurring VEGFs.
 CC AAU08446-AAU08454 represent the peptides A1-A9 which are encoded by human
 CC VEGF-A forward primers used in the methods of the present invention
 XX

SQ Sequence 13 AA;

Query Match 59.4%; Score 79; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LOHKKCECRPKD 23
 DB 1 LOHKKCECRPKD 13

RESULT 3
 AAB10862
 ID AAB10862 standard; protein; 21 AA.

XX AAB10862;
 XX
 DT 02-FEB-2001 (first entry)
 XX
 DE ScVEGF2 construct protein fragment SEQ ID NO: 34.
 XX
 KW MVP; multivalent protein; treatment; dressing; skin; mucus; musculature;
 KW nervous system; inner organ; hematopoietic system; immune system; joint;
 KW support tissue; immunization.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO200053790-A1.
 XX
 PD 14-SEP-2000.
 XX
 PF 26-FEB-2000; 2000WO-EP001612.
 XX
 PR 10-MAR-1999; 99DE-01010419.
 XX
 PA (AVET) AVENTIS PHARMA DEUT GMBH.
 XX
 PI Kontermann R, Nettelbeck D, Sedlacek H, Mueller R;
 XX
 DR WPI; 2000-572272/53.
 DR N-PSDB; AAA98171.
 XX
 XX Cell specific multivalent proteins useful for targeting specific cells
 PT for the treatment of disease.
 PT
 XX
 PS Example 2; Page 63-64; 81pp; German.
 XX
 CC This invention describes a method for the production of a novel cell
 CC specific multivalent protein (MVP). The invention also describes (1) a
 CC nucleic acid construct, which encodes an MVP; (2) a bacterium, yeast or
 CC mammalian cell, in which the nucleic acid construct of (1) is introduced;
 CC (3) the MVP bound to a vector; (4) production of an MVP; (5) an MVP
 CC comprising a scFv with a binding site for the adenoviral fibre protein or
 CC CD3 molecule and two VEGF units, bound by a peptide linker; and (6) a
 CC complex comprising at least two MVPs as above (in which each single
 CC ligand can be 0-1). The MVP, optionally bound to a vector, is useful for
 CC production of a remedy to treat cells outside tissue by dressings for
 CC skin, mucus, nervous systems, inner organs, hematopoietic systems, immune
 CC systems, musculature, support tissues or joints and to immunize to

CC prevent or treat diseases
XX
SQ Sequence 21 AA;

Query Match 56.4%; Score 75; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QHNKCECRPKKD 23
Db 1 QHNKCECRPKKD 12

RESULT 4

AA010860
ID AAB10860 standard; protein; 21 AA.

XX
AC AAB10860;

XX 02-FEB-2001 (first entry)

XX ScVEGF2 construct protein fragment SEQ ID NO: 29.

XX MVP; multivalent protein; treatment; dressing; skin; mucus; musculature;
XX nervous system; inner organ; hematopoietic system; immune system; joint;
XX support tissue; immunization.

XX Synthetic.

XX Homo sapiens.

XX WO200063790-A1.

XX 14-SEP-2000.

XX 26-FEB-2000; 2000WO-EP001612.

XX 10-MAR-1999; 99DE-01010419.

XX (AVET) AVENTIS PHARMA DEUT GMBH.

XX Kontermann R, Nettelbeck D, Sedlacek H, Mueller R;

XX WPI; 2000-572272/53.

XX N-PSDB; AAA98168.

XX Cell specific multivalent proteins useful for targeting specific cells
PT for the treatment of disease.

XX Example 1; Page 58; 81pp; German.

XX This invention describes a method for the production of a novel cell
CC specific multivalent protein (MVP). The invention also describes (1) a
CC nucleic acid construct, which encodes an MVP; (2) a bacterium, yeast or
CC mammalian cell, in which the nucleic acid construct of (1) is introduced;
CC (3) the MVP bound to a vector; (4) production of an MVP; (5) an MVP
CC comprising a scfv with a binding site for the adenoviral fibre protein or
CC CD3 molecule and two VEBF units, bound by a peptide linker; and (6) a
CC complex comprising at least two MVPs as above (in which each single
CC ligand can be 0-1). The MVP, optionally bound to a vector, is useful for
CC production of a remedy to treat cells outside tissue by dressings for
CC skin, mucus, nervous systems, inner organs, hematopoietic systems, immune
CC systems, musculature, support tissues or joints and to immunize to
CC prevent or treat diseases

XX Sequence 21 AA;

Query Match 56.4%; Score 75; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QHNKCECRPKKD 23
Db 1 QHNKCECRPKKD 12

RESULT 5

AAW23802
ID AAW23802 standard; peptide; 12 AA.

XX
AC AAW23802;

XX 12-SEP-1997 (first entry)

XX VEGF/VPF antigen sequence SFLQHNKCECRP.

XX Vascular endothelial cell growth factor; VEGF; VPF; antigen;
XX vascular permeability factor; anti-VEGF; monoclonal antibody; cancer.

XX Homo sapiens.

XX JP09124697-A.

XX 13-MAY-1997.

XX 01-NOV-1995; 95JP-00308184.

XX 01-NOV-1995; 95JP-00308184.

XX (TOAG) TOA GOSEI CHEM IND LTD.

XX WPI; 1997-316574/29.

XX Human vascular endothelial cell growth factor-vascular permeability
PT factor antigen - and monoclonal antibody against it, useful for diagnosis
PT and treatment of cancer.

XX Claim 1; Page 6; 8pp; Japanese.

XX A total of 67 overlapping peptides, each of 12 amino acids in length,
CC were synthesised to cover the 121 amino acid sequence of human vascular
CC endothelial cell growth factor/vascular permeability factor (VEGF/VPF).
CC Five of the peptides reacted with an anti-VPF monoclonal antibody. Three
CC of these antigenic peptides all included the sequence Lys-Pro-Ser-Cys-Val
CC -Pro-Leu-Met-Arg (AAW23801). The other two 12mers had the sequences Ser-
CC -Pro-Leu-Gln-His-Asn-Lys-Lys-Cys-Glu-Cys-Arg-Pro (AAW23802) and Lys-Cys-Glu-
CC Cys-Arg-Pro-Lys-Lys-Asp-Arg-Ala-Arg (AAW23803). The antigenic peptides
CC are claimed and are useful as diagnostic and therapeutic agents for
CC diseases such as cancer

XX Sequence 12 AA;

Query Match 54.9%; Score 73; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SFLQHNKCECRP 20

Db 1 SFLQHNKCECRP 12

RESULT 6

AAW53383
ID AAW53383 standard; peptide; 12 AA.

XX
AC AAW53383;

XX 06-JUL-1998 (first entry)

XX Tumour metastasis inhibitor peptide 2.

XX Tumour metastasis inhibitor; human; VEGF; metastasis therapy;
XX vascular endothelial cell growth factor; monoclonal antibody.

XX Synthetic.

XX Homo sapiens.

XX

PN JPI0087509-A.
XX
PD 07-APR-1998.
XX
PF 23-JUN-1997; 97JP-00181769.
XX
PR 15-JUL-1996; 96JP-00202765.
XX
PA (TOAG) TOA GOSEI CHEM IND LTD.
XX
DR WPI; 1998-267032/24.
XX
PT Tumour metastasis inhibitor - consists of vascular endothelial cell
PT growth factor inhibitor.
XX
PS Claim 4; Page 2; 12pp; Japanese.
XX
CC The present sequence represents a tumour metastasis inhibitor peptide
CC from the present invention. The present invention describes a tumour
CC metastasis inhibitor consisting of vascular endothelial cell growth
CC factor (VEGF) inhibitor. In an example, anti-vascular endothelial cell
CC growth factor polyclonal antibody was produced, and an antibody-
CC producing cell was prepared. A myeloma cell was prepared and cell fusion
CC was carried out. The hybridoma was selected and cultured. The monoclonal
CC antibody was collected and purified. The reaction site of the monoclonal
CC antibody was identified. A peptide corresponding to part of the amino
CC acid sequence of vascular endothelial cell growth factor was prepared. A
CC peptide reacting with the monoclonal antibody was identified. The
CC monoclonal antibody was used as a tumour metastasis inhibitor. The drug
CC can be effectively applied in metastasis therapy
XX
SQ Sequence 12 AA;
XX
Query Match 54.9%; Score 73; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 LQHNKCECRPKK 22
DB 1 LQHNKCECRPKK 12
XX
RESULT 8
AAW74627
ID AAW74627 standard; peptide; 12 AA.
XX
AC AAW74627;
XX
DT 21-DEC-1998 (first entry)
XX
DE Amino acid sequence of the VEGF/VPF peptide 2.
XX
KW Vascular endothelial growth factor; VEGF; vascular permeability factor;
KW VPF; inhibition; malignant tumour; benign tumour; liver cirrhosis;
XX inflammation of peritoneum.
XX
OS Homo sapiens.
XX
PN JPI0245347-A.
XX
PD 14-SEP-1998.
XX
PF 28-FEB-1997; 97JP-00062443.
XX
PR 28-FEB-1997; 97JP-00062443.
XX
PA (TOAG) TOA GOSEI CHEM IND LTD.
XX
DR WPI; 1998-551156/47.
XX
PT An inhibitory agent for the re-retention of body fluid - useful for
PT treating this side-effect of associated disease states.
XX
PS Claim 3; Page 2; 8pp; Japanese.
XX
CC Amino acid sequence of a vascular endothelial growth factor/vascular
CC permeability factor (VEGF/VPF) peptide used in the method of the
CC invention as an inhibitory agent. The inhibitory agent is used for the
CC treatment of retention of body fluid during disease states, e.g.
CC malignant and benign tumours, inflammation of peritoneum, ascites, and
CC liver cirrhosis
XX
SQ Sequence 12 AA;
XX
Query Match 54.9%; Score 73; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 SFLOHNKCECRP 20
DB 1 SFLOHNKCECRP 12
XX
RESULT 7
AAW53444
ID AAW53444 standard; peptide; 12 AA.
XX
AC AAW53444;
XX
DT 06-JUL-1998 (first entry)
XX
DE Vascular endothelial cell growth factor peptide 61.
XX
KW Tumour metastasis inhibitor; human; VEGF; metastasis therapy;
KW vascular endothelial cell growth factor; monoclonal antibody.
XX
OS Homo sapiens.
XX
PN JPI0087509-A.
XX
PD 07-APR-1998.
XX
PF 23-JUN-1997; 97JP-00181769.
XX
PR 15-JUL-1996; 96JP-00202765.
XX
PA (TOAG) TOA GOSEI CHEM IND LTD.
XX
DR WPI; 1998-267032/24.
XX
PT Tumour metastasis inhibitor - consists of vascular endothelial cell
PT growth factor inhibitor.
XX
PS Disclosure; Page 6; 12pp; Japanese.

XX The present sequence represents a vascular endothelial cell growth factor
CC peptide from the present invention. The present invention describes a
CC tumour metastasis inhibitor consisting of vascular endothelial cell
CC growth factor (VEGF) inhibitor. In an example, anti-vascular endothelial
CC cell growth factor polyclonal antibody was produced, and an antibody-
CC producing cell was prepared. A myeloma cell was prepared and cell fusion
CC was carried out. The hybridoma was selected and cultured. The monoclonal
CC antibody was collected and purified. The reaction site of the monoclonal
CC antibody was identified. A peptide corresponding to part of the amino
CC acid sequence of vascular endothelial cell growth factor was prepared. A
CC peptide reacting with the monoclonal antibody was identified. The
CC monoclonal antibody was used as a tumour metastasis inhibitor. The drug
CC can be effectively applied in metastasis therapy
XX
SQ Sequence 12 AA;
XX
Query Match 54.9%; Score 73; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 LQHNKCECRPKK 22
DB 1 LQHNKCECRPKK 12
XX
RESULT 8
AAW74627
ID AAW74627 standard; peptide; 12 AA.
XX
AC AAW74627;
XX
DT 21-DEC-1998 (first entry)
XX
DE Amino acid sequence of the VEGF/VPF peptide 2.
XX
KW Vascular endothelial growth factor; VEGF; vascular permeability factor;
KW VPF; inhibition; malignant tumour; benign tumour; liver cirrhosis;
XX inflammation of peritoneum.
XX
OS Homo sapiens.
XX
PN JPI0245347-A.
XX
PD 14-SEP-1998.
XX
PF 28-FEB-1997; 97JP-00062443.
XX
PR 28-FEB-1997; 97JP-00062443.
XX
PA (TOAG) TOA GOSEI CHEM IND LTD.
XX
DR WPI; 1998-551156/47.
XX
PT An inhibitory agent for the re-retention of body fluid - useful for
PT treating this side-effect of associated disease states.
XX
PS Claim 3; Page 2; 8pp; Japanese.
XX
CC Amino acid sequence of a vascular endothelial growth factor/vascular
CC permeability factor (VEGF/VPF) peptide used in the method of the
CC invention as an inhibitory agent. The inhibitory agent is used for the
CC treatment of retention of body fluid during disease states, e.g.
CC malignant and benign tumours, inflammation of peritoneum, ascites, and
CC liver cirrhosis
XX
SQ Sequence 12 AA;
XX
Query Match 54.9%; Score 73; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 SFLOHNKCECRP 20


```

Db      1 SFLOHNKCECRP 12
|||||
RESULT 9
AAW74688
ID AAW74688 standard; peptide; 12 AA.
XX
XX
AC AAW74688;
XX
XX 21-DEC-1998 (first entry)
XX
XX Amino acid sequence of the VEGF/VPF peptide 63.
XX
XX Vascular endothelial growth factor; VEGF; vascular permeability factor;
XX VPF; inhibition; malignant tumour; benign tumour; liver cirrhosis;
XX inflammation of peritoneum.
XX
XX Homo sapiens.
XX
XX JP10245347-A.
XX
XX 14-SEP-1998.
XX
XX 28-FEB-1997; 97JP-00062443.
XX
XX 28-FEB-1997; 97JP-00062443.
XX
XX (TOAG ) TOA GOSEI CHEM IND LTD.
XX
XX WPI; 1998-551156/47.
XX
XX An inhibitory agent for the re-retention of body fluid - useful for
XX treating this side-effect of associated disease states.
XX
XX Example 3; Page 5; 8pp; Japanese.
XX
XX Amino acid sequence of a vascular endothelial growth factor/vascular
XX permeability factor (VEGF/VPF) peptide used in the method of the
XX invention as an inhibitory agent. The inhibitory agent is used for the
XX treatment of retention of body fluid during disease states, e.g.
XX malignant and benign tumours, inflammation of peritoneum, ascites, and
XX liver cirrhosis
XX
XX Sequence 12 AA;
XX
XX Query Match 54.9%; Score 73; DB 2; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 0.00015;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 11 LOHNKCECRPKK 22
Db 1 LOHNKCECRPKK 12
|||||
RESULT 10
AAW5950
ID AAW5950 standard; peptide; 12 AA.
XX
XX AAW5950;
XX
XX 22-JUL-1998 (first entry)
XX
XX Human vascular permeability factor peptide 61.
XX
XX Human; vascular permeability factor; VPF; mitomycin; cisplatin;
XX vascular endothelial growth factor; VEGF; carcinostatic; anti-tumour;
XX monoclonal antibody; MAB; MV 833.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX JP09301888-A.
XX
XX Query Match 54.9%; Score 73; DB 2; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 0.00015;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 11 LOHNKCECRPKK 22
Db 1 LOHNKCECRPKK 12
|||||
RESULT 11
AAW5949
ID AAW5949 standard; peptide; 12 AA.
XX
XX AAW5949;
XX
XX 22-JUL-1998 (first entry)
XX
XX Human vascular permeability factor peptide 60.
XX
XX Human; vascular permeability factor; VPF; mitomycin; cisplatin;
XX vascular endothelial growth factor; VEGF; carcinostatic; anti-tumour;
XX monoclonal antibody; MAB; MV 833.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX JP09301888-A.
XX
XX 25-NOV-1997.
XX
XX 14-MAY-1996; 96JP-00143621.
XX
XX 14-MAY-1996; 96JP-00143621.
XX
XX (TOAG ) TOA GOSEI CHEM IND LTD.
XX
XX WPI; 1998-059107/06.
XX
XX Carcinostatic comprises anti-vascular endothelial growth factor antibody
XX - and mitomycin or cisplatin.
XX
XX Example; Page 4; 7pp; Japanese.
XX
XX The present sequence represents a peptide fragment from human vascular
XX permeability factor (VPF), which is used in the example of the present
XX invention to produce a monoclonal antibody against human VPF. The
XX monoclonal antibody produced was designated MV 833. The monoclonal
XX antibody was used in a novel carcinostatic of the present invention,
XX comprising an anti-vascular endothelial growth factor (VEGF)/VPF antibody
XX (Ab), and mitomycin or cisplatin. The carcinostatic improves the effect
XX of the known anti-tumour agents
XX
XX Sequence 12 AA;
XX
XX Query Match 54.9%; Score 73; DB 2; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 0.00015;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 11 LOHNKCECRPKK 22
Db 1 LOHNKCECRPKK 12
|||||
RESULT 12
AAW5949
ID AAW5949 standard; peptide; 12 AA.
XX
XX AAW5949;
XX
XX 22-JUL-1998 (first entry)
XX
XX Human vascular permeability factor peptide 60.
XX
XX Human; vascular permeability factor; VPF; mitomycin; cisplatin;
XX vascular endothelial growth factor; VEGF; carcinostatic; anti-tumour;
XX monoclonal antibody; MAB; MV 833.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX JP09301888-A.
XX
XX 25-NOV-1997.
XX
XX 14-MAY-1996; 96JP-00143621.
XX
XX 14-MAY-1996; 96JP-00143621.
XX
XX (TOAG ) TOA GOSEI CHEM IND LTD.
XX
XX WPI; 1998-059107/06.
XX
XX Carcinostatic comprises anti-vascular endothelial growth factor antibody
XX - and mitomycin or cisplatin.
XX
XX Example; Page 4; 7pp; Japanese.
XX
XX The present sequence represents a peptide fragment from human vascular
XX permeability factor (VPF), which is used in the example of the present
XX invention to produce a monoclonal antibody against human VPF. The

```

CC monoclonal antibody produced was designated MV 833. The monoclonal
CC antibody was used in a novel carcinostatic of the present invention,
CC comprising an anti-vascular endothelial growth factor (VEGF)/VPF antibody
CC (Ab), and mitomycin or cisplatin. The carcinostatic improves the effect
CC of the known anti-tumour agents
XX
XX Sequence 12 AA;

Query Match 54.9%; Score 73; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SFLQHNKCECRP 20
|||
Db 1 SFLQHNKCECRP 12

RESULT 12

AAW97382
ID AAW97382 standard; peptide; 12 AA.

XX AC AAW97382;

XX DT 14-MAY-1999 (first entry)

XX DE A VEGF/VPF antagonist used in an anticancer agent.

XX KW Antagonist; vascular endothelial growth factor; VEGF;
KW vascular permeability factor; VPF; anticancer agent; growth inhibition;
KW tumour.

XX OS Synthetic.

XX PN JP11049701-A.

XX PD 23-FEB-1999.

XX PF 04-AUG-1997; 97JP-00223063.

XX PR 04-AUG-1997; 97JP-00223063.

XX PA (TOAG) TOA GOSEI CHEM IND LTD.

XX PA (IATR) IATRON LAB INC.

XX DR WPI; 1999-210773/18.

XX PT New anticancer agent - comprises VEGFF/VPF and bFGF antagonists.

XX PS Claim 3; Page 2; 12pp; Japanese.

XX CC AAW97381-82 represent antagonist of vascular endothelial growth factor
CC (VEGF)/vascular permeability factor (VPF). The peptides are used in an
CC anticancer agent, which is used to inhibit growth of a tumour
XX

XX SQ Sequence 12 AA;

Query Match 54.9%; Score 73; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SFLQHNKCECRP 20
|||
Db 1 SFLQHNKCECRP 12

RESULT 13

AAW57613
ID AAW57613 standard; peptide; 12 AA.

XX AC AAW57613;

XX DT 08-MAR-2000 (first entry)

DE Human VEGF/VPF peptide SEQ ID NO:2.

XX Human; vascular endothelial cell growth factor; VEGF; VPF; VEGF-121;
KW vasopermeability factor; tumour; monoclonal antibody; chemotherapy;
KW cancer; angiogenesis; cytostatic; tumourigenesis; inhibition;
KW proliferation; suppression; antitumour.

XX OS Homo sapiens.

XX PN JP11310537-A.

XX PD 09-NOV-1999.

XX PF 27-APR-1998; 98JP-00134665.

XX PR 27-APR-1998; 98JP-00134665.

XX PA (TOAG) TOA GOSEI CHEM IND LTD.

XX DR WPI; 2000-057134/05.

XX KW Thermotherapy for treatment of various cancers - involves destroying the
KW tumor site by hot temperature and inhibiting angiogenesis effect by
KW VEGF/VPF antagonist.

XX PS Claim 3; Page 2; 8pp; Japanese.

XX CC A thermotherapy method has been developed which involves destroying the
CC tumour site by hot temperature and administering vascular endothelial
CC cell growth factor (VEGF)/ vasopermeability factor (VPF) antagonist. The
CC method is useful for the treatment of various cancers. The VEGF/VPF
CC antagonist has cytostatic activity and is a tumourigenesis inhibitor.
CC Proliferation of the tumour is suppressed effectively. AAY57612 to
CC AAY57614 represent specifically claimed human VEGF/VPF peptides. AAY57615
CC to AAY57679 represent human VEGF-121 peptides used in the exemplification
CC of the present invention
XX

XX SQ Sequence 12 AA;

Query Match 54.9%; Score 73; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SFLQHNKCECRP 20
|||
Db 1 SFLQHNKCECRP 12

RESULT 14

AAW57674
ID AAY57674 standard; peptide; 12 AA.

XX AC AAY57674;

XX DT 08-MAR-2000 (first entry)

XX DE Human vascular endothelial cell growth factor 121 peptide #60.

XX KW Human; vascular endothelial cell growth factor; VEGF; VPF; VEGF-121;
KW vasopermeability factor; tumour; monoclonal antibody; chemotherapy;
KW cancer; angiogenesis; cytostatic; tumourigenesis; inhibition;
KW proliferation; suppression; antitumour.

XX OS Homo sapiens.

XX PN JP11310537-A.

XX PD 09-NOV-1999.

XX PF 27-APR-1998; 98JP-00134665.

XX PR 27-APR-1998; 98JP-00134665.

PA (TOAG) TOA GOSEI CHEM IND LTD.
 XX WPI; 2000-057134/05.
 XX
 PT Thermoherapy for treatment of various cancers - involves destroying the
 PT tumor site by hot temperature and inhibiting angiogenesis effect by
 PT VEGF/VPF antagonist.
 XX
 PS Disclosure; Page 6; 8pp; Japanese.
 CC
 CC A thermoherapy method has been developed which involves destroying the
 CC tumour site by hot temperature and administering vascular endothelial
 CC cell growth factor (VEGF)/ vasopermeability factor (VPF) antagonist. The
 CC method is useful for the treatment of various cancers. The VEGF/VPF
 CC antagonist has cytostatic activity and is a tumourigenesis inhibitor.
 CC Proliferation of the tumour is suppressed effectively. AAY57612 to
 CC AAY57614 represent specifically claimed human VEGF/VPF peptides. AAY57615
 CC to AAY57679 represent human VEGF-121 peptides used in the exemplification
 CC of the present invention
 XX
 SQ Sequence 12 AA;

Query Match 54.9%; Score 73; DB 3; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 LQHNKCECRPKK 22
 DB 1 LQHNKCECRPKK 12

RESULT 15
 AAY59616
 ID AAY59616 standard; peptide; 12 AA.
 AC AAY59616;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Vascular endothelial cell growth factor peptide 61.
 XX
 KW Vascular endothelial cell growth factor; vessel permeability factor; VPF;
 KW angiogenesis inhibitor; minocycline; tumour; diabetic retinopathy;
 KW intraocular angioenic disease; aging muscular degeneration; psoriasis;
 KW rheumatoid arthritis; Kaposi's sarcoma; cancer; arteriosclerosis; VEGF.
 XX
 OS Homo sapiens.
 XX
 XX JP11302193-A.
 XX
 PD 02-NOV-1999.
 XX
 PF 22-APR-1998; 98JP-00129646.
 XX
 PR 22-APR-1998; 98JP-00129646.
 XX
 PA (TOAG) TOA GOSEI CHEM IND LTD.
 XX
 XX WPI; 2000-065707/06.
 XX
 PT Angiogenesis inhibitor for treating tumors and cancers - contains
 PT vascular endothelial cell growth factor or vessel permeability factor
 PT antagonist and minocycline as active ingredient.
 XX
 PS Example 1; Page 6; 8pp; Japanese.
 XX
 CC This sequence is a fragment of human vascular endothelial cell growth
 CC factor (VEGF)/vessel permeability factor (VPF). The peptide is used to
 CC identify the site at which an anti-VEGF antibody binds to VEGF. The
 CC antibody is used in the method of the invention, which relates to the use
 CC of an angiogenesis inhibitor. The inhibitor contains a VEGF antagonist
 CC (preferably the anti-VEGF antibody) and minocycline. The angiogenesis
 CC inhibitor can be used as a therapeutic agent against tumours. The

CC inhibitor can also be used as a therapeutic agent against, intraocular
 CC angioenic diseases such as diabetic retinopathy and aging muscular
 CC degeneration. Diseases such as rheumatoid arthritis, psoriasis, Kaposi's
 CC sarcoma, and arteriosclerosis, can also be treated using the angiogenesis
 CC inhibitor
 XX
 SQ Sequence 12 AA;

Query Match 54.9%; Score 73; DB 3; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 LQHNKCECRPKK 22
 DB 1 LQHNKCECRPKK 12

Search completed: March 8, 2004, 11:46:25
 Job time : 53 secs

US-09-795-006A-136
; Sequence 136, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 136
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-795-006A-136

Query Match 59.4%; Score 79; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LOHNKCECRPKD 23
Db 1 LOHNKCECRPKD 13

RESULT 3
US-09-795-006A-135
; Sequence 135, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 135
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-795-006A-135

Query Match 40.6%; Score 54; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQHIGEMSF 10
Db 5 QQHIGEMSF 14

RESULT 4
US-10-216-484-36
; Sequence 36, Application US/10216484
; Publication No. US20030103976A1

; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 36
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-484-36

Query Match 28.6%; Score 38; DB 14; Length 20;
Best Local Similarity 55.6%; Pred. No. 66;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 12 QHNKCECRP 20
Db 8 QNTKCRCKP 16

RESULT 5
US-10-384-933-36
; Sequence 36, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 36
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-384-933-36

Query Match 28.6%; Score 38; DB 14; Length 20;
Best Local Similarity 55.6%; Pred. No. 66;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 12 QHNKCECRP 20
Db 8 QNTKCRCKP 16

RESULT 6
US-10-313-986-546
; Sequence 546, Application US/10313986
; Publication No. US20030236209A1
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.

; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 546
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-546

Query Match 25.6%; Score 34; DB 15; Length 20;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QGOHIGEMS 9
Db 5 QGOHINQUS 13

RESULT 7

US-09-795-006A-145
; Sequence 145, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/3597B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 145
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
US-09-795-006A-145

Query Match 24.8%; Score 33; DB 9; Length 13;
Best Local Similarity 45.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 13 HNKCECRPKD 23
Db 3 HTSCRCMSKLD 13

RESULT 8

US-10-216-484-44
; Sequence 44, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Hanyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Pas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662

; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 44
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-484-44

Query Match 24.1%; Score 32; DB 14; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 15 KCECRP 20
Db 1 KCRCKP 6

RESULT 9

US-10-384-933-44
; Sequence 44, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817A1ufusa
; APPLICANT: Hanyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Pas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 44
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-384-933-44

Query Match 24.1%; Score 32; DB 14; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 15 KCECRP 20
Db 1 KCRCKP 6

RESULT 10

US-10-215-759-2
; Sequence 2, Application US/10215759
; Publication No. US20030059430A1
; GENERAL INFORMATION:
; APPLICANT: Mascarenhas, Desmond
; TITLE OF INVENTION: IGF-BINDING PROTEIN-DERIVED PEPTIDE OR
; FILE REFERENCE: 51490200200
; CURRENT APPLICATION NUMBER: US/10/215,759
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/323,267
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

us-09-761-636a-4.closed.rapb

Mon Mar 8 13:10:53 2004

```
;
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(20)
; FEATURE:
; NAME/KEY: METAL
; LOCATION: (8)...(19)
; US-10-264-672-2

Query Match      24.1%; Score 32; DB 14; Length 20;
Best Local Similarity 50.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      13 HNKCECRPKK 22
       : | : | | |
Db      3 YKKQCRPSK 12

RESULT 11
US-10-216-484-37
; Sequence 37, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 37
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-216-484-37

Query Match      24.1%; Score 32; DB 14; Length 20;
Best Local Similarity 66.7%; Pred. No. 5.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      15 KCECRP 20
       : | : |
Db      1 KCRCKP 6

RESULT 12
US-10-264-672-2
; Sequence 2, Application US/10264672
; Publication No. US20030161829A1
; GENERAL INFORMATION:
; APPLICANT: MASCARENHAS, Desmond
; TITLE OF INVENTION: IGF-BINDING PROTEIN-DERIVED PEPTIDE OR
; SMALL MOLECULE
; FILE REFERENCE: 514902000200
; CURRENT APPLICATION NUMBER: US/10/264,672
; CURRENT FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US 10/215,759
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/323,267
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(20)
; FEATURE:
; NAME/KEY: METAL
; LOCATION: (8)...(19)
; US-10-264-672-2

Query Match      24.1%; Score 32; DB 14; Length 20;
Best Local Similarity 50.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      13 HNKCECRPKK 22
       : | : | | |
Db      3 YKKQCRPSK 12

RESULT 13
US-10-384-933-37
; Sequence 37, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 37
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-384-933-37

Query Match      24.1%; Score 32; DB 14; Length 20;
Best Local Similarity 66.7%; Pred. No. 5.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      15 KCECRP 20
       : | : |
Db      1 KCRCKP 6

RESULT 14
US-10-215-759-7
; Sequence 7, Application US/10215759
; Publication No. US20030059430A1
; GENERAL INFORMATION:
; APPLICANT: MASCARENHAS, Desmond
; TITLE OF INVENTION: IGF-BINDING PROTEIN-DERIVED PEPTIDE OR
; SMALL MOLECULE
; FILE REFERENCE: 514902000200
; CURRENT APPLICATION NUMBER: US/10/215,759
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/323,267
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/323,267
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

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```

; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(22)
; OTHER INFORMATION: Capable of directing cellular internalization of
; OTHER INFORMATION: unrelated proteins.
; FEATURE:
; NAME/KEY: METAL
; LOCATION: (10)...(21)
; OTHER INFORMATION: Selectively binds zinc and nickel
; US-10-215-759-7

```

```

Query Match      24.1%; Score 32; DB 14; Length 22;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 13 HNKCECRPK 22
   :|:|:|:|
Db 5 YKKQCRPSK 14

```

```

RESULT 15
US-10-264-672-7
; Sequence 7, Application US/10264672
; Publication No. US20030161829A1
; GENERAL INFORMATION:
; APPLICANT: MASCARENHAS, Desmond
; TITLE OF INVENTION: IGF-BINDING PROTEIN-DERIVED PEPTIDE OR
; FILE REFERENCE: 514902000220
; CURRENT APPLICATION NUMBER: US/10/264,672
; CURRENT FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US 10/215,759
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/323,267
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(22)
; OTHER INFORMATION: Capable of directing cellular internalization of
; OTHER INFORMATION: unrelated proteins.
; FEATURE:
; NAME/KEY: METAL
; LOCATION: (10)...(21)
; OTHER INFORMATION: Selectively binds zinc and nickel
; US-10-264-672-7

```

```

Query Match      24.1%; Score 32; DB 14; Length 22;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 13 HNKCECRPK 22
   :|:|:|:|
Db 5 YKKQCRPSK 14

```

Search completed: March 8, 2004, 11:53:02
Job time : 33 secs